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ASAS WESTERN SECTION GRADUATE STUDENT PAPER COMPETITION

0001 Effects of maternal nutritional status on nutrient transporter expression in bovine utero-placental tissue on days 16 to 50 of gestation. M. S. Crouse*[1], K. J. McLean[1], M. R. Crosswhite[2], N. Negrin Pereira[1], A. K. Ward[1], L. P. Reynolds[1], C. R. Dahlen[1], B. W. Neville[3], P. P. Borowicz[1], and J. S. Caton[1], *[1]Department of Animal Sciences, North Dakota State University, Fargo, [2]North Dakota State University, Fargo, [3]North Dakota State University, Streeter.*

We hypothesized that maternal nutrition and day of gestation would impact mRNA expression of nutrient transporters *GLUT1*, *CAT-1*, *CAT-2*, and *CAT-3* in beef heifers. Crossbred Angus heifers (n = 49) were synchronized, bred via AI, assigned to nutritional treatment (CON = 100% of requirements for 0.45 kg/d gain and RES = 60% of CON) and ovariohysterectomized on d 16, 34, or 50 of gestation (n = 6 to 9/d); nonpregnant (NP) controls were not bred and ovariohysterectomized on d 16 of the synchronized estrous cycle (n = 6). The resulting arrangement of treatments was a 2 × 3 factorial + 1. Caruncle (CAR), intercaruncular endometrium (ICAR), and fetal membranes (FM), were obtained from the pregnant uterine horn immediately following ovariohysterectomy. For NP controls, only CAR and ICAR were obtained. Relative expression of the glucose transporter *GLUT1* and cationic amino acid transporters *CAT-1*, *CAT-2*, and *CAT-3* was determined for each tissue utilizing NP-CAR and NP-ICAR tissue as the baseline. For FM, NP endometrium served as the baseline. There was no interaction of day and treatment in FM for any genes ($P \geq 0.05$). Expression of *GLUT1* and *CAT-1* both showed a day effect, being greater ($P < 0.05$) in FM on d 34 and 50, compared with d 16. In CAR there was no day × treatment interaction and *CAT-3* expression tended ($P = 0.06$) to be greater in CON vs. RES heifers. Additionally, expression of *GLUT1*, *CAT-1*, and *CAT-2* in CAR were greater ($P < 0.01$) on d 16 compared with d 34 and 50, d 34 compared with d 50, and d 16 and 34 compared with d 50, respectively. In ICAR, *CAT-2* showed a day × treatment interaction, being greater ($P = 0.01$) on d 50 CON compared with all other groups. Transporter *CAT-3* tended ($P = 0.09$) to be greater in day × treatment in ICAR on d 16 CON compared with all other days and treatments. The expression of *GLUT1* was greater ($P < 0.01$) in ICAR on d 16 than all other days. Arginine transporter *CAT-1* was greater ($P < 0.01$) in ICAR on d 34 and 50 compared with d 16. These results partially support our hypothesis and indicate that day was a more influential factor for mRNA expression of utero-placental glucose and cationic amino acid transporters than maternal nutritional status in heifers during early pregnancy.

Key Words: arginine, gestation, glucose, maternal nutrition, transporters

0002 Effects of dried distiller's grains and lasalocid on feedlot lamb growth, carcass traits, nutrient digestibility, ruminal fluid volatile fatty acid concentrations, and ruminal hydrogen sulfide concentration. A. R. Crane*[1,2], R. R. Redden[3], K. C. Swanson[2], B. M. Howard[2], T. J. Frick[2], K. R. Maddock-Carlin[4], and C. S. Schauer[1], *[1]Hettinger Research Extension Center, Hettinger, ND, [2]Department of Animal Sciences, North Dakota State University, Fargo, [3]Texas A&M AgriLife Research and Extension Center, San Angelo, TX, [4]North Dakota State University, Fargo.*

Our hypothesis was increasing the inclusion level of dried distiller's grains with solubles (DDG) to feedlot lambs would increase growth, while the inclusion of lasalocid (LAS; Bovatec, Alpharma, LLC, Bridgewater, NJ) would increase ADG and G:F while not affecting digestibility, ruminal VFA concentration, and pH in the rumen fluid. Furthermore, we hypothesized that rations including LAS and higher levels of DDG would cause increased ruminal hydrogen sulfide gas (H_2S) concentrations. To test this hypothesis, 240 crossbred (Suffolk × Rambouillet) lambs (31.9 ± 5.87 kg BW; approximately 90 d of age) were allocated to six treatments in a completely random design with a 3 × 2 factorial arrangement of treatments. Lambs were placed into 24 feedlot pens (four pens/treatment; 10 lambs/pen) for a 111-d finishing study. Main effects included concentration of DDG (0, 15, or 30% DM basis) and inclusion of LAS (0 or 20 g/t LAS) resulting in treatments of (1) 0% DDG without LAS (0DDG-NL), (2) 0% DDG with LAS (0DDG-L), (3) 15% DDG without LAS (15DDG-NL), (4) 15% DDG with LAS (15DDG-L), (5) 30% DDG without LAS (30DDG-NL), and (6) 30% DDG with LAS (30DDG-L). Two-day weights were taken at the beginning and end of the trial. Two hundred and eighteen lambs (63.7 ± 8.78 kg) were harvested on d 112 at a commercial abattoir and carcass data collected after a 24 h chill. The inclusion of LAS increased ($P \leq 0.02$) final BW, ADG, G:F, and HCW. As DDG in the ration increased to 30%, DMI decreased linearly ($P = 0.03$) while G:F increased linearly ($P = 0.03$). A second study was conducted utilizing the same treatments to evaluate N and S balance, ruminal VFA and H_2S concentration, and ruminal pH in 24 crossbred wethers (Suffolk × Rambouillet; 41.2 ± 12.23 kg BW). Daily urinary sulfur excretion and H_2S production were linearly increased ($P < 0.001$) as DDG increased in the ration. Total ruminal VFA concentration linearly decreased ($P = 0.002$) as DDG increased in the ration. The inclusion of LAS increased ($P = 0.02$) ruminal pH. The results confirm our hypothesis that LAS increased overall growth and increasing DDG increased ruminal H_2S concentration, however, DDG

inclusion did not increase growth. Additionally, we reject the hypothesis that the combined effects of LAS and DDG would have no effect on rumen pH and VFA concentrations.

Key Words: dried distiller's grains with solubles, ionophores, lambs

0003 Impacts of stocking density on growth and puberty attainment of replacement beef heifers. K. M. Schubach[*1], R. F. Cooke[1], A. P. Brandao[1,2], K. Lippolis[1], R. Marques[1], M. T. Hinchliff[1], D. W. Bohnert[1], *[1]Oregon State University- EOARC Burns, Burns, OR, [2]UNESP-FMVZ, Botucatu, Brazil.*

Sixty Angus × Hereford heifers were ranked by age and BW (210 ± 2 d and 220 ± 2 kg, respectively) on d 0, and assigned to: (A) 1 of 3 drylot pens (10 × 14 m pens; 10 heifers/pen) resulting in a stocking density of 14 m^2/heifer (HIDENS), or (B) 1 of 3 pastures (1-ha pastures; 10 heifers/pasture), resulting in a stocking density of 1000 m^2/heifer (LOWDENS). Before the beginning of the experiment, pastures were harvested for hay, leaving no forage available for grazing for LOWDENS heifers. All heifers received the same diet consisting of (as-fed basis) 5 kg alfalfa hay and 3.5 kg of corn per heifer/d. On d 0, heifers were fitted with a pedometer (HJ-321; Omron Healthcare, Inc., Bannockburn, IL). Each week for the duration of the experiment (d 0 to d 161), pedometer results were recorded, heifer BW was measured, and blood samples were collected. Heifer shrunk BW (after 16 h of water and feed deprivation) was also collected on d –5 and 162 of the experiment. Puberty onset was determined according to plasma progesterone concentration. Heifers were considered pubertal when plasma progesterone concentration was >1.0 ng/mL for two consecutive weeks. A treatment × day interaction was detected ($P < 0.01$) for BW, considering HIDENS heifers were, on average, 10 ± 4 kg heavier than LOWDENS heifers beginning on d 28. This difference in body weight can be attributed to increased physical activity of LOWDENS heifers, as they exhibited more ($P < 0.01$) steps compared with HIDENS heifers. However, ADG using shrunk BW values did not differ ($P = 0.49$) among treatments. Treatment × day interactions were detected for plasma cortisol ($P < 0.01$) and IGF-1 ($P < 0.01$), given that concentration of these hormones were greater for LOWDENS compared with HIDENS heifers on d 84 ($P < 0.01$) and d 140 ($P \leq 0.04$). A treatment × day interaction was also detected ($P < 0.01$) for puberty attainment, considering a greater proportion of LOWDENS heifers reached puberty compared with HIDENS cohorts during the experiment (54.6 vs. 3.4% of heifers pubertal by d 161, respectively; $P < 0.01$, SEM = 5.3). In conclusion, heifers reared in a low-stocking density exhibited hastened puberty attainment, despite the observed decrease in heifer BW attributed to increased physical activity, compared with heifers reared in high stocking density.

Key Words: beef heifers, growth, puberty, stocking density

0004 Physiologic, health and production responses of dairy cows supplemented with an immunomodulatory feed ingredient during the transition period. A. P. Brandao[*1,2], R. F. Cooke[1], F. N. Correa[3], M. B. Piccolo[2], R. Gennari[4], T. Leiva[2], and J. L. M. Vasconcelos[5], *[1]Oregon State University–EOARC Burns, Burns, [2]UNESP- FMVZ, Botucatu, Brazil, [3]Department of Animal Sciences, University of Florida, Gainesville, [4]UNESP- FMVZ, Botucatu, FL, [5]Sao Paulo State University, Botucatu, Brazil.*

This study compared physiological, health, and productive parameters in dairy cows supplemented or not with Omnigen-AF® (OMN) during the transition period. Thirty-eight nonlactating, multiparous, pregnant Holstein × Gir cows were ranked by BW and BCS, and assigned to receive ($n = 19$) or not (CON; $n = 19$) OMN at 56 g/cow daily (as-fed basis) beginning 35 d before calving. Before calving, cows had ad libitum access to corn silage, and received (as-fed basis) 3 kg/cow daily of concentrate. After calving, cows were milked twice daily, offered (as-fed basis) 35 kg/cow daily of corn silage, and individually received a concentrate formulated to meet their nutritional requirements. Cows received OMN individually as top-dressing into the morning concentrate feeding. Before calving, cow BW and BCS were recorded weekly and blood samples collected every 5 d beginning on d –35 relative to calving. After calving and until 46 d in milk (DIM), BW and BCS were recorded weekly, individual milk production was recorded, and milk samples were collected daily. Blood was sampled daily from 0 to 7 DIM, every other day from 9 to 21 DIM, and every 5 d from 26 to 46 DIM. On 30 and 46 DIM, cows were evaluated for endometritis via cytobrush technique, based on percentage of polymorphonuclear (PMN) cells in 100 total cell count (PMN + endometrial cells). On 48.7 ± 1.6 DIM, nine cows/treatment received a lipopolysaccharide (LPS) injection (0.25 μg/kg of BW), and blood was sampled hourly from –2 to 8 h, at 12-h intervals from 12 to 72 h, and at 24-h intervals form 96 to 120 h relative to LPS administration. No treatment differences were detected on BW, BCS, and serum concentrations of cortisol, NEFA, insulin, glucose, haptoglobin, cortisol, and IGF-I ($P \geq 0.15$). Cows receiving OMN had greater ($P \leq 0.04$) milk yield (30.3 vs. 27.1 kg/d; SEM = 0.9) and percentage of PMN cells in endometrial cell population (12.2 vs. 3.9%; SEM = 2.9) compared with CON cows. After LPS administration, cows receiving OMN had greater ($P \leq 0.04$) mean serum haptoglobin (212 vs. 94 μg/mL; SEM = 38) and serum concentration of tumor necrosis factor α at 1, 2, and 3 h relative to LPS injection compared with CON cows. In conclusion, OMN supplementation during the transition period enhanced innate immunity parameters and increased milk production in dairy cows.

Key Words: inflammation, milk production, Omnigen-AF, transition cows

0005 Bioavailability of supplemental ruminally-protected leucine in sheep. J. G. Castro*, J. B. Alford, K. E. Quinn, F. A. Lopez, S. L. Pillmore, E. J. Scholljegerdes, and C. A. Loest, *New Mexico State University, Las Cruces*.

The objective of this study was to evaluate the effects of rumen-protected L-Leu on plasma branched-chain AA concentrations and rumen fermentation characteristics of lambs. Four ruminally-cannulated wether lambs (34 ± 2.4 kg BW) were used in a 4 × 4 Latin square. Each period consisted of 7 d: 5 d for adaptation, 1 d for collections, and 1 d of rest. Lambs were fed a basal diet (corn grain and alfalfa hay; 0.6 kg/d DM) and supplements (0.1 kg/d DM) containing no added leucine (CON), 6 g/d of unprotected L-Leu (UP-LEU), and 18 g/d ruminally-protected L-Leu (RP-LEU), or postruminally infused with 6 g/d of L-Leu (INF-LEU). Blood and rumen fluid samples were collected on d 6 of each period at 0, 3, 6, and 9 h after feeding. The statistical model included period, sheep, treatment, hour, and treatment × hour. Lambs receiving INF-LEU had plasma Leu concentrations that were greater at 3 and 6 h, but not different at 9 h compared with CON, UP-LEU, and RP-LEU (treatment × h; $P < 0.01$). Plasma Ile concentrations were lower for RP-LEU than CON, UP-LEU, and INF-LEU at 0 h, lower for INF-LEU than CON, UP-LEU, RP-LEU and at 3 h, not different among treatments at 6 h, and lower for RP-LEU and INF-LEU than CON and UP-LEU at 9 h (treatment × h, $P = 0.02$). Rumen fluid acetate (mol/100 mol) tended to be lower for RP-LEU than CON, UP-LEU, and INF-LEU at 0 h, lower for UP-LEU than CON, RP-LEU, and INF-LEU at 3 h, not different among treatments at 6 h, and greater for UP-LEU than CON, RP-LEU, but not INF-LEU, at 9 h (treatment × h, $P < 0.01$). Rumen isovalerate (mol/100 mol) was greatest for RP-LEU, intermediate for UP-LEU, and lowest for INF-LEU and CON ($P < 0.01$). Rumen fluid pH, NH_3, total VFA, and molar proportions of propionate, isobutyrate, butyrate, valerate, and acetate:propionate ratio were not altered by treatments ($P \geq 0.01$). Although supplementation of RP-LEU was unable to elevate plasma Leu concentrations, decreases in plasma Ile concentrations are likely due to the antagonistic effects of postabsorptive L-Leu on plasma Ile concentrations. This data implies that the ruminally-protected Leu was absorbed by the gastrointestinal tract of lambs. Altered rumen fermentation also demonstrated that the ruminally-protected L-Leu source was not entirely protected from rumen microorganisms.

Key Words: leucine, rumen-protected, sheep

0006 Key metabolic pathways associated with differences in weight maintenance and gain in mature cow skeletal and adipose tissue. *H. C. Cunningham*[*1], K. J. Austin[1], K. M. Cammack[1], H. C. Freetly[2], A. K. Lindholm-Perry[2], [1]Department of Animal Science, University of Wyoming, Laramie, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

During the production year of a cow, the majority of nutrients are used to support maintenance. Differences in feedstuff utilization and metabolism can impact the ability of the cow to meet maintenance requirements. Tissue specific metabolism is critical to energy homeostasis of the animal, and therefore, regulation of metabolism is critical to understand. The objective of this research was to determine whether cows that differ in efficiency of weight maintenance and weight gain differ in the relative abundance of transcripts associated with protein and lipid turnover of skeletal muscle and adipose tissue, respectively. Crossbred cows ($n = 121$) were feed restricted for 112 d followed by an ad libitum feeding period for 98 d. Individual feed intake was monitored and body weights were collected to estimate ADG. Adipose and muscle biopsies were collected at d 105 of restricted feeding and at d 49 of ad libitum feeding. Total RNA was extracted from these tissues of the cows with the highest ($n = 6$) and the lowest ($n = 6$) ADG during the ad libitum period. The Affymetrix GeneAtlas microarray system was used to determine relative transcript abundance differences between ADG classes within feeding periods and tissue type. Subsequent analyses using the Database for Annotation, Visualization, and Integrated Discovery (DAVID) and Ingenuity Pathway Analysis (IPA) programs identified key gene clusters and pathways associated with differential gene expression, largely including pathways associated with lipid and carbohydrate metabolism, cell-cell signaling and interaction, and cellular function and maintenance. These data suggest key metabolic pathways may be critical to differences in weight maintenance and gain.

Key Words: adipose tissue, metabolism, skeletal muscle

0007 Effects of grazing intensity and advancing season on chemical composition and in vitro organic matter disappearance in steers grazing mixed-grass prairie. K. E. Chilcoat*, *Animal Sciences Dep., North Dakota State University, Fargo.*

A study was conducted to evaluate the influence of advancing season and grazing intensity on dietary chemical composition and in vitro organic matter disappearance (IVOMD) in beef steers grazing mixed-grass prairie in the Missouri Coteau of south central North Dakota. Five sampling periods were conducted from mid-May to early September 2015. Twelve ruminal cannulated crossbred steers were used to collect diets while 188 crossbred steers were used to maintain specific

grazing intensities on 12 pastures. Treatments were light (LT), moderate (MOD), heavy (HVY), and extreme (EXT) grazing intensities. Each treatment was assigned to 3 pastures. Grazing treatment × sampling period interactions were not present ($P \geq 0.29$) for all variables measured except IVOMD ($P < 0.01$). There were no main effects of grazing treatment for NDF, ADF, total N, soluble N (SN), insoluble N (IN), and ADIN. Responses to grazing season were evaluated with linear, quadratic, and cubic contrasts. Neutral detergent fiber increased linearly ($P < 0.01$) and cubically ($P = 0.01$), while ADF tended ($P = 0.17$) to increase linearly with advancing season. Dietary N decreased linearly ($P < 0.01$), quadratically ($P = 0.01$), and cubically ($P = 0.01$). Soluble N and IN expressed a linear ($P < 0.001$) and quadratic ($P = 0.03$) decrease across advancing season, while IN also showed a cubic response ($P < 0.001$). Acid detergent insoluble N did not change as season advanced ($P > 0.14$). In vitro OM digestibility decreased from May to September ($P < 0.01$) in all sampling periods, but did not show any trends across treatments ($P = 0.82$). However, IVOMD did show a treatment × period interaction ($P < 0.01$). In summary, these data indicate increases ($P < 0.001$) in dietary NDF and decreases ($P < 0.001$) in N, SN, IN, and IVOMD with advancing season. These data suggest seasonal factors are a more important driver of grazed masticate forage nutrient composition than the grazing intensities evaluated in this study.

Key Words: dietary nutrient composition, grazing intensity, season

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0008 Altering the time of vaccination against respiratory pathogens to enhance vaccine efficacy, health, and performance of feedlot cattle.

K. Lippolis*[1], R. F. Cooke[1], K. M. Schubach[1], A. P. Brandao[1,2], R. Marques[1], M. T. Hinchliff[1], and D. W. Bohnert[1], *[1]Oregon State University–EOARC Burns, Burns, [2]UNESP- FMVZ, Botucatu, Brazil.*

Ninety Angus × Hereford calves were ranked by gender, BW, and age, and assigned to 1 of 3 vaccination schemes against respiratory pathogens: (1) vaccination at weaning (d 0) and at feedlot entry (d 30; CON, $n = 30$), (2) vaccination 15 d before weaning (d –15) and 15 d before feedlot entry (d 15; EARLY, $n = 30$), and (3) vaccination 15 d after weaning (d 15) and 15 d after feedlot entry (d 45; DELAYED, $n = 30$). From d –15 to 6, calves were maintained on pasture. On d 7, calves were placed according to treatments into 1 of 18 drylot pens (6 pens/treatment; 5 calves/pen), and fed a forage-based preconditioning diet. On d 30, calves were transported 1440 km in a livestock trailer and returned to different drylot pens for a 45-d receiving period. Calves were fed a forage + concentrate diet during the receiving period. Blood samples and BW were collected on d –15, 0, 15, 30, 45, 60, and 75. Additional BW was collected on the day after blood sampling so two consecutive BW were recorded and averaged. There were no treatment effects on BW preweaning, weaning, or during the preconditioning and receiving periods ($P \geq 0.59$). The EARLY calves had less ($P \leq 0.05$) ADG preweaning, however had greater ($P \leq 0.04$) ADG during feedlot receiving compared with the other treatments. During preconditioning, CON had greater ($P = 0.05$) DMI compared with EARLY and DELAYED calves, but there were treatment effects ($P \geq 0.20$) on DMI during the feedlot receiving. There were no treatment effects ($P \geq 0.16$) on G:F, morbidity, or mortality. By 15-d after initial vaccination, DELAYED calves had the greatest ($P < 0.01$) antibody titers against *Mannheimia haemolytica,* and EARLY calves had the lowest ($P \leq 0.05$) antibody titer against this pathogen. By revaccination, there was no difference ($P = 0.82$) between DELAYED or CON for antibody titers against *M. haemolytica* titers, while EARLY titers remained the lowest ($P < 0.01$). However, by 45-d after initial vaccination, EARLY calves had the greatest antibody titers ($P \leq 0.05$) against *M. haemolytica*, which remained the greatest until 60-d after initial vaccination. These data suggest that while preweaning ADG may be inhibited by vaccination before weaning, vaccination before weaning and revaccination before feedlot receiving can improve overall antibody titer to *M. haemolytica* and ADG during feedlot receiving.

Key Words: feeder cattle, health, performance, vaccination

0009 Evaluation of genetic structure across five U.S. climate zones using prominent AI sires of two British *Bos taurus* breeds.

B. C. Krehbiel*[1,2], M. G. Thomas[1], H. D. Blackburn[2], S. E. Speidel[1], R. M. Enns[1], and L. Keenan[3], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]National Animal Germplasm Program ARS-USDA, Fort Collins, CO, [3]Red Angus Association of America, Denton, TX.*

Cattle performance in diverse climates can be problematic if they cannot adapt to climate variability. Previous research showed Hereford cattle to have genetic substructure associated with U.S. climates: cool arid (CA), cool humid (CH), transition zone (TZ), warm arid (WA), and warm humid (WH). Allele frequencies of 66 SNP from BovineSNP50 (Illumina BeadChip) were associated with the following traits: mature cow body weight, heat stress, milk yield, heifer conception rate, and early embryonic survival. Knowledge of these genotype to phenotype associations were queried from CattleQTLdb. The GENALEX (6.501) software was used to estimate population genetic results. To characterize the diversity in another British *Bos taurus* breed, population genetic characteristics were estimated in Red Angus bulls ($n = 175$) that were included in the 2000 Bull Project. Similar software, climate zone regions, and SNP were used in the analyses. The number of sires in the climates zones of CA, CH, TZ, WA, and WH were 126, 32, 11, 5, and 1, respectively. We hypothesized

Red Angus bulls would possess genetic substructure across the five climatic zones as observed in Hereford bulls. ARLEQUIN (3.5.2.2) software was used to estimate Hardy-Weinberg Equilibrium (HWE) and conduct an analysis of molecular variance for genotype to phenotype associations. The number of significant ($P < 0.05$) SNP for the traits of milk yield, early embryonic survival, and mature cow body weight were 4, 1, and 1, respectively. Based on the results and genotypes from the bulls studied in the 2000 Bull Project, we reject our hypothesis that Red Angus bulls possess genetic substructure similar to Hereford bulls across five U.S. climate zones. These results provide evidence to suggest that Red Angus cattle in the United States appear to be preferred in beef production systems in cooler climate zones, whereas Hereford cattle populate these regions as well as drier climate zones.

Key Words: *Bos taurus*, genetic diversity management, molecular markers

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0010 Effect of processing of supplemental corn on metabolizable protein of beef cows grazing winter wheat pasture. C. S. Hebbert*[1], M. A. Lopez-Baca[2], L. Avendaño-Reyes[2], U. Macias-Cruz[2], and S. A. Soto-Navarro[1], *[1]New Mexico State University, Las Cruces, [2]Instituto de Ciencias Agricolas, Universidad Autonoma de Baja California, Ejido Nuevo Leon, Baja California, Mexico.*

Eight ruminally and duodenally cannulated, Angus-crossbred cows (587 ± 49.0 kg) grazing winter wheat pasture (WWP) were used in a completely randomized design with the objective of evaluating effects of processing of supplemental corn (ground vs. steam-flaked) on forage intake and metabolizable protein. The experiment was conducted from 23 Mar. through 6 Apr. 2015. Cows grazed a single WWP with ground corn (GC) or steam-flaked corn (SFC) offered individually at 0.4% of BW, once daily at 0700 h. Forage DM intake and total DM intake were greater ($P = 0.01$) for SFC than for GC supplementation. Forage OM, CP, and NDF intake was greater ($P = 0.01$) for SFC than for GC supplementation. Total OM, CP, and NDF intake was greater ($P < 0.02$) for SFC than for GC supplementation. Although feed CP flow to the small intestine was not affected ($P = 0.97$) by corn processing method, microbial CP synthesis was greater ($P = 0.01$) for SFC than for GC supplementation. Therefore, total CP flow to the small intestine (metabolizable protein) was greater ($P = 0.03$) for SFC than for GC supplementation. Total tract digestibility of OM, CP, and NDF (expressed as g/d) were greater ($P < 0.02$) for SFC than for GC supplementation. In conclusion, forage intake, microbial protein synthesis, and metabolizable protein improved by steam-flaking as compared with grinding supplemental corn for cattle grazing WWP. Steam flaking, as compared with grinding supplemental corn, may improve performance of cattle grazing WWP by improving forage intake and microbial CP synthesis.

Key Words: grain processing, metabolizable protein, winter wheat pasture

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0011 Does adaptive grazing management influence dietary quality of yearlings during the grazing season on western Great Plains rangelands? T. R. Plechaty*[1], J. D. Scasta[1], J. D. Derner[2], *[1]University of Wyoming, Laramie, [2]USDA–Agricultural Research Service, Cheyenne, WY.*

Grazing management decisions, such as timing of herd movements, can have a direct impact on the diet quality and nutritional plane of cattle. The variation in diet quality relative to adaptive versus continuous grazing strategies can lead to differences in cattle weight gains which directly impacts the profit margin for livestock producers. Near Infrared Reflectance Spectroscopy (NIRS) was used on fecal samples collected weekly from yearlings during the 2015 grazing season (May through October) to evaluate if differences occurred in measurements of dietary quality (crude protein and digestible organic matter) between adaptive grazing and continuous, season-long grazing in two rangeland ecosystems of the western Great Plains: shortgrass steppe and northern mixed-grass prairie. Yearling cattle under traditional grazing management at a moderate stocking rate had a 1.2 to 2.4% higher dietary crude protein ($P < 0.003$, $P < 0.001$) and a 0.5 to 1.4% higher digestible organic matter ($P < 0.1$, $P < 0.001$) than yearling cattle under adaptive grazing management across the season at HPGRS and CPER, respectively, with maximum differences for both protein and digestibility exceeding 5% at times. At CPER, adaptive grazing management caused a two- to greater-than-fourfold steeper decline in digestibility between rotations compared with traditional grazing management.

Key Words: beef cattle, diet quality, grazing management

0012 Long-term progesterone influence on feed efficiency, body composition, nonesterified fatty acids, and metabolic hormones in mature Rambouillet ewes. M. R. Herrygers*, J. M. Thomson, K. A. Perz, P. J. Merta, M. Knerr, K. Metcalf, K. B. Herrygers, and J. G. Berardinelli, *Montana State University, Bozeman.*

The objectives of this study were to evaluate the effects of long-term progesterone (P4) treatment on changes in feed efficiency, BW, body composition, NEFA and metabolic hormones in mature Rambouillet ewes. Thirty multiparous 5- and 6-yr-old Rambouillet ewes were stratified by age and metabolic BW and assigned randomly to receive long-term P4 administration using a sequential replacement of either a P4-containing controlled internal drug release device (CIDR) or non-P4-containing CIDR (CIDRX). Initially, ewes were

synchronized for estrus using a 7 d CIDR and $PGF_{2\alpha}$ protocol. All ewes exhibited estrus within 72 h after $PGF_{2\alpha}$. Twelve days after estrus (d = 0), each ewe received either a CIDR (n = 15) or a CIDRX (n = 15). Every 14 d thereafter, the CIDR or CIDRX was removed from each ewe and replaced with a new CIDR or CIDRX for 126 d. Jugular venous blood samples were collected from each ewe at the time of CIDR or CIDRX replacement. Serum samples were assayed for P4, NEFA, insulin (INS), triiodothyronine (T3), and thyroxine (T4). Individual feed intake was recorded using GrowSafe units, beginning at d 0 following a 3-wk adaptation period. Ewes were fed a mixed grass hay diet ad libitum that met the nutrient requirements for maintenance. BW for each ewe was collected every 14 d when CIDR or CIDRX were replaced. Back fat (BF) and rib-eye area (REA) were measured for each ewe every 28 d using ultrasonography. BW, residual feed intake, BF and REA did not differ ($P > 0.10$) between CIDR- and CIDRX-treated ewes. Calculated estimates of body composition did not differ ($P > 0.10$) between CIDR- and CIDRX-treated ewes. NEFA, T3, and T4 concentrations did not differ ($P > 0.10$) between CIDR- and CIDRX-treated ewes. However, INS concentrations did differ ($P < 0.05$) between CIDR- and CIDRX-treated ewes. In conclusion, long-term P4 treatment did not appear to alter feed efficiency and partitioning of nutrients. However, maintaining P4 may alter the homeostatic relationship between INS and carbohydrate metabolism in ewes.

Key Words: carcass traits, ewe, metabolism, progesterone, residual feed intake

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0013 Health evaluation of immune-stimulated and hay-supplemented feedlot receiving calves as assessed by blood gas analysis.

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This study evaluated blood parameters, health, and performance of immune-stimulated and hay-supplemented feedlot receiving calves. Heifers (n = 705; 179 ± 0.58 kg BW) were blocked by six truckloads and assigned to 48 pens and four treatments in a randomized complete block design. Treatments were a factorial arrangement of hay (+HAY vs. –HAY) and immunostimulation (+IMMUN vs. –IMMUN). Pens assigned +HAY received supplemental alfalfa hay to the receiving ration for the first 14 d. Calves assigned +IMMUN received a DNA immunostimulant on d 0. On d 0, 14, and 28, BW, rectal temperatures, and venous blood were collected. Health was recorded throughout the 56-d study, and pen weights on d 56. No HAY × IMMUN interactions occurred ($P \geq 0.18$). During the first 14 d, calf ADG was greater ($P < 0.01$) for +HAY than-HAY, but d 14 to 28 ADG was lower ($P < 0.01$) for +HAY than-HAY. Calf ADG was lower ($P \leq 0.01$) for +IMMUN than –IMMUN from d 28 to 56 and from d 0 to 56. Total DMI was greater ($P < 0.01$) for +HAY than –HAY from d 0 to 14, but lower ($P \leq 0.04$) from d 14 to 28 and from d 28 to 56. Gain efficiency of +HAY calves was greater (less negative; $P < 0.01$) from d 0 to 14, but lower ($P < 0.01$) from d 14 to 28 when compared with –HAY. Gain efficiency was lower ($P \leq 0.02$) for +IMMUN than –IMMUN calves from d 28 to 56 and d 0 to 56. Calf morbidity, mortality, and blood parameters (pH, glucose, lactate, hemoglobin saturated with oxygen [sO_2]) were not affected ($P \geq 0.18$) by treatments. Blood sO_2 was lower ($P < 0.01$) on d 0 than d 14 and 28, and glucose was greater ($P < 0.01$) on d 28 than d 0 and 14. Blood sO_2 correlated ($P < 0.05$) with glucose (R^2 = 0.09), lactate (R^2 = –0.12), and mortality (R^2 = 0.08). Glucose correlated with lactate (R^2 = 0.61), and first (R^2 = –0.22) and second (R^2 = –0.13) medical treatment. Lactate correlated ($P < 0.05$) with first medical treatment (R^2 = –0.12) and mortality (R^2 = –0.12). In conclusion, hay supplementation and immune stimulation did not affect calf health, performance, or blood gas parameters. Changes in calf health can be observed in measures of blood parameters.

Key Words: calves, hay, immunostimulant

0014 Effect of postweaning heifer development system on average daily gain, pregnancy rates, and subsequent feed efficiency as a pregnant heifer.

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A 4-yr study was conducted using Angus-based, spring born heifers. In yr 1, weaned heifers grazed corn residue (CR, n = 50) or were fed in a drylot (DLHI, n = 50). In yr 2, 3, and 4, heifers grazed CR (n = 75), upland range (RANGE, n = 75), or were fed diets differing in energy, high (DLHI, n = 75) or low (DLLO, n = 75), in a drylot. Percentage of mature BW before the breeding season was greater (P = 0.01) for DLHI (67%) compared with Range (59%), CR (60%), and DLLO (63%). Pregnancy rates to AI were similar (P = 0.39) among treatments (67, 63, 61, 49 ± 7.2%; RANGE, CR, DLHI, DLLO), and final pregnancy rates were also similar (84, 90, 91, 91 ± 5.4%; Range, CR, DLHI, DLLO; P = 0.59). A subset of AI pregnant heifers from each treatment was placed in a Calan gate system. Heifers were allowed a 20 d acclimation period before beginning the 90 d trial at approximately gestational d 170. Heifers were offered ad libitum hay; amount offered was recorded daily and orts collected weekly. Initial BW was not different (P = 0.35) among treatments (451, 457, 472, 464 ± 10 kg; RANGE, CR, DLHI, DLLO). Body weight at the end of the trial was also similar (P = 0.24; 488, 497, 511, 502 ± 14 kg; RANGE, CR, DLHI, DLLO). Intake was similar, either as DMI (P = 0.27; 9.74, 9.97, 10.18, 10.00 ± 0.76 kg; RANGE, CR, DLHI, DLLO) or residual feed intake (P = 0.61; 0.094, 0.091, –0.056, –0.0743 ± 0.160 kg; RANGE, CR, DLHI, DLLO). There was no difference in ADG (P = 0.36; 0.38, 0.45, 0.43, 0.41 ± 0.17 kg/d; RANGE, CR, DLHI, DLLO)

among treatments. Although the development cost was not different among treatments ($P = 0.41$; \$166, 141, 160, 171 ± 12, RANGE, CR, DLHI, DLLO), there was a \$30 numerical difference between the most (DLHI) and least (CR) expensive treatment. Developing heifers to a greater prebreeding BW did not influence subsequent AI or overall pregnancy rates or feed efficiency as a pregnant heifer.

Key Words: beef heifers, feed conversion, heifer development

0015 Comparison of timed insemination vs. modified estrus detection protocol in beef heifers.

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Angus-based, crossbred heifers (n = 972, 346 kg ± 14 kg) were assigned to either a fixed-time AI (FTAI) protocol or modified estrus detection with fixed-time AI (MTAI) to evaluate synchronization, conception, and pregnancy rates. During the prebreeding development period, heifers were fed to achieve a target of 60 ± 5% mature BW at breeding. Heifers were synchronized via melengestrol acetate-prostaglandin $F_{2\alpha}$ (MGA-PG) protocol and received an estrus detection aid (patch) at PG administration. A patch score was recorded for each heifer at AI to reflect what percentage of rub-off coating had been removed. Heifers in the FTAI treatment received 2 mL GnRH injection and were AI 72 ± 2 h following PG. Heifers in MTAI treatment were observed for estrus at 58 ± 2 and 70 ± 2 h after PG. Approximately 72 ± 2 h after $PGF_{2\alpha}$, heifers in MTAI were AI in the following order: heifers in estrus at 58 h post-PG, heifers in estrus at 70 h post-PG, and heifers not expressing estrus at either estrus observation. Heifers not expressing estrus received GnRH at AI. Pregnancy was determined via transrectal ultrasonography. Heifers exhibiting estrus had greater ($P < 0.01$; 71 and 66 ± 5% for FTAI vs. MTAI, respectively) AI conception rates than heifers not expressing estrus in both FTAI and MTAI treatments vs. 47 and 53 ± 9% AI conception rates in nonestrus heifers for FTAI and MTAI, respectively. However, overall AI conception rate (62 ± 5%, $P = 0.49$) and final pregnancy rates were similar ($P = 0.98$; 96 and 97 ± 3% for FTAI vs. MTAI, respectively). Similar AI conception rates were achieved without estrus detection.

Key Words: beef heifers, estrus synchronization, timed artificial insemination

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0016 Growth and reproductive performance of yearling beef heifers implanted with Revalor G in the Nebraska Sandhills.

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Crossbred beef heifers (n = 3242), approximately 12 mo of age, were managed at three locations in the Nebraska Sandhills and randomly assigned to be implanted with Revalor G (40 mg of trenbolone acetate and 8 mg estradiol, IMP), while the control group (CON) did not receive an implant. Heifers (238 ± 2 kg) grazed native Sandhills range for the duration of the trial (164 ± 4 d). Eighty-two ± 2 d following trial initiation, heifers were synchronized for estrus and AI followed with clean-up bulls as part of a 25 d breeding season. Body weight was measured at the beginning and end of trial. Pregnancy detection occurred 45 d following bull removal at the conclusion of the summer grazing period. Implanted heifers gained more and were heavier ($P < 0.05$; 0.68 vs. 0.64 ± 0.01 kg/d and 347 vs. 340 ± 3 kg, IMP vs. CON, respectively) at the end of the trial. However, pregnancy rate was greater ($P < 0.01$) for CON vs. IMP (64 vs. 46 ± 3%, respectively). Implanted heifers also had a lower pregnancy rate in their second breeding season ($P = 0.02$; 93 vs. 96 ± 2%, IMP vs. CON, respectively). Implanting beef heifers with Revalor G at approximately 12 mo of age increased ADG and summer BW gain; however, it decreased initial and subsequent pregnancy rate compared with heifers not implanted.

Key Words: beef heifers, fertility, growth implants

0017 Performance and net energy in high and low RFI beef cattle.

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The objective of this study was to relate feed efficiency to performance and net energy in beef cattle. To identify animals with greater or lesser feed efficiency, 98 weaned Angus cross beef calves (71 steers and 27 heifers) were fed individually for 56 d. Feed offered and refused were measured daily, body weights were taken at 14 d intervals, and ultrasound measures (longissimus muscle area and subcutaneous fat over the 12th to 13th ribs) were taken at the beginning, middle and end of the trial. Feed was delivered twice a day, on an ad libitum basis. Residual feed intake (RFI) was determined as the residual of the regression of DMI on mid-test $BW^{0.75}$ and ADG. High and low RFI groups were defined as >0.5 SD above or below zero, respectively, with intermediate animals classified as medium RFI. As expected, RFI groups had similar initial and final BW and ADG, and different DMI, gain:feed and RFI ($P < 0.001$). Fat gain, protein gain, and recovered energy (RE) were not different between RFI groups, although subcutaneous fat over the 12th and 13th rib was 0.19 cm higher in high RFI than low RFI cattle ($P = 0.012$). Heat energy (HE),

Table 0017.

Table 2. Performance, body composition, and net energy in RFI groups and sex after 56 days *ad libitum* feeding.

	RFI			Sex			P-value		
Trait	High	Medium	Low	H	S	SD	RFI	Sex	Sex x RFI
Initial BW, kg	279.3	272.3	277.2	261.3	291.2	30.2	0.67	< 0.001	0.53
Final BW, kg	382.6	370.1	382.4	346.7	410.0	35.9	0.33	< 0.001	0.32
ADG, kg/d	1.844	1.747	1.878	1.524	2.122	0.238	0.11	< 0 .001	0.32
DMI, kg/d	9.06	8.17	7.84	7.63	9.08	0.866	< 0.001	< 0.001	0.16
Gain:feed	0.203	0.212	0.239	0.202	0.235	0.02	< 0.001	< 0.001	0.96
RFI, kg/d	0.590	-0.006	-0.634	0.014	-0.047	0.25	< 0.001	0.29	0.29
Ribeye area, cm^2	67.52	65.18	67.80	63.82	69.85	6.26	0.23	< 0.001	0.35
12^{th}-13^{th} rib fat, cm	0.94	0.84	0.75	0.85	0.84	0.18	0.002	0.81	0.09
Fat gain, kg/d	0.64	0.61	0.61	0.517	0.722	0.17	0.65	< 0.001	0.17
Protein gain, kg/d	0.22	0.21	0.23	0.179	0.258	0.05	0.26	< 0.001	0.62
Fat:protein	3.02	2.81	2.73	2.892	2.817	0.67	0.29	0.62	0.06
RE, Mcal/d	7.25	6.89	7.00	5.860	8.231	1.78	0.63	< 0.001	0.19
RE, Mcal $kg^{0.75}$	0.102	0.099	0.098	0.089	0.112	0.02	0.77	< 0.001	0.28
HE, Mcal/d	19.40	17.14	16.08	16.58	18.50	2.69	< 0.001	< 0.001	0.40
HE, Mcal $kg^{0.75}$	0.274	0.248	0.228	0.250	0.250	0.03	< 0.001	0.91	0.55
NEm, Mcal/$kg^{0.75}$	0.103	0.087	0.077	0.098	0.081	0.03	0.001	0.002	0.75

defined as the difference between metabolizable energy intake (MEI) and RE was lower in low RFI cattle ($P < 0.001$). Estimated NE_m requirement (Mcal/$kg^{0.75}$) was lower in low than in high RFI cattle ($P = 0.001$). Overall heifers gained less than steers; however, there were no sex × RFI class interactions. Low RFI cattle have similar weights and weight gains, but lower intakes and higher feed efficiencies as high RFI cattle. This may be partially due to decreased maintenance requirement and heat production.

Key Words: efficiency, net energy, residual feed intake

0018 Impact of maternal protein restriction in first-calf heifers during mid- to late- gestation on gene expression, feedlot performance, and carcass characteristics of progeny.

J. J. Kincheloe*[1], M. J. Webb[2], R. N. Funston[3], K. R. Underwood[2], M. G. Gonda[2], A. D. Blair[1], and K. C. Olson[1], *[1]South Dakota State University, Rapid City, [2]South Dakota State University, Brookings, [3]University of Nebraska, West Central Research and Extension Center, North Platte.*

Maternal nutrient restriction in beef cows impacts developmental processes in the fetus that may influence postnatal performance. This study investigated impacts of MP restriction in mid- and late-gestation on the transcriptome of neonatal muscle tissue and subsequent feedlot performance and carcass characteristics of progeny. One hundred eight Angus × Simmental heifers were blocked by BW and method of conception (AI or natural service, based on fetal age at ultrasound) and allocated to 12 pens in a randomized complete block design with a 2 × 2 factorial treatment structure including two stages of gestation (mid- and late-) and two levels of dietary protein (control [CON]; approximately 102% of MP requirements and restricted [R]; approximately 80% of MP requirements). Pens were randomly assigned to CON or R treatments within blocks during mid- and/or late-gestation. Heifers were removed from treatments after calving and managed as a common group. Within 48 h of birth, LM biopsy samples were collected from a subset of three male AI calves from each treatment combination for analysis of gene expression using RNA-Seq technology. Following weaning, calves were backgrounded for 2 wk then finished in a GrowSafe feeding system on a common finishing diet. Individual carcass measurements were recorded. Genes found in pathways associated with muscle tissue development were up-regulated ($P \leq 0.02$) in calves born to dams on the CON treatment throughout mid- and late- gestation. Genes involved in adipogenesis were up-regulated in calves born to dams on the R-R treatment ($P = 0.05$). No differences were observed for calf BW, DMI, ADG, G:F, or residual feed intake (RFI) due to maternal nutritional treatments across the entire feeding period ($P > 0.10$). Hot carcass weight, adjusted 12th rib fat thickness, KPH, marbling score, and proportion of carcasses in each USDA quality grade were not influenced ($P > 0.10$) by maternal diet during gestation. Progeny of dams on the R treatment in late gestation had greater LM area ($P = 0.05$) vs. progeny from CON dams. There was a tendency ($P = 0.06$) for a mid- by late-gestation treatment interaction for

yield grade, with lower yield grades in progeny from dams on CON-R or R-CON treatments vs. CON-CON. Differences in gene expression, animal performance, and carcass characteristics indicate MP restriction during mid- and late-gestation may impact developmental programming.

Key Words: beef cattle, MP restriction, gene expression

ASAS WESTERN SECTION UNDERGRADUATE STUDENT POSTER COMPETITION

0019 Development of an immunohistochemical technique to determine presence and localization of glucose transporter GLUT3 in bovine utero-placental tissues from days 16 to 50 of gestation.

J. Osei*, M. S. Crouse, K. J. McLean, J. A. Flaten, P. P. Borowicz, L. P. Reynolds, J. S. Caton, and C. R. Dahlen, *Department of Animal Sciences, North Dakota State University, Fargo.*

Before the establishment of transplacental exchange, nutrients must be transported to the embryo via nutrient transporters. Glucose transporter *GLUT3* is known as a higher affinity, facilitated diffusion glucose transporter found in high glucose demanding tissues such as the brain, placenta, sperm, pre-implantation embryos, and some cancers. The objectives of our current study were (1) develop an immunohistochemistry technique to localize *GLUT3* in bovine utero-placental tissues, and (2) confirm the presence and location of *GLUT3* in bovine utero-placental tissues. We hypothesized that *GLUT3* would be present in utero-placental tissues from d 16 to 50 of gestation. To test this hypothesis, crossbred Angus heifers (n = 49), were synchronized, bred via AI, randomly assigned to nutritional treatment beginning at AI (CON; heifers receiving 100% of requirements to gain 0.45 kg daily) or (RES; 60% of CON), then ovariohysterectomized on d 16, 34, or 50 of gestation (n = 6 to 7/d/treatment), or were not bred and ovariohysterectomized on d 16 of a synchronized estrous cycle (n = 6) to serve as nonpregnant (NP) controls. Uterine cross-sections were obtained from the pregnant horn, fixed in neutral buffered formalin, and embedded in paraffin for histology. Rabbit primary antibody for *GLUT3* (Abcam) followed by fluorescently labeled, goat nonrabbit secondary antibody (Alexa Fluor 633; Abcam) was used to localize *GLUT3* transporter. A DAPI stain was used to counterstain cell nuclei. Photomicrographs were taken with a Zeiss Imager.M2 epifluorescence microscope using a 10× objective and AxioCam HR camera with a Zeiss piezo automated stage. To describe localization of *GLUT3*, the mosaic image of a large tissue area covering the whole cross-section of the uterus with fetal membranes (12 × 3 pictures) on the slide was taken using the MosaiX module of Zeiss AxioVision software. We localized *GLUT3* in fetal membrane [chorioallantois], uterine endometrium [caruncles and intercaruncular endometrium] interglandular (stromal) tissue, superficial glands, deep glands, as well as myometrium in NP, CON, and RES tissues on d 16, 34, and 50. These results accomplished our objectives and clearly supported our hypothesis that *GLUT3* is present in uterine tissues from d 16 to 50 of gestation. Further research and more detailed measurements using fluorescence intensity in utero-placental tissues across day and treatments is needed to determine impacts of maternal nutrition status and day of early gestation on localization as well as concentration of the *GLUT3* transporter within utero-placental tissues.

Key Words: bovine, glucose, immunohistochemistry, utero-placental tissue

0020 Do ewes born with a male co-twin have greater longevity with lambing over time?

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Based on a recent analysis of historical records, ewes born co-twin to a ram had greater lifetime reproductive performance than ewes born co-twin to an ewe. We are interested in determining what component(s) of lifetime reproductive performance may be associated with a ewe's co-twin sex. As an initial indicator of longevity in the flock, we hypothesized that co-twin sex will affect the age at which ewes consistently appear in the lambing records (i.e., recorded as having lambed). Therefore, the objective was to determine the percentage of ewes, born with a female or male co-twin, that appear in the lambing records at ages 1 to 7 yr. Using the USDA–ARS, U.S. Sheep Experiment Station database, lambing records from 1994 to 1997 were queried for ewes that were either born with a male or female co-twin. A total of 4442 ewes were identified, and breeds included Columbia (n = 417), Polypay (n = 627), Rambouillet (n = 446), and Targhee (n = 427). For each age class, Chi square analysis was used to compare the expected percentage of ewes lambing that were either born to a female or male co-twin. Of ewes born as a twin and subsequently recorded as having lambed, we expected that, within each age class (1 to 7 yr), 50% of the ewes were originally born as a co-twin to a female (FF) and 50% born as a co-twin to a male (FM). The observed percentage of FF (52.7%) or FM (47.3%) ewes did not differ, regardless of age or breed; $P > 0.10$). Within breed, no differences between percentages were observed in Columbia (FF = 53.8% and FM = 46.2%; $P > 0.10$), Rambouillet (FF = 55.2% and FM = 44.8; $P > 0.60$), and Targhee (FF = 46.3% and FM = 53.7%; $P > 0.30$) ewes regardless of age. However, in 2-yr-old Polypay ewes, there were more FF ewes recorded as having lambed compared with FM ewes (FF = 55% and FM = 45%; $P < 0.01$), but no differences were found at any other age. We suggest that the percentage of ewes having a female or male co-twin did not vary from the expected percentage, thus ewes having a male

co-twin did not have greater longevity with lambing compared with ewes with a female co-twin.

Key Words: co-twin, longevity, lambing

0021 Effect of postweaning brewers grain supplementation on growth and reproductive performance of angus and red angus heifers.

S. E. Butterfield*, J. M. Wisniewski, D. A. Daley, S. P. Doyle, and K. L. DeAtley, *California State University, Chico.*

Objectives of this study were to determine the effects of supplemental brewers grain on growth performance and reproductive characteristics of Angus and Red Angus heifers in a 3-yr study. A total of 85 spring-born, weaned heifers were randomized via gate cut and placed on an 84 d supplementation trial. Treatment groups were either control (CON; $n = 43$; initial BW = 311.90 ± 8.57 kg) or wet brewers grain (WBG; $n = 42$; initial BW = 309.43 ± 8.57 kg) groups. Heifers were housed on adjacent improved pastures (TDN, 56.5%; CP, 11.19%; NDF, 64.8%) and supplemented once daily at 1800 with either the control (CON, alfalfa hay + corn silage; TDN, 52.4%, CP, 8.2%, NDF, 65.6%) or WBG (Alfalfa hay + corn silage + wet brewers grain; TDN, 53.6%, CP: 9.8%, NDF, 66.2%) ration. Diets were balanced to target 0.68 kg ADG/head and were offered on an ad libitum basis. Fifteen days after supplementation period, heifers were synchronized using the 14 d controlled internal drug release-PG + heat detection + timed AI protocol. Traits collected were: BW at d 0, 28, 56, and 84; total gain; ADG; response to synchronization protocols; and ultrasound pregnancy rate. During yr 2, weekly blood serum samples were collected via jugular venipuncture for determination of serum progesterone concentration. Age at puberty was defined as heifer age in days on date of second consecutive progesterone values > 1 ng/mL. Growth performance measures were analyzed as a completely randomized block design (block = year of study) and age at puberty was analyzed as a completely randomized design. No difference ($P > 0.05$) was detected between the control and treatment groups for heifer BW on d 28 (325.97 ± 8.88 vs. 324.86 ± 8.88 kg), d 56 (341.54 ± 8.57 vs. 341.84 ± 8.57 kg), d 84 (361.42 ± 8.21 vs. 360.38 ± 8.21 kg), and ADG (0.14 ± 0.01 vs. 0.14 ± 0.01 kg). Age of puberty did not differ ($P > 0.05$) between treatment groups. Results indicate that heifers supplemented with brewer's grain showed no deviation in development compared with heifers fed the control ration. Cumulative results suggest that WBG could be used as part of a heifer development ration to help offset costs associated with diet ingredients; however, economic analyses of ration and development costs need to be investigated further.

Key Words: heifer development, growth, supplementation

0022 Growth performance and feed efficiency of commercial and half-blood lowline-angus steers in backgrounding and finishing phases.

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Objectives of this study were to measure growth performance and feed efficiency of commercial ($n = 20$) and half-blood Lowline-Angus ($n = 20$) steers during the backgrounding and finishing growth phases. A total of 40, spring-born steers were delivered to the CSU, Chico cattle feeding facility 30 d postweaning and randomly assigned to three 7 × 18 m pens equipped with GrowSafe feed intake system for a 28 d adaption period. Commercial ($n = 20$) and half-blood Lowline-Angus ($n = 20$) steers were fed a forage-based backgrounding ration (CP, 15.6%; TDN, 56.22%; NDF, 52%, DM basis) for 58 d and allowed ad libitum access to feed and water. Cattle were transitioned to the finishing ration (CP, 11.9%; TDN, 72.58%; NDF, 20.21%, DM basis) over a 16 d period. Finishing phase trial was 72 d and weights were taken on d 0, 1, 35, 71, and 72. Data were analyzed as a randomized block design (block = pen). Breed × pen effect was not significant ($P > 0.05$). In the backgrounding phase, dry matter intake tended ($P = 0.06$) to be greater for commercial steers (DMI; 9.16 ± 0.36 kg) compared with half-blood Lowline-Angus (DMI; 8.17 ± 0.36 kg) steers. ADG, metabolic mid-weight, residual feed intake and feed conversion ratio were not different ($P > 0.05$) between breed groups in the backgrounding phase. In the finishing phase, commercial and half-blood Lowline-Angus steers had different ($P < 0.05$) ADG (1.82 ± 0.05 kg vs. 1.53 ± 0.05 kg), metabolic mid-weight (MMWT; 72.30 ± 1.18 kg vs. 68.16 ± 1.18 kg), DMI (10.12 ± 0.20 kg vs. 8.65 ± 0.20 kg), residual feed intake (RFI; 0.24 ± 0.13 kg vs. –0.22 ± 0.13 kg) and end weight (464.41 ± 9.28 kg vs. 423.16 ± 9.25 kg). Results indicate that backgrounding phase performance may not be an accurate predictor for finishing phase performance. Lack of significance in the backgrounding phase between breed groups may be a function of half-blood steers being F1 generation. Further research should be conducted to assess feed efficiency performance during the backgrounding phase in commercial and half-blood Lowline-Angus steers.

Key Words: GrowSafe, growth performance, steer

0023 Utilization of wet brewers grain as a winter feed supplement for beef cows grazing native annual grasslands. K. N. Bohn*[1], S. P. Doyle[1], J. Davy[2], D. K. Flavell[3], N. Schweitzer[3], K. L. DeAtley[1], *[1]California State University, Chico, [2]University of California, Cooperative Extension Service, Red Bluff, [3]University of California, Cooperative Extension Service, Browns Valley.*

Objectives of this study were to determine the effects of wet brewers grain (WBG) as a winter supplement on cow and calf performance while grazing native annual grasslands. The study was conducted at the Sierra Foothill Research and Extension Center (Browns Valley, CA) during 2014–2015 and 2015–2016 winter grazing seasons (i.e., November through January). A total of 92, fall-calving Angus × Hereford cows grazing native annual pastures (12.12 ha/pair for 84 d; 3.56% CP, 39.3% TDN, 75.3% NDF) were supplemented with either molasses low moisture protein block, available ad libitum (CON; n = 28; CP, 26%) or WBG (fed 3 times/wk; formulated to offer 0.68 kg CP head/d on DM basis; CP, 26%). Treatment groups were housed in adjacent pastures during the 84 d supplementation period and weights were taken in 28 d intervals. Dependent variables included: cow and calf BW and cow BCS. Data were analyzed as a randomized block design where block = year of study. Treatment × block interaction was not significant ($P > 0.05$). Calves were born before beginning of study each year and calf date of birth was fit as a covariate. Brewers grain supplemented cows were heavier on d 56 compared with CON cows (560.63 vs. 529.86 ± 13.99 kg; $P = 0.03$). Similarly, WBG calves were also heavier on d 56 compared with CON calves (117.97 vs. 110.06 ± 3.72 kg; $P = 0.03$). Calves born to WBG supplemented cows tended ($P < 0.10$) to be heavier than those of CON supplemented cows on d 0 (57.96 vs. 58.81 ± 2.73 kg) and d 86 (141.64 vs. 152.03 ± 3.74 kg). Results indicate that cows and calves supplemented with WBG recovered weight more quickly than those consuming liquid protein supplement. Therefore, WBG may have considerable potential as a winter protein supplement on California grasslands; however, economic analyses need further investigation.

Key Words: annual grasslands, feed supplementation, wet brewers grain

0024 Derivation of economic values for feedlot performance traits in commercial and lowline-influenced angus steers. L. C. Huffaker*, K. L. DeAtley, J. N. Brimlow, and S. P. Doyle, *California State University, Chico.*

Feed costs and market volatility make identifying cattle biological types and performance traits with significant economic impact at the feedlot imperative. Thus, the objective of this study was to determine the economic values of feedlot performance traits in commercial Angus (n = 20), half-blood Lowline-influenced Angus (n = 20), and full-blood Lowline Angus (n = 8) steers. Steers were fed for 72-d after a 28-d adjustment period at the CSU, Chico Agricultural Teaching and Research Center's beef cattle feeding facility. Upon delivery, steers were randomly assigned to three, 7 × 18 m pens, each fitted with two GrowSafe feed nodes and allowed ad libitum access to water and finishing ration (CP = 11.9%, TDN = 72.58%, NDF = 20.20%). After the 72-d GrowSafe trial, steers continued in their assigned GrowSafe pens until slaughter. Feedlot performance traits with significant economic impact were identified using stepwise, multiple-trait linear regression of net revenue onto residual feed intake (RFI), ADG, DMI, slaughter weight, and dummy variables representing breed type. Net revenue was defined as gross revenue minus feed costs. Gross revenue for each steer was determined by multiplying each animal's slaughter weight by market price at the time of sale ($3.26/kg). Costs included yardage ($.50/hd/d), billed daily feed consumption, and average feeder price ($3.68/kg) multiplied by delivery weight. Average net revenue (±SD, USD) for the commercial Angus, half-blood Lowline-influenced and full-blood Lowline Angus steers were $10.13 ± 86.97, $–44.30 ± 69.98, and $–105.05 ± 86.97, respectively. Multiple linear regression results identified slaughter weight, DMI, and ADG as significant predictors of feedlot net revenue ($R^2 = 0.41$; $P < 0.05$). Coefficients representing economic values for slaughter weight, DMI and ADG were $0.66, $–32.92, and $71.30, respectively. Results suggest that slaughter weight, DMI, and ADG are key predictors of feedlot net revenue, and deserve consideration in the development of breeding objectives with the goal of improving feedlot profitability.

Key Words: economic values, feedlot cattle, performance

ASAS WESTERN SECTION YOUNG SCHOLARS

0025 Effects of organic or inorganic Co, Cu, Mn, and Zn supplementation to late-gestating beef cows on productive and physiological responses of the offspring. R. Marques*[1], R. F. Cooke[1], M. C. Rodrigues[1], B. I. Cappellozza[1], R. R. Mills[2], C. K. Larson[3], P. Moriel[4], and D. W. Bohnert[1], *[1]Oregon State University–EOARC Burns, Burns, [2]Oregon State University Extension Service, Pendleton, [3]Zinpro Corporation, Eden Prairie, MN, [4]UF/IFAS Range Cattle Research and Education Center, Ona, FL.*

Eighty-four multiparous, nonlactating, pregnant Angus × Hereford cows were ranked by pregnancy type (AI = 56, natural service = 28), BW, and BCS, and allocated to 21 drylot

pens at the end of their second trimester of gestation (d 0). Pens were assigned to receive forage-based diets containing: (1) sulfate sources of Cu, Co, Mn, and Zn (INR), (2) an organic complexed source of Cu, Mn, Co, and Zn (AAC; Availa®4; Zinpro Corporation, Eden Prairie, MN), or (3) no supplemental Cu, Co, Mn, and Zn (CON). Diets were offered from d 0 until calving, and formulated to meet requirements for energy, protein, macrominerals, Se, I, and vitamins. The INR and AAC diets provided the same daily amount of Cu, Co, Mn, and Zn. Cow BW and BCS were recorded, and liver samples were collected on d –10 and 2 wk (d 75) before the calving season. Within 3 h after calving, calf BW was recorded, liver samples were collected, and the expelled placenta was retrieved (n = 47 placentas). Calves were weaned on d 283 of the experiment, preconditioned for 45 d (d 283 to 328), transferred to a growing lot on d 328, and moved to a finishing lot on d 440 where they remained until slaughter. Liver Co, Cu, and Zn concentrations on d 75 were greater ($P \leq 0.05$) for INR and AAC compared with CON cows, whereas INR had reduced ($P = 0.04$) liver Co but greater ($P = 0.03$) liver Cu compared with AAC cows. In placental cotyledons, Co concentrations were greater ($P \leq 0.05$) in AAC and INR compared with CON cows, whereas Cu concentrations were only increased ($P = 0.05$) in AAC compared with CON cows. Calves from INR and AAC had greater ($P < 0.01$) liver Co concentrations at birth compared with calves from CON cows. Liver Cu and Zn concentrations at birth were greater ($P \leq 0.05$) in calves from AAC compared with cohorts from CON cows. Weaning BW was greater ($P \leq 0.05$) in calves from AAC compared with cohorts from CON cows, and this difference was maintained until slaughter. In the growing lot, calves from AAC cows had reduced ($P < 0.01$) incidence of bovine respiratory disease compared with CON and INR cohorts. Collectively, these results suggest that feeding the AAC diet to late-gestating beef cows stimulated programming effects on postnatal offspring growth and health compared with the CON diet. Therefore, supplementing late-gestating beef cows with an organic complexed source of Co, Cu, Zn, and Mn instead of no supplementation appears to optimize offspring productivity in beef production systems.

Key Words: trace mineral, beef cow, supplementation

0026 Altered rumen microbial populations in response to high sulfate water in lambs.

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Water is involved directly or indirectly in essentially every bodily process. Therefore, access to quality water sources is critical for livestock wellbeing. In the western United States, however, high sulfate (SO_4^{2-}) water sources are frequently encountered. High SO_4^{2-} water can cause overproduction of ruminal H_2S and result in compromised health and performance of the host. An initial trial (Trial 1) was conducted to determine the impact of high SO_4^{2-} drinking water on the rumen microbiome of growing lambs. A follow-up trial (Trial 2) then sought to confirm rumen microbial species involved in the response to high SO_4^{2-} drinking water and additionally identify species that adapt to SO_4^{2-} challenges. Each trial consisted of individually penned Hampshire-cross lambs (n = 43 in Trial 1; n = 16 in Trial 2) which had access to ad libitum feed and high SO_4^{2-} water (3000 mg SO_4^{2-}/L) for a 28 d period. Trial 2 also included a 7 d posttreatment period to obtain recovery data for later analysis. DNA was extracted and sequenced from d 0, 7, and 28 rumen samples and then compared with known 16S rDNA reads for microbial identification. Operational taxonomic units (OTU) were defined as sequence clusters with ≥97% identity and analyzed for the fixed effect of sampling day using the GENMOD procedure of SAS. Trial 1 resulted in a total of 145 OTU found in at least one of the 24 sequenced samples (eight lambs; three sampling dates); eight OTU were affected ($P \leq 0.05$) by sampling day. Trial 2 resulted in 287 OTU identified in at least one of the 24 sequenced samples (eight lambs; three sampling dates), with sampling day affecting ($P \leq 0.05$) 38 of those OTU. Collectively, these results indicate a shift in rumen microbe relative abundance in response to high SO_4^{2-} water. Abundance variation may confer differences in host animal ability to tolerate and adapt to high SO_4^{2-} water. Similarities in microbial abundance changes across the two trials suggest that particular species are especially reactive to high ruminal SO_4^{2-} and are likely important to host response. Furthermore, certain microbial species demonstrated greater potential to adapt over time to a high SO_4^{2-} environment. Greater understanding of the rumen microbes involved in the response to high SO_4^{2-} drinking water is necessary for development of effective treatment and prevention strategies for ruminant livestock maintained in high SO_4^{2-} water regions.

Key Words: DNA sequencing, microbes, rumen, sheep, sulfate

0027 Immunological implications of pregnancy: A focus on inflammatory cytokines.

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The present studies aim to (1) determine expression of (C-X-C motif) Ligand 12 (CXCL12), CXCR4, and inflammatory cytokines in corpus luteum (CL) and fetal-maternal interface during early pregnancy and when CXCR4 signaling is inhibited in ewes, and (2) determine alterations in CL cytokine expression using an in vivo model with hCG-stimulated P4 levels. Several human studies highlight CXCL12-CXCR4 signaling in regulating cytokine production, but whether similar mechanisms occur in livestock is uncertain. Our laboratory

reported activation of CXCL12-CXCR4 signaling axis at the fetal-maternal interface in sheep but whether this axis is involved in modifying reproductive tissue or peripheral blood inflammatory responses is uncertain. We hypothesized CXCL12-CXCR4 signaling acts as a potentiator during early pregnancy in ewes by altering cytokine populations at the fetal-maternal interface and the luteal microenvironment. To test this hypothesis, CL tissue was collected from NP (d 10 of estrous cycle) and pregnant ewes on d 20 and 25. In a separate study, we utilized AMD3100, a potent CXCR4 antagonist, to disrupt CXCR4 signaling to determine inhibition effects on fetal-maternal cytokines. Mini-osmotic pumps were surgically installed on d 12 of gestation and delivered AMD3100 or PBS into the uterine lumen ipsilateral to CL for 7 d. Endometrium (caruncular and intercaruncular) and fetal membrane tissues were collected on d 23 of gestation. Gene expression of inflammatory cytokines were investigated using real time PCR. During gestation, proinflammatory cytokines increased ($P < 0.05$) in CL from pregnant compared with NP ewes. Similarly, CXCL12 and CXCR4 increased ($P < 0.05$) on d 20 of gestation in pregnant compared with NP ewes. Under hCG stimulation, interferon γ (IFNG) decreased ($P < 0.01$) on d 25 in CL tissue compared with control ewes. In AMD3100-treated ewes, transcripts for tumor necrosis factor (TNF; $P < 0.05$) and interleukin 12 (IL12A; $P < 0.01$) increased in caruncle, while transforming growth factor β 1 (TGFB1) and IL12A tended ($P = 0.2$) to increase in intercaruncular endometrium compared with control. Interleukin 10 (IL10) transcript from treated ewe fetal membrane tended ($P = 0.1$) to increase compared with control. Using immunofluorescence, IL10 protein was localized to uterine luminal and glandular epithelium, and TNF to uterine glandular epithelium and stroma. Using flow cytometry, we established peripheral blood T lymphocytes are CXCR4-positive. Our results highlight the role CXCL12-CXCR4 signaling may play in regulating localized inflammation at the fetal-maternal interface and immune cell trafficking in peripheral blood, contributing to pregnancy maintenance.

Key Words: chemokine receptor 4, cytokines, inflammation

MEETING TODAY'S ANIMAL CARE STANDARDS: ARE YOU READY?

0028 New *Ag Guide*—What should we expect?

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The first edition of the *Ag Guide* was published in 1988 to define standards of care for agricultural animals used in agricultural research and teaching. These standards were to accomplish two important objectives. One was to ensure that the agricultural animals used for research and teaching are fit subjects so as not to compromise outcomes by having poor condition. The other objective was to give regard to and preserve the wellbeing of these animals based on our growing recognition that they, by their nature, ought to be in the realm of human moral concern. The second edition of the *Ag Guide* came out in 1999, with an expanded authorship and chapters devoted to specific types of agricultural animals. The current third edition (2010) has 62 authors and additional chapters covering institutional policies and principles related to health care, husbandry, environmental enrichment, and handling and transport. The title of the third edition was changed to *Guide for the Care and Use of Agricultural Animals in Research and Teaching*, on the principle that the standards therein are applicable to agricultural animals in all research and teaching situations, not just those seen as strictly agricultural. The *Ag Guide* has become the reference document for agricultural animals by IACUC's nationwide, and has been adopted by AAALAC as a primary standard to evaluate animal care and use programs. At the last meeting of the FASS Scientific Advisory Committee on Animal Care (SACAC) in May 2015, it was decided to revise the *Ag Guide* to produce a fourth edition. Items were identified for each chapter and a tentative timeline was developed. The sale of ASAS and PSA interests in FASS to ADSA in 2015 provided for transfer of ownership of the *Ag Guide* to ADSA, ASAS, and PSA and dissolved the SACAC, temporarily suspending action on the *Ag Guide*. As of the writing of this abstract, the revision process has been initiated, but a determinable timeline for publication has not been established. The three societies recognize the vital importance of an up-to-date *Ag Guide* and intend to jointly publish a revised fourth edition.

Key Words: *Ag Guide*

0029 How ag research and teaching differs from "rodent" studies in AAALAC international accreditation.

J. J. McGlone*, *Texas Tech University, Lubbock.*

Ethical care of farm animals is required for conduct of farm animal research and teaching, journal article submission, and production on commercial farms. The highest standard of animal care is provided when an agricultural research and teaching institution becomes accredited by AAALAC International. Some people in animal agriculture are leery of AAALAC accreditation because they have experienced laboratory animal ethics applied to farm animal research and teaching. Here I argue that the fundamental ethical principles underlying farm animal care are often different than those that underpin laboratory animal care. The laboratory animal community lean heavily on the 3 R's (reduce, replace, and refine). I argue that these are not appropriate for farm animals as they are for laboratory animals. Agricultural research doesn't reduce the sample size, it optimizes the sample size. Agricultural animal researchers don't often replace animal models with a "lower" model species (say using a mouse rather than a chimp for a

human disease), they use the actual target species (say using a pig for pig research). Sample size is often optimized, not set at the lowest numbers possible. Field studies may use the building or barn as the experimental unit which greatly increases numbers of animals in an appropriate manner. Retailers and consumers may set ethical requirements on the entire market or niche markets that require certain production practices. Finally, animals used in teaching have entirely different ethical standards depending on if the learning is meant to be a demonstration or if the student is expected to be proficient at an animal procedure. In addition to budgetary pressures for university farms, animal science programs must determine if they can justify model animal farms for teaching purposes. In conclusion, laboratory animal ethical principles are different in some ways than the standards for agricultural animals used in farm animal research or teaching. Using laboratory animal standards like the 3 R's may not help and may harm farm animal welfare. AAALAC International utilizes the *Ag Guide* as its guiding document for farm animals in teaching and research. As long as overseeing bodies use the appropriate ethical framework, farm animal care will be protected in both farm animal research and teaching.

Key Words: animal care, accreditation, ethics

0030 Getting along with your IACUC and helping them understand agricultural species research.
J. Salak-Johnson*, *University of Illinois, Urbana.*

The Institutional Animal Care and Use Committee (IACUC) is responsible for ensuring the humane use and care of farm animals in research and teaching at Universities. Despite, the challenges IACUCs face in oversight of farm animals used in research in terms of the diverse animal facilities or farm or production settings, this does not change the acceptable guidelines for ensuring animal farm well-being. Farm animal care and use in research and teaching requires the same science-based practices that are outlined and supported by the *Guide for Care and Use of Agricultural Animals in Research and Teaching* (*Ag Guide*, 2010). It is necessary for IACUCs to have expertise on their committees that understand how to best apply these standards specifically to species in question in a particular setting. An IACUC that is adequately informed to consider species-specific issues within the context of the specific research being conducted can better ensure proper animal care while maximizing farm animal welfare. But, this can only be achieved if an IACUC has explicit knowledge of each species for which it has oversight which can be accomplish only if there is knowledgeable representation on the committee. The past few years, IACUCs have been faced with challenges from the public and other committee members that lack knowledge and understanding of the importance of the *Ag Guide* and animal unit specific standard operating procedures (SOPs) for farm animals. The objective is to give an overview of the importance of a good working relationship between IACUCs and animal scientists to ensure successful research programs that use agricultural species in research and teaching by emphasizing importance of *Ag Guide*, development of species-specific SOPs derived from science-based data and approved by IACUC, and when issues need to be addressed that a subcommittee of experts are part of the decision making process. Animal scientists and IACUCs must work together to ensure the best care for farm animals used in research and teaching at their respective universities.

Key Words: animal care, research, welfare

0031 Applying AAALAC international's peer review program to support agricultural research programs.
J. Bradfield*, *AAALAC International, Frederick, MD.*

Agricultural animal research is arguably more important today than ever before. The challenge of providing food for the world's population in a sustainable, ethical manner is no small task. Public awareness regarding animal production is increasingly focused on humane treatment and methods, while at the same time there is a significant lack of understanding about production animals, their needs, and the best practices to rear and care for them. Institutions that engage in animal research and production must ensure that high standards of animal care and use are used both to meet expectations of society and to be ethical stewards of the animals with which we work. AAALAC International provides a third party, peer review of all facets of the animal care and use program that has proven to be an effective mechanism to ensure institutions meet the standards of the *Ag Guide*, undergo continuous improvement, and demonstrate institutional commitment to high standards of animal care and use. Data from 671 AAALAC site visits highlight the common challenges faced by animal care and use programs and provide information to aid those engaged in research animal program management. Findings data in each of the six main areas of the animal program will be provided: institutional commitment and resources, personnel expertise and training, husbandry and veterinary care, occupational health and safety, facilities, and effective oversight by the institutional animal care and use committee. An AAALAC review by peers who are experienced in agricultural animal research is collegial, confidential, and outcome-based. It is designed to help identify strengths and weaknesses of the program, with the aim of ensuring high quality scientific outcomes and a high level of animal welfare.

Key Words: AAALAC, review, welfare

0032 AAALAC international agricultural animal research program accreditation at Purdue University: "The good, the bad, and the ugly." J. S. Radcliffe*, *Purdue University, West Lafayette, IN.*

Admittedly, most production animal researchers at Purdue where scared when Purdue decided to move forward with AAALAC International Agricultural Animal Research Program accreditation. Two main concerns dominated: (1) How would AAALAC deal with the unique issues of animals in a production setting versus a laboratory setting? And (2) Would AAALAC accreditation interfere with our research? Particular emphasis was placed on cost of accreditation in terms of making or keeping programs compliant, facility maintenance, enhanced workload on researchers, and the possibility of excessive or "unnecessary" oversight. As we navigated through the accreditation process, we found that expense was manageable and, that if the program was well run, already it easily fit within the AAALAC guidelines and, if improvements were needed, it helped to have the need for accreditation as the reason to force the necessary improvements. We also found that AAALAC itself was willing to have open discussions about issues specific to production animal research and work with Purdue to create solutions to any issues. Today, AAALAC accreditation and maintenance of our accreditation status allows Purdue to promote and advertise our high standards for research and animal care across all species, demonstrate our commitment to public accountability, lobby the university for continuous improvement, and market our accreditation to federal and industry funding sources.

Key Words: AAALAC accreditation, Purdue, welfare

ADSA PRODUCTION DIVISION SYMPOSIUM: ROBOTIC DAIRYING: ADAPTING FARM AND BUSINESS MANAGEMENT

0033 Changes in dairy farm management strategies with the adoption of robotic milking. J. Rodenburg*, *DairyLogix, Woodstock, ON, Canada.*

Adoption of robotic milking on dairies of up to 250 cows is improving the lifestyle of dairy families, and it is an effective way to reduce labor in herds of all sizes. Since milking is voluntary, and feed delivered during milking is the main enticer for attendance, feeding strategies that offer palatable pelleted concentrate in the milking stations, combined with low starch mixed feeds or forage at the feed fence, improve milking frequency and production. Barn layouts that encourage low-stress access by providing adequate open space near the milking stations and escape routes for waiting cows also improve milking frequency and reduce the number of cows requiring fetching. Lame cows present themselves less often for milking and produce less milk. Preventing lameness with comfortable stalls, clean alley floors, and effective foot bathing and treatment protocols is given greater emphasis on robotic dairies. Variable milking times create challenges for foot bathing, sorting and handling, and dealing with special-needs cows. These challenges must be addressed with appropriate cow routing and separation options at the milking stations, if the expected labor savings are to be realized. With less work, all protocols and the layout and gating of the barn should make it possible to complete handling tasks alone. Unattended milking demands reliance on sensors to monitor health and performance; but this, along with computer control of milking intervals and feeding levels, creates new opportunities to manage cows individually. Much of the potential to improve the productivity, health, and longevity of dairy cows, and to decrease feed costs through combining the use of sensor data with individual feeding and milking, is as yet unrealized. Free traffic and guided traffic systems have been adopted, and results are similar when excellent management is applied. In less-ideal circumstances, guided traffic and the use of commitment pens results in long standing times and stress, particularly for lower-ranking cows, while poor management with free traffic results in more labor for fetching nonattending cows. Robotic dairies require a smaller labor force than conventional dairies, but function best with skilled workers than can perform a variety of tasks.

Key Words: automatic milking, robotic milking

0034 Opportunities and challenges for herd health and reproduction with robotic milking. S. J. LeBlanc*, *Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

There has been a rapid increase in the number of herds with automatic milking systems (AMS). This technology is a well-established means to harvest milk from cows. Robotic milking offers potential advantages in labor per cow, increased milking frequency, and integration of sensors and data collection that assist with estrus detection, and might help with detection of health problems or lameness. Activity monitoring (AM) systems (in AMS or parlor-milked freestall barns) have been shown to produce, on average, comparable herd pregnancy rates to alternative approaches to reproductive management. However, AM requires supplemental interventions for timely AI for approximately 20% of inseminations. AMS provide streams of a variety of data on activity, milking frequency and timing, quarter-level milk yield, and conductivity, and the daily cow-level variation in these metrics. The systematic collection of these data offers the promise of detection of some health problems earlier and with less variation. However, selection of valid, actionable indicators of health from

AMS data remains a work in progress, and a balancing act of adequate detection and false alerts. As with conventional systems, the associations of AMS with cow health, welfare, and performance are confounded by their human managers. There is little data on measures of health with AMS. More research is needed on the predictive value of indicators of mastitis from AMS. Research on approaches to and outcomes of treatment of mastitis with AMS-based detection is lacking. Reports indicate a similar prevalence of lameness to non-AMS freestall barns, with similar stall- and bedding-related factors associated with lameness, injuries, and lying time. Processing of multiple data inputs, mostly related to cow activity and milking performance, has been shown to have reasonable accuracy for detection of lameness, which if successfully implemented, would likely be earlier and more thorough. Preliminary data indicate a higher prevalence of ketosis in herds with AMS. Feeding behavior is generally driven by feed delivery as in non-AMS barns, such that feeding space requirements are similar. Timely detection of metabolic disease such as ketosis may be aided but not replaced by AMS-derived data, and detection of reproductive disease still requires daily observation of the cows by skilled people; pen design and cow handling equipment are needed to facilitate interactions with the cows.

Key Words: health, disease detection, precision technology

0035 Nutritional approaches in robotic herds.

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Cows in herds equipped with conventional milking parlor systems follow a structured, consistent, and social milking and feeding routine. Furthermore, in most cases, cows in these systems receive all their nutrients from a TMR, whereas in herds equipped with robotic or automatic milking systems (AMS), cows receive a fraction of their nutrients during milking, mainly as a means to attract them to the milking system. In this regards, the AMS presents both a challenge and an opportunity for feeding cows. The main challenge resides in maintaining a minimum and relatively constant milking frequency in AMS. Hover, milking frequency is dependent on many factors, including the social structure of the herd, the farm layout design, the type of traffic imposed to cows, the type of flooring, the health status of the cow (especially lameness, but also mastitis, metritis, etc.), the stage of lactation, the parity, and the type of ration fed at the feed bunk and the concentrate offered in the AMS. Uneven milk frequency has been associated with milk losses and increased risk of mastitis, but most importantly, with a lost opportunity for milking the cow. On the other hand, the opportunity from AMS resides in the possibility of milking more frequently, and feeding cows more precisely or closely to their nutrient needs (in an individual basis), potentially resulting in a more profitable production system. However, feeding cows in the parlor or AMS has many challenges by itself. On one side, feeding starchy, high-palatable ingredients, may upset rumen fermentation or alter feeding behavior after milking, and feeding high-fiber concentrates may compromise total energy intake and ultimately milking performance. Nevertheless, AMS (and some milking parlors, especially rotary ones) offer the possibility of feeding the cows to their estimated individual nutrient needs with the aim of maximizing profits (rather than milk yield). This approach requires that not only the amount of feed offered, but also the composition of the feed for each individual cow need to change according to the nutrient needs. The change in composition can be achieved by combining several feed ingredients or concentrates on real-time as the cow enter the AMS (or the milking parlor). This review discusses the opportunities and pitfalls of milking and feeding cows in an AMS and summarizes different feeding strategies to maximize profits by managing the nutrition of the cows individually.

Key Words: modeling, precision feeding, optimization

0036 Finances and returns for robotic dairies.

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Automatic or robotic milking systems (AMS) are being adopted by dairy producers at a relatively fast rate. Previous studies of the economic returns of AMS compared with parlor milking systems (PMS) are scarce and offer mixed results mostly because of the assumptions used by the researchers. The key parameters that affected these results pertained to the costs and economic life of AMS, and the prospect of the AMS to increase milk production and decrease labor. Another key factor affecting profitability of AMS is milk production per AMS milking unit. Increasing average milk flow rate and reducing milking preparation time, along with increasing the percentage of milking box occupation time, has been shown to increase milk production per AMS unit. The nonfinancial lifestyle improvement factor is another consideration that influences the decision to install an AMS. We developed a simulation model to compare the economics of alternative milking systems under current Minnesota conditions. As an example, for a 120-cow operation currently switch milking in a tiestall barn, the most profitable alternative is to build a new freestall barn and install a retrofit PMS (double 8) in the old building. A new PMS is slightly less profitable because of the higher cost of investment. Another factor affecting profitability in our model is how much money is spent on the freestall barn. Many AMS freestall barns constructed in cold climates are warm barns and have expensive manure handling systems (slatted floors or automatic scrapers). An AMS is less profitable than a PMS under those circumstances, if milking and chore labor is valued at $15/h. It would require a labor rate of around $50/hour to make the AMS and PMS equally profitable. Including inflation in labor rate also increases the

profitability of AMS systems compared with PMS because of the labor saved. If the barn is equipped more like a typical parlor operation, an AMS may be similar to a PMS in profitability. Those results assume a labor reduction and a milk production increase with the AMS compared with the PMS. Surveys have shown that most farmers are happy with the decision to install AMS. Much of the satisfaction is not based on economic returns, but on improved lifestyle. Maximizing milk per robot by optimizing cow numbers and milking speed, along with improved labor efficiency and increased milk production per cow, will maximize dairy farm returns.

Key Words: automatic milking systems, profitability

ADSA-SAD (STUDENT AFFILIATE DIVISION) UNDERGRADUATE STUDENT ORAL COMPETITION: DAIRY FOODS

0037 Milk is milk, isn't it? J. M. Madigan* and S. P. Washburn, *North Carolina State University, Raleigh.*

This paper examines the differences in beverages from almonds or soybeans compared with milk from cows. There are some people that argue plant-based beverages hold the same nutritional aspects as milk and are overall better for the consumer. Through examination of multiple research papers on cow-based milk and plant-based "milk" products, discussion and analysis of potential benefits and limitations of each product is examined. One key point of analysis is that soymilk was shown to reduce cholesterol (Meyer et al., 2004), but in another study showed no effect even with increased isoflavone in samples taken (Onuegbu et al., 2011). Almond milk seemed to cause hyperoxaluria and genitourinary disorders in children due to richness in oxalate, though showed to be a good option for lactose intolerant individuals (Ellis and Lieb, 2015). Though almond based beverages can be an alternative for lactose intolerant people, NC State University's Department of Food, Bioprocessing, and Nutrition discovered that the use of *Lactobacillus acidophilus* bacteria can help make milk acceptable to lactose intolerant individuals (Sanders and Klaenhammer, 2001). A study also showed that people who consumed cow milk more than once a day had a lower likelihood to have type 2 diabetes (Morcillo et al., 2012). A key nutrient, protein, was shown to be lacking in almond milk, which has less than 1 g per cup vs. 2% milk with 8 g per cup (USDA). Milk is also a better source for essential fatty acids than either soymilk or almond milk (USDA, nutritiondata.self.com). From the data collected over multiple studies and databases, a conclusion is reached that, though plant based "milk" products such as beverages made from almonds and soybeans have some nutritional promise, they have a difficult time replacing milk from a cow.

Key Words: milk, milk substitutes, nutrition

0038 Health benefits of *Lactobacillus helveticus* in dairy foods. C. Kenny*, *Louisiana State University, Baton Rouge.*

Lactic acid bacteria (LAB) are often used as a starter culture in the production of cheeses. These LAB produce biopeptides by breaking down proteins in milk that have positive effects on the functions of the body. One specific LAB, *Lactobacillus helveticus,* which is used in the production of many Italian cheeses such as Swiss, Provolone, Mozzarella, and Parmesan, has many extremely valuable health benefits. *Lactobacillus helveticus* is able to survive after being eaten, and adheres to epithelial cells in the gastrointestinal tract. Because of this, *L. helveticus* can stimulate the digestive tract and reduce lactose intolerance, and inhibit the absorption of some pathogens while also increasing the absorption of certain nutrients. However, the two most valuable benefits of *L. helveticus* are its nontumorogenic and nonhypertensive properties. *Lactobacillus helveticus* has been shown in research studies to inhibit the growth of colon cancer cells and breast cancer cells in vivo. Because of these studies, *L. helveticus* is being considered to be a potential anticancer treatment. Further, *L. helveticus* is an angiotensin converting enzyme (ACE) Inhibitor, meaning that it prevents the release of Angiotensin II, which constricts blood vessels. This keeps blood vessels and the heart healthy, which prevents high blood pressure. From all angles of human health, *L. helveticus* has many benefits when consumed.

Key Words: lactic acid bacteria, cheese, health benefits

0039 A2 milk marketing and human health. J. Nystrom* and D. R. Winston, *Virginia Tech, Blacksburg.*

Although butter and cheese sales have been increasing over recent years, fluid milk sales have been declining in the United States since 1970. With declines in per capita milk consumption, and changes in the export market, the dairy industry has to be creative in developing products to increase milk sales. Recent products like Fairlife® ultra-filtered milk is an example of an innovative fluid milk product that demonstrates adaptability of the dairy industry to consumer preferences. In the U.K., Australia, New Zealand, and recently, California, A2 milk has been introduced as a functional dairy food. A2 milk contains a homozygous A2 β-casein protein, whereas conventional milk contains a heterozygous combination of A1 and A2 β-casein proteins. While A2 milk has been available in U.K. since 2012 and previously in New Zealand and Australia, it has just recently made its way to the U.S. markets. Research on digestibility of A2 milk is ongoing; however, the A2 Milk Company is a processor that only sells 100% A2 milk in New Zealand and also exports to the U.K., China, the United States, and Australia. In the first human trial of A2 versus A1 milk digestion, conducted by Ho et al., A2 and A1 milk was significantly higher in digestibility than A1 milk. Almost all cows have the A2 gene, but the majority have an A1/A2 combination. The

Guernsey breed naturally produces a higher percentage of A2 milk, which may create a new niche market and therefore increase demand for Guernseys nationwide. In conclusion, A2 β-casein milk is a new way to use genetics to create a niche market, potentially increasing sales of fluid milk nationwide.

Key Words: A2 milk

0040 Ultrasonic separation of milk to select for fat globule size distribution. S. P. Itle* and D. R. Olver, *Pennsylvania State University, University Park.*

The size of fat globules is important in manufacturing dairy products such as cheese and butter. Smaller fat globules result in a smooth texture and mouthfeel in cheese, while butter production better utilizes larger globule sizes. Although the cream separator is most commonly used in dairy processing operations to separate cream from milk, centrifugal technology is not commonly used for selecting for a specific fat globule size distribution. This is due to the complexity and nearly-perfect timing needed to control g-forces. Some artisan cheese producers have opted to utilize gravity separation to isolate smaller fat globules, but this process can take many hours while imposing a food safety risk. A new technology, ultrasonic separation, promises faster separation of fat globule fractions than gravity separation. This method utilizes sound waves that can rapidly separate the fat components of milk with a high specificity in globule sizes. In a recent Australian study, ultrasonic separation by dual transducers operating at 2 MHz achieved appreciable fractionation after 20 min and resulted in a 0.9 μm decrease in fat globule size.

Key Words: ultrasonic separation, dairy processing, fat globule fractionation

ADSA-SAD (STUDENT AFFILIATE DIVISION) UNDERGRADUATE STUDENT ORAL COMPETITION: DAIRY PRODUCTION

0041 Gene therapy and the prevention of mastitis in dairy cattle. K. Boudreaux*, *Louisiana State University, Baton Rouge.*

Mastitis in dairy cattle is an inflammation of the mammary gland and surrounding udder tissue, often an immune response to a pathogen invading the teat canal. It can also be a result of chemical, mechanical, or thermal injury to the udder. Mastitis can present clinically or subclinically, so routine testing and examinations are done to prevent the spread of infection. This infection is most often treated with antibiotics, but during antibiotic treatment, the cow's milk is not able to consumed or sold, because it contains antibiotic residues. It is an ongoing epidemic in the dairy industry, and monetary losses are accrued from the milk that must be disposed of due to antibiotic usage, reduction in milk yields due to permanent damage to the udder as a result of infection, labor costs to tend to infected cows, veterinary and medicinal costs, and in extreme cases, premature culling costs. Studies are being conducted to show that gene therapy may be a possible solution to prevent mastitis. Research has been done in an attempt to transfect the udders of dairy cattle with cercropin B, a lytic peptide found in Cercropia moths, that has broad spectrum bactericidal properties. This technology has been applied to other species through different experimental procedures and has yielded favorable outcomes and a decrease in targeted infectious diseases. The research with dairy cattle has not yet yielded favorable results, but with some experimental modifications, could be proven effective in preventing mastitis. This practice, once perfected, could be incorporated in routine dairy farm procedures, such as vaccine administration, and could reduce or eliminate antibiotic treatment of mastitis and reduce the losses of milk unable to be sold because of residual antibiotic contamination.

Key Words: gene therapy, mastitis, dairy cattle

0042 The importance of mastitis management practices in maintaining milk quality in the United States. K. Bochantin* and J. M. Bewley, *University of Kentucky, Lexington.*

Dairy producers strive to achieve optimal milk quality in an effort to provide the highest quality product possible to consumers. Milk quality is highly influenced by management practices used on farms. Poor milk quality may lead to decreased cheese yield and reduced shelf life for all dairy products. Measurements of milk quality include somatic cell count (SCC), bulk tank bacterial counts, antibiotic residues, and nutrient values. Lowered milk quality in certain regions of the United States within the past few years has caused some concerns within the industry, leading to renewed efforts toward improving milk quality. Such changes are centered on key management practices, including mastitis treatment and prevention. Mastitis is one of the most prevalent and costly diseases within the dairy industry, impacting both cows' health and milk quality. Awareness of the disease and its economic impact can increase motivations for change. Prevention of mastitis is key to management of the disease. Management of the environment (including housing and routine procedures) and cleanliness of the parlor can reduce the spread of mastitis-causing pathogens and decrease the risk of contamination. Housing and bedding should be kept clean and dry. In-parlor milking procedures, which include pre- and post-teat dip with proper germicides, can help remove existing bacteria from the udder and lower the risk of mastitis. Heifers are also at risk for mastitis and infection can lead to reduced milk yield during lactation. Prevention strategies include proper management, nutrition, and attention to prepartum udder health. Dry cows have a higher risk of mastitis infections than lactating cows.

Prevention of mastitis for dry cows at drying off includes treating all quarters with antibiotic products designed specifically for dry cow therapy. Vaccinations are also available to prevent against certain strains of mastitis-causing bacteria. Detection and awareness of mastitis is important for proper, timely treatment. Treatment methods can vary based on the severity of the case and can influence milk yield, quality, and overall cow health and performance. Dairy Herd Information Association (DHIA) records can help with somatic cell count management. Culturing of milk to determine bacteriological causes of mastitis can be useful for designing pathogen-specific prevention and treatment strategies.

Key Words: mastitis management, milk quality, United States

0043 The impact of amount and quality of colostrum and subsequent transition milk on calf health and growth. J. Hardy*[1], K. M. Daniels[2], and D. R. Winston[1], [1]*Virginia Tech, Blacksburg,* [2]*Virginia Polytechnic Institute and State University, Blacksburg.*

In the United States, the current "gold standard" is to deliver colostrum to newborn calves at 10% of BW within the first 2 h of life. In practice, many farmers simply offer calves 1.89 L of colostrum within 12 h of birth. For a 43 kg calf, this is about 4.5% of the calf's weight—not even half of the recommended amount. Colostrum ingestion is critical for passive transfer of immunity in the form of immunoglobulins (Ig). Researchers in Ireland examined the effects of feeding different volumes of colostrum (7, 8.5, or 10% of BW within 2 h of birth) and subsequent feedings (0, 2, or 4) of transition milk on serum IgG and health status. Ninety-nine calves were enrolled. They found that calves fed 8.5% of BW within 2 h of birth achieved the highest levels of IgG transfer. Following the initial feeding of colostrum, offering transition milk to calves appears to have positive impacts on calf health. Calves fed two or four subsequent feedings of transition milk seemed to have a lower risk of getting assigned poor nasal and eye scores (Conneely et al., 2014). The researchers were right to focus on measurement of serum IgG concentration in their project calves, as serum IgG is a major indicator of calf health because calves are born agammaglobulinemic. Therefore, when calf Ig measurements are obtained after consumption of colostrum, they reflect Ig content of colostrum and absorptive ability of the calf's small intestine. Colostral Ig absorption is highest in the first 24h of life and declines sharply; this has to do with permeability of the calf's small intestine to large molecules such as Ig. This process is termed passive transfer of immunity and it is key in protecting the calf against pathogens that the dam was previously exposed to, before the calf's own immune system maturing and becoming more functional (Godden, 2008). In conclusion, if colostrum quality is sufficient and calves are managed properly, calves seem to excel at 8.5% of their body weight at birth and when offered a few feedings of transition milk will have improved health and be less prone to disease in the first three to 4 wk of life (Conneely et al., 2014). For a 43 kg Holstein calf, this equates to 3.66 L of colostrum.

Key Words: dairy calf, immunoglobulin

0044 A future for genomics in animal health through the Bovine Respiratory Disease Complex: Coordinated Agricultural Project. S. J. Thomsen* and J. F. Bohlen, *University of Georgia, Athens.*

Whether through animal welfare and antibiotic residual concerns from the public, or the Veterinary Feed Directive, antibiotic use in animal agriculture is increasingly scrutinized and restricted. As such, it is essential for the future of the dairy industry to consider options to reduce the prevalence of disease on farm with new technology while decreasing their dependence on antibiotics. The 5-yr Bovine Respiratory Disease Complex: Coordinated Agricultural Project (BRD:-CAP) funded by the USDA and formed with the help of several universities, scientists and agriculturalists is searching to find new methods of addressing Bovine Respiratory Disease (BRD). Once determining that BRD has moderate heritability at 0.21, the goal of the BRDC:CAP is to utilize new genetic technology and the bovine genome to determine genetic markers for the susceptibility and resistance of Bovine Respiratory Disease and consider the financial impact of BRD genetic selection. Despite increased knowledge regarding BRD and progress in vaccine and preventative technology, BRD continues to be a financial liability of over $692 million dollars to the industry and contributes to 46% of the deaths among weaned calves, while having long-term influences of animal performance and health for affected individuals. Understanding the science behind BRDC:CAP will provide a gateway to analyzing the practicality of such genetic research on the farm. This may provide for its inclusion as a single selection criterion or as part of an index, such as Net Merit, for a sire proof. With this genetic selection for reduction in BRD incidence rates, the average dairy producer could see reduction in financial costs from treatment, calf mortality, and the resulting implications poor heifer development will have on future lactation performance. Continued work is necessary to ascertain the reliability and usefulness of genomics with regards to infectious diseases such as BRD. Increased farm profitability may be realized with proven ability to practically apply this information to the dairy industry.

Key Words: genomics, bovine respiratory disease, farm profitability

0045 Breeding for strength may create frail cows.
A. N. Gabel* and C. D. Decho, *The Pennsylvania State University, University Park.*

The Purebred Dairy Cattle Association Dairy Cow Unified Scorecard assigns 25% of weight to the dairy strength category, which is described as "a combination of dairyness and strength that supports sustained production and longevity." Stronger cattle are assumed by many breeders to have longer herd-life, but data from several studies suggest otherwise. In a 2003 study, relative culling risks (RCR) were assigned based on strength scores (1 = weak to 50 = strong) from 268,008 Jersey cows. A score of 25 equated to a RCR of 1.00. RCR values below or above 1.00 indicated low or high culling risks, respectively. Scores from 11 to 20 were optimal, whereas cows with a score of 41 to 45 were at most risk of being culled (RCR = 1.30). A similar analysis was performed in a study of 891,524 Holstein cows (Caraviello et. al., 2003; 2004), and strength scores higher than 25 were associated with significantly elevated RCR. These two studies indicate that "stronger" cattle have greater culling risk, which may partially be attributed to unfavorable associations with disease. Genetic correlations of strength with displaced abomasum, ketosis, mastitis, and cystic ovaries indicated that selection for strength would elevate disease risks (Zwald et. al., 2004). A 2015 analysis (Dechow) compared chest width and body condition score (BCS) in Canadian Holstein genetic evaluations with the Canadian dairy strength trait and U.S. productive life (PL) and daughter pregnancy rate (DPR). In this study, 527 bulls with Canadian and U.S. daughters were divided into groups based on chest width and BCS. Sires that transmitted wide chests and low BCS had the highest dairy strength scores (+9.5), followed by wide chest and average BCS sires (+6.5). These groups had the lowest PL (–2.5 and –1.6 mo, respectively) and DPR (–2.75% and –1.6%, respectively). In contrast, sires that transmitted narrow chests and high BCS scored lowest for dairy strength (–5.5), highest for PL (+1.1 mo), and highest for DPR (+0.4%). Therefore, high scores for strength suggest decreased longevity and reproductive efficiency. This counterintuitive relationship of dairy strength with health and survival may result from poorly defined measures of strength in linear scoring programs; cows with extremely low BCS have minimal muscle mass but are still considered to have high dairy strength if they have a wide skeletal system. Dairy producers should take caution when breeding for strength.

Key Words: strength, longevity, genetics

0046 The links between uterine infection and infertility.
N. Walker*, *University of Florida, Gainesville.*

The objective of this presentation is to explain the impact that uterine infections have on female reproductive fertility and dairy production. Uterine infections such as metritis and endometritis are prevalent among Holsteins primarily after parturition. Anatomical barriers act as a natural defense against bacterial pathogens, but during parturition these barriers are compromised. While these infections can be treated, they pose lasting negative effects on fertility. *Escherichia coli* and *Trueperella pyogenes* are the most common pathogens that cause uterine infections. These pathogens initiate an inflammatory response in the endocrine signaling system, the endometrium, and the ovaries. The inflammatory responses in these organs, coupled with innate immunity, can overload the female reproductive tract and lead to infertility. It is not known why reproductive fertility is compromised even after the uterine infection is treated. Further research is needed to better understand the exact mechanisms that lead to infertility. When those mechanisms are discovered, there is a potential to intervene before fertility is compromised. There are also current developments for metritis vaccines to prevent uterine infections. Until further advancements are made in those areas, implementing good management practices such as nutrition and hygiene during partition are feasible solutions.

Key Words: cow, immunity, fertility, infection, uterus

ADSA-SAD (STUDENT AFFILIATE DIVISION) UNDERGRADUATE STUDENT ORAL COMPETITION: ORIGINAL RESEARCH

0047 Comparison of calving data among Jersey, Jersey × Holstein crosses, and Norwegian Red × Holstein × Jersey crosses.
S. M. Royal*, K. A. E. Mullen, and S. P. Washburn, *North Carolina State University, Raleigh.*

The dairy at the Center for Environmental Farming Systems (CEFS) has been a pasture-based herd of Holstein (H), Jersey (J), and crosses of those breeds, but now is transitioning into three breed groups: Group A includes pure J and mostly J being bred to become pure Jerseys; Group B includes a two-way criss-cross of H and J breeds by alternating sire breeds each generation; whereas Group C is a three-way rotational cross with Norwegian Red (NR) introduced as the third breed in 2014. The objective of the study is to examine differences in calving characteristics among breed groups across two calving years. Groups included: A (83 calves, J sires), Bh (48 calves, H sires), Bj (60 calves, J sires), and C (94 calves, NR sires), respectively. Breed group ($P < 0.05$), interaction of parity × calving year ($P < 0.01$), and the three-way interaction (breed group × parity × year; $P < 0.05$) significantly affected gestation length. Least squares means for birth weight for groups A, Bj, Bh, and C, respectively were: 26.8 kg ± 0.5 kg, 27.7 kg ± 0.7 kg, 32.9 kg ± 0.7 kg, and 34.5 kg ± 0.5 kg. Parity ($P < 0.001$), breed group ($P < 0.001$), and calf gender ($P < 0.001$) all affected birth weight. Multiparous cows had heavier calves than first parity cows ($P < 0.001$). Group C calves were heavier

than Group Bj ($P < 0.001$) and Group A ($P < 0.001$) calves. Group Bh calves were also heavier than Group A calves. Male calves weighed more than female calves ($P < 0.001$). Breed group was associated with calving difficulty ($P < 0.05$). Cows delivering NR crossbred calves had more difficulty than cows having Group Bj calves ($P < 0.05$). Based on current data and earlier studies, use of either NR or H sires results in heavier birth weights and potentially more challenges at calving.

Key Words: crossbreeding, gestation, calving

0048 Effects of a low moisture block supplement on cow distribution and time budget. A. J. DiGennaro*, A. R. Lee, B. A. Wadsworth, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this study was to compare the visitation effects of cows between a low moisture block supplement barrel (LMB; Buffer-lyx®, Ridley Block Operations, Flemingsburg, KY) and an empty control barrel (ECB). The study was conducted in two freestall pens ($n = 40$ and $n = 43$) at the University of Kentucky Coldstream Dairy from January 21, 2015 to February 25, 2015. Both LMB and ECB were placed in low traffic areas in the pens. All cows were exposed to a 7 d acclimation period with an ECB, an initial 14 d period with either LMB or ECB (P1), a 7 d washout period with ECB, and a second 14 d period of the opposite treatment (P2). Cows receiving LMB followed by ECB were characterized as treatment control (TC) and cows receiving ECB followed by LMB were characterized as control treatment (CT). Time spent around the barrels was measured using SmartBow (MKW Electronics, Jutogasse, Austria), an eartag based real-time location system. Smartbow recorded per second XY coordinate data to calculate cow location within the housing facility in h/d. When a cow entered or exited the 3 m radius around either barrel, a start or stop time was recorded. All collected data was analyzed using a mixed linear model performed with the MIXED procedure of SAS 9.3 (SAS Institute, Inc., Cary, NC). Cows spent more time around the LMB than the ECB (16.49 ± 1.57 and 4.98 ± 1.62 min, $P < 0.01$). Period (P1: 15.68 ± 1.62 and P2: 5.78 ± 1.57 min, $P < 0.01$) and sequence (TC: 19.79 ± 1.84 and CT: 1.67 ± 1.82 min, $P < 0.01$) effects were also observed. Period and sequence effects may be attributed to inclement weather during P2 or cows becoming conditioned to expect the ECB. Strategic placement of LMB appears to modify dairy cattle movement and behavior in a freestall setting. Dairy farmers may consider the use of LMB to entice cows toward an automated milking system.

Key Words: low moisture block, real-time location system

0049 The influence of age and weaning on the structure of the gastrointestinal epithelium in Holstein bull calves. S. I. Pletts*, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The objective of this study was to characterize how age and weaning influence structural adaptations of the gastrointestinal tract (GIT) in calves. Tissues from the GIT were taken from 21 Holstein bull calves that were randomly assigned to 1 of 3 treatments: preweaned calves sampled at d 16 (PRE; $n = 7$); weaned calves sampled at d 42 (WN; $n = 7$); and control calves sampled at d 42 (CON; $n = 7$). A step down weaning approach was used (from d 35 to d 42 of life), while CON calves were not weaned. Histological analysis was performed on the rumen, duodenum, jejunum, ileum, proximal and distal colon, and the cecum. Tissues were processed and fully imaged under 40×, and minimum of 10 images under 100×. Measurements were taken of rumen sloughing, papillae dimensions, crypt depth throughout the small intestines, mucosal width in the hindgut, and goblet cell counts in all intestinal compartments. Treatments were compared using the mixed procedure in the statistical analysis system. Weaning effects were most notable in the rumen and duodenum: rumen sloughing scores were highest ($P < 0.01$) in WN (2.64 ± 0.25) relative to CON (1.50 ± 0.25) and PRE (1.51 ± 0.25); duodenal villi length was longer ($P = 0.02$) in CON (356.5μm ± 32.67) than in WN (218.9μm ± 32.67). Crypt depths were consistently deeper ($P < 0.01$) for duodenum, jejunum, proximal, and distal colon of PRE calves compared with CON and WN. Mucosa thickness in the hindgut compartments was greater ($P < 0.01$) in the PRE group. There were no treatment differences on goblet cell count except in the proximal colon, with PRE (0.08 ± 0.01) having less ($P < 0.01$) goblet cells in 100μm^2 than WN (0.15 ± 0.01) and CON (0.15 ± 0.01). These data suggest that during weaning there is significant structural alteration in the rumen and intestine. The most notable differences were detected in the rumen and the beginning of the small and large intestine. Future research is needed to assess the functional adaptation of the entire GIT, and how these adaptations may relate to calf health and performance.

Key Words: GIT, weaning, histology

0050 Effects of supplementing a commercial blend of anaerobic probiotic bacteria, MBiotix Calf, on the growth and health of preweaned and immediately postweaned Holstein calves. R. E. Hudson*, Y. Liang, T. L. Harris, K. P. Sharon, and M. A. Ballou, *Texas Tech University, Lubbock, TX.*

The objectives of these studies were to determine the effects of supplementing a blend of anaerobic bacteria on the growth and health of preweaned and immediately postweaned Holstein calves. Holstein calves within 1 d of birth were randomly

assigned to 1 of 2 dietary treatments ($N = 35$). Treatments included a negative Control and MBiotix Calf (BTX) treatment, which was administered in the milk replacer and top-dressed on the starter during the preweaned and immediately postweaned periods, respectively. The BTX treatment dose was 2×10^9 CFU/d of a proprietary blend of *Lactobacillus casei* and *Enterococcus faecium* strains; however, during the first 3 d of the study, the BTX calves were given a 10× dose. The study was conducted in 3 periods ($n = 20$ Control and $n = 15$ BTX). Calves were individually housed and fed between 250 and 350 g depending on the period of a 22% CP and 20% fat milk replacer twice daily at 0730 and 1630. Calves had ad libitum access to a calf starter and water. Calves were individually housed until they were weaned at 56 d when they were grouped by treatment for an additional 28 d. Peripheral blood samples were collected on d 0, 7, 21, 56, 70, and 84, and analyzed for hematology. Data were analyzed as a repeated measures ANOVA with treatment, time, and treatment × time as the fixed effects and period as a random effect. Calf nested within treatment was the subject of the repeated statement. Data are reported as Control vs. BTX, respectively. There was a treatment × time interaction ($P = 0.001$) on calf starter intake during the preweaned period, whereas BTX calves began to consume more starter during the fourth week of life, and the difference in starter intake was different ($P \leq 0.05$) during the sixth to eighth week of life. BTX calves were consuming more starter at weaning (1.065 vs. 1.305 ± 0.141 kg/d; $P = 0.025$). Further, the BTX calves had greater ADG during the 84 d observation period (0.701 vs. 0.883 ± 0.079 kg/d; $P = 0.016$). There were no treatment or treatment × time effects on hematocrit percentage (34.3 vs. 35.9 ± 1.98%; $P \geq 0.235$). Further, there were no treatment or treatment × time effects ($P \geq 0.178$) on any hematological variable. These data indicated that supplementing MBiotix Calf improved calf starter intake and average daily gain during the preweaned and immediate postweaned periods.

Key Words: calf, health, nutrition, probiotic

0051 Assessing the correlation between teat end scores and presence of mastitis in lactating Holstein cows. K. J. Alward*, J. F. Bohlen, L. O. Ely, and S. C. Nickerson, *University of Georgia, Athens.*

Mastitis is an inflammation of the mammary gland caused by bacteria that affects one in every three cows, and costs the producer an average of $180/cow/year. Penetration of bacteria into the teat canal causing mastitic infections may be enhanced by hyperkeratosis, a thickening of the teat canal keratin, which provides a breeding ground for bacteria. The objective of this project was to determine if a correlation exists between elevated teat end scores (degree of hyperkeratosis) and presence of mastitis as indicated by elevated somatic cell counts (SCC). Purebred Holstein cows ($n = 30$) were assessed and sampled between 30 and 100 d in milk. Each animal was given a teat end score (TES) at sampling on a scale of 1 (smooth) to 4 (rough ring) according to level of severity, and teat canal swabs as well as milk samples were collected aseptically from each quarter for microbiological examination to determine infection status and, if infected, the pathogen(s) present. All milk samples were further evaluated for SCC using a DeLaval Cell Counter. The association of TES, infection status, and SCC was analyzed using the CORR procedure of SAS. A strong positive correlation was seen between level of infection and SCC for each quarter ($P = 0.001$) and for TES and age of the cow ($P = 0.001$). The average TES for uninfected quarters was 2.00, while the average TES for infected quarters was 2.42. However, there was no correlation between presence of infection and TES ($P = 0.444$) or SCC and TES ($P = 0.439$). When infected quarters were compared for pathogen and average TES, the following observations were made: CNS (TES = 1.9), *Streptococcus* (TES = 2.), *Prototheca* (TES = 2.0), *S. aureus* (TES = 2.6), mold (TES = 3.0) and *E. coli* (TES = 3.0). While no correlation was found for the presence of infection and teat end scores, the observation regarding the presence of specific mastitis causing bacteria and elevated teat end scores is an area for future investigation. This observation also suggests that teat end hyperkeratosis is associated with presence of mastitis caused by certain pathogens and that management practices should be in place to promote healthy teat ends for decreased mastitis incidence rates.

Key Words: hyperkeratosis, somatic cell count, mastitis pathogens

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0052 Evaluating the effects of heat stress on rumen pH and temperature. L. Beckett*, R. R. White, and M. D. Hanigan, *Virginia Tech, Blacksburg.*

As the climate changes, heat stress is becoming an increasing concern for heavily utilized agriculture assets like dairy cattle. The goal of this study is to evaluate the effects of ambient temperature change on ruminal pH and temperature. The study was conducted using eight Holstein heifers (250 kg) housed in climate-controlled rooms (four heifers per room). Heifers were housed at a thermoneutral (20°C) temperature for 2 wk after which room temperature was raised to 30°C. Measurements were taken with a ruminal pH and temperature bolus that was manually inserted into the reticulum through a rumen cannula. Each bolus wirelessly transmitted ruminal pH and temperature every 10 min for the duration of the study. Response variables included: hourly mean, minimum, and maximum pH; proportion of hourly time spent below 5.5 or 5.75; and mean, minimum, and maximum rumen temperature. Data was used from 2 d prior and 2 d after changing the ambient temperature to specifically assess this temperature transition. A mixed-effect model was used to evaluate the data with fixed effects for group (heat stress; HS; or thermoneutral; TN), period (thermoneutral, P1; stressed, P2), and group by period interaction and a random effect for cow. The results

Table 0052.

Table 1. Mean and significance of differences between group and periods

Response[1]	Group 1		Group 2		*P*-Values		
	P1 (20 °C)	P2 (30 °C)	P1 (20 °C)	P2 (20 °C)	Group	Period	Group x Period
Time Below 5.5, h/h	0.06	0.01	0.13	<0.01	0.662	0.067	0.418
Time Below 5.75, h/h	0.25	0.07	0.29	0.16	0.560	0.074	0.778
Min. pH	6.16	6.09	6.25	6.23	0.010	0.055	0.266
Mean pH	6.28	6.20	6.36	6.34	0.077	0.004	0.053
Max. pH	6.40	6.30	6.47	6.45	0.060	<0.001	0.005
Max. T, °C	39.7	39.7	39.5	39.4	0.019	0.044	0.165
Mean T, °C	39.5	39.4	39.3	39.2	0.101	0.010	0.310
Min. T, °C	39.2	39.1	39.1	38.9	0.384	0.057	0.241

[1]Response variables included minimum (min.), mean, and maximum (max.) pH and temperature (T; °C), proportion of time pH was below 5.5 and 5.75 (hour/hour).

are summarized in Table 1. The significance of the group by period interaction for mean ($P = 0.053$) and maximum ($P = 0.005$) pH demonstrates that that heat stress lowers average rumen pH by reducing the height of pH peaks occurring in between digestion events. However, this pH shift is not associated with decreases in minimum pH or a change in time spent below cutoff pH values ($P > 0.05$). Further work must be conducted to evaluate what effects this pH shift has on rumen fermentation kinetics during heat stress.

Key Words: heat stress, rumen pH, rumen temperature

ADSA-SAD (STUDENT AFFILIATE DIVISION) UNDERGRADUATE STUDENT POSTER COMPETITION

0053 Validation of a commercially available β-hydroxybutyrate meter for assessing rumen development in dairy calves. M. A. Richard*[1], C. C. Williams[2], R. M. Orellana[1], S. J. Blair[1], and A. H. Dolejsiova[2], [1]*Louisiana State University, Baton Rouge,* [2]*Louisiana State University AgCenter, Baton Rouge.*

Previous research has shown that glucometers used for testing blood glucose levels in humans are accurate for testing blood glucose in dairy calves and cows. Ketone monitors have been developed for assessment of ketoacidosis in human diabetics. Both acetoacetatic acid and β-hydroxybutyric acid (BHBA) are classified as ketones, but BHBA is the metabolite of interest when assessing rumen development. The Abbot Precision Xtra meter measures BHBA in whole blood. Thus, this instrument would be beneficial from both a basic and applied standpoint in dairy calf nutrition and management. The objective of this experiment was to validate the use of a commercially available hand held β-hydroxybutyrate meter for assessing rumen development in young dairy calves. Blood was collected from 24 Holstein calves at the LSU Dairy Farm via jugular venipuncture during weeks 2, 4, 6, 8, 10, and 12 for analysis of BHBA. Blood was immediately tested for BHBA concentrations using the Abbot Precision Xtra meter. The remainder of each sample was separated and frozen until analyzed for BHBA using a commercial spectrophotometric kit. The BHBA concentrations obtained with the Abbot Precision Xtra meter were strongly correlated with overall plasma BHBA concentrations. Correlations were good when monitoring BHBA concentrations in different age groups. The meter values were not accurate when compared with plasma BHBA concentrations. Beta-hydroxybutyrate meters can be useful tools for monitoring changes in blood ketone concentrations but are not accurate for use in research data collection.

Key Words: β-hydroxybutyrate, dairy calves, ketone monitors

0054 The effect of the liquid nitrogen level on the temperature in a semen storage tank. A. Hale*[1], A. Ahmadzadeh[1], B. Shafii[1], and J. Dalton[2], [1]*University of Idaho, Moscow,* [2]*University of Idaho, Caldwell.*

The temperature in semen storage tanks is critical to maintain the viability of semen stored within the tanks. The objective was to investigate the effect of liquid N level on the temperature in a semen storage tank. Using an electronic thermometer, semen tank temperature was measured at three locations: (a) 2 cm below the top of the neck, (b) 7 cm below the top of the neck (below the frost line), and (c) 2 cm above the level of liquid N. Liquid N volume in the tank was incrementally decreased from 45 to 19 L. The experiment was repeated twice, and temperatures at each location and N level were recorded four times. The data on the effects of N level, location, and two-way interaction on the tank's temperature were analyzed using a general linear mixed model and procedure GLIMMIX in SAS. There was an effect of location and volume by location interaction on tank temperature ($P < 0.01$). Mean tank temperature was greater ($P < 0.01$) 2 cm below the top of the neck as compared with 7 cm below the top of the neck (below the frost line; 6.3 ± 0.1°C vs. –38.4 ± 0.3°C). Results showed that the

effect of liquid N volume on tank temperature was not consistent across locations. As N levels decreased, the temperature gradient remained above 0°C and did not change at 2 cm below the top of the neck. However, as liquid N level decreased, the temperature gradient increased ($P < 0.05$; from –41 ± 1 to –36 ± 1°C) at 7 cm below the top of the neck (below the frost line). Similarly, as N levels decreased, the temperature gradient increased ($P < 0.05$; –187 ± 0.3 to –185 ± 0.3°C) at 2 cm above the level of liquid N. Based on covariance parameters estimated, the temperature gradient below the frost line in the neck of the tank demonstrated the most variability. Data provide evidence of an increase in temperature gradient at 7 cm below the top of the neck (below the frost line) as the liquid N level decreases over time. Therefore, as liquid N level in the tank decreases, removal of semen straws should be done efficiently, to preserve semen viability via minimization of semen exposure to increased temperatures in the neck of the tank.

Key Words: semen storage tank, nitrogen level, temperature gradient

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0055 Evaluating the effects of a sodium hypochlorite post milking teat disinfectant on teat condition using a split udder trial. N. Lind*, *University of Kentucky, Lexington.*

The objective of this study was to compare the effects of sodium hypochlorite, DX 648, (GEA Farm Technologies, Naperville, Illinois) and 1% iodine postmilking teat disinfectants on teat condition. Sixty-two primiparous and multiparous lactating Holstein cows averaging 209.63 ± 128.12 d in milk, from the University of Kentucky Coldstream Dairy Farm, were included in an 8-wk study from 27 Nov. 2015 to 21 Jan. 2016. A split udder trial was used to control for cow effects and maximize the number of experimental units. The teats on the left side of the udder were dipped in DX 648 while the teats on the right side were dipped in iodine. All teats were dipped using nonreturn dip cups. Teat end condition and teat skin condition were scored weekly after milking. Teat end condition was scored on a scale of 1 to 4 (1 = no ring, 2 = smooth or slightly rough ring, 3 = rough ring, and 4 = very rough ring). Teat skin condition was scored on a scale of 1 to 3 (1 = normal, 2 = dry, and 3 = rough). The MIXED procedure of SAS 9.4 was used to evaluate the fixed effects of week and teat dip on teat end and teat skin condition. Data was repeated by week with teat within cow as subject using a compound symmetry covariance structure. Teat skin condition scores were not significantly different ($P = 0.98$) between teats dipped with sodium hypochlorite (1.04 ± 0.01) and iodine (1.04 ± 0.01). Teat end condition scores were not significantly different ($P = 0.40$) between teats dipped with sodium hypochlorite (2.45 ± 0.05) and iodine (2.45 ± 0.05). The DX 648 teat dip performed similarly to iodine regarding teat end and teat skin condition, indicating that this dip may be used without adverse effects.

Key Words: postmilking teat dip, sodium hypochlorite, teat condition

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0056 The effect of ergothioneine-containing mushroom powder (MP) on sensory acceptability and probiotic survivability in yogurt. B. Blain, C. Boothroyd*, D. R. Roberts, and E. Furumoto, *The Pennsylvania State University, University Park.*

L-ergothioneine, produced by certain fungi and bacteria, is known to have protective effects for both microorganisms and humans due to nonoxidative capabilities. Commercial preparations of L-ergothioneine are derived from mushrooms and can also serve as a source of vitamin D. The objective of this work was to determine if addition of commercial mushroom powder (ErgoD2) could be used as a natural source of vitamin D and antioxidant in yogurt. To test this hypothesis, control and treatment probiotic-containing yogurts (composition: 12% milk solids nonfat, 0.5% milk fat, 3% sucrose) were produced in the Food Science Pilot plant. Mixes were homogenized at 2000 psi and pasteurized at 85°C for 30 min. Mushroom powder (2.5 mg/g ergothioneine) was added at 0.02% by weight to the treatment sample before pasteurization. The pH was monitored throughout fermentation and viable counts of *Streptococcus thermophilus*, *Lactobacillus delbrueckii* subsp. *bulgaricus*, and the probiotic *Bifidobacterium animalis* ssp. *lactis* Bb-12 were monitored at the beginning and end of fermentation. The pH of yogurt and probiotic survival were also monitored weekly for 5 wk. Hedonic liking and preference tests were conducted on both control and treatment products with 106 participants. Yogurt containing mushroom powder fermented at a similar rate to the control. Addition of mushroom powder did not affect growth of Bb-12, *S. thermophilus*, or *L. delbrueckii* subsp. *bulgaricus*. Although counts of Bb-12 decreased during storage, the rate of decline was similar in control and treatment yogurts throughout the 5 wk storage period. No significant differences were observed in acceptability between control and treatment products. Results suggest mushroom powder containing L-ergothonine and vitamin D could be used successfully in yogurt.

Key Words: ergothioneine, yogurt, probiotic

STRATEGIES FOR MANAGING HEIFERS IN THE SOUTHEAST

0057 Influences of feeding and housing practices on the behavior and performance of dairy calves.
E. K. Miller-Cushon*[1] and T. J. DeVries[2], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

Approaches to rearing replacement dairy heifers vary widely between farms across the Southeast, and the behavior and performance of the calf early in life is highly subject to management practices. There is also increasing evidence that early life environment and experiences can have longer-term effects on the performance and health of the growing heifer and mature cow. This presentation will review the current understanding of the short and longer-term behavioral and performance implications of early life management factors that may vary on-farm, including milk feeding method, solid feed provision, and social housing. First, on-farm milk-feeding levels typically range between conventional restricted feeding programs to free-access feeding. From a behavioral standpoint, milk feeding level influences milk meal frequency and diurnal patterns of feeding time before weaning. Early rate of weight gain is dependent on milk feeding level, and there is evidence that differences in performance may be maintained postweaning and have later benefits in life. A main goal of rearing replacement heifers is to wean them successfully from milk to solid feed, and early solid feed intake is critical for this transition. Solid feed types and presentation directly affect intake and feeding patterns, and there is evidence that feed experiences during the milk-feeding stage may have a longer-term influence on feeding behavior of weaned dairy calves. For example, postweaning feed sorting behavior appears to depend on feed preferences, which are formed by prior feed experiences, as well as an early opportunity to perform this behavior, as provided by access to a mixed diet. Finally, the housing environment can be highly influential in the social development of the calf and may also interact with feeding methods, having both immediate and longer-term effects on performance and behavior. Social contact has been demonstrated to be beneficial in encouraging early solid feed intake and supporting weight gain through weaning. Further, early social environment influences social development, and may have longer-term effects on the behavior of the calf. Group-housing facilities introduce the possibility of competition for feed access, and this may also influence the development of social and feeding behavior. The extent to which all of these early rearing factors may influence long-term behavioral development and performance into lactation remains largely unknown and requires further investigation.

Key Words: behavior, dairy calf, feeding

0058 Developing replacement heifers that get pregnant and maintain pregnancy.
K. G. Pohler*[1], M. H. Pereira[2], S. Reese[1], and J. L. M. Vasconcelos[3]. [1]*The University of Tennessee, Knoxville,* [2]*UNESP-FMVZ, Botucatu, Brazil,* [3]*Sao Paulo State University, Botucatu, Brazil.*

Reproductive failure is one of the most substantial barriers to profitability in dairy herds. Management issues, cow infertility, bull infertility, heat stress, embryonic mortality (EM), and poor heifer development are all contributing factors to reproductive inefficiency. Developing heifers that successfully establish and maintain a pregnancy, give birth to live offspring, and stay in the herd for a number of years is critical. In addition to proper selection of these heifers, minimizing reproductive inefficiency, specifically EM, is vital. Embryonic mortality is generally considered to be the primary factor limiting conception rates in cattle and occurs early (<d 25) or late (≥d 25) during gestation (d 0 = estrus). In cattle, the incidence of early EM is approximately 25% and the incidence of late EM is varied, approximately 3.2 to 42.7%. However, in heifers, these numbers are thought to be decreased but are still a major issue. Significant effort has been directed toward understanding the mechanisms resulting in early EM; however, relatively little is known about the causes or mechanisms associated with late EM, most of which occurs around the time of placentation. Mechanisms associated with reproductive loss around the time of placentation may be associated with inadequate placental development or function. Binucleate trophoblast cells constitute 15 to 20% of the ruminant placenta trophoblast population, appear around d 19 to 20 of gestation in cattle, and secrete pregnancy associated glycoproteins (PAGs), along with other products. Bovine PAGs are commonly used to diagnose pregnancy success in cattle and have recently been reported to be a potential marker of late EM in dairy cattle (Pohler et al., 2015). Based on positive and negative predicative value analysis, we have identified circulating concentrations of PAG that are 95% accurate in predicting EM at d 28 of gestation. This talk will highlight some of the work our group, as well as others, are focusing on with regard to selecting high fertility heifers, as well as management strategies to decrease reproductive loss in those heifers using PAG testing. In summary, based on the experiments and relevant literature, PAGs seem to be a good marker for predicting EM, but also may provide a useful tool for selection of high fertility heifers. Advancements in our understanding of the mechanisms associated with EM may lead to development of strategies to overcome these reproductive losses.

Key Words: cattle, pregnancy, placenta, embryonic mortality

0059 Benefits of fly control in dairy heifers.
S. C. Nickerson*, *University of Georgia, Athens.*

This presentation discusses the role of the horn fly (*Haematobia irritans*) in the initiation and spread of staphylococcal mastitis among dairy heifers, how this insect vector can be managed, and the benefits of control for animal health and well-being, as well as producer profits. The horn fly is an irritant to livestock, and in response to the incessant painful biting, blood sucking, and stress, cattle expend a great deal of energy in defensive behavior, resulting in elevated heart and respiratory rates, reduced grazing time, decreased feeding efficiency and rate of gain, and reduced milk production. Additionally, the horn fly can serve as a disease vector, such as in the initiation and spread of mastitis in dairy heifers. As such, it is one of the most economically important pests of cattle worldwide. In the United States, $700 M to $1 B in losses are attributed to the horn fly each year, while additional $60 M is spent annually on parasite control. Herd surveys have revealed that the prevalence of mastitis in heifers is markedly lower in dairy herds using some form of fly control compared with herds without a pest control program. The horn fly has a demonstrated role in the development of teat lesions on heifers that develop into chronic *Staphylococcus aureus* mastitis, which is then spread among heifers by these same insect vectors. Such infections, if left untreated, negatively affect the development of milk-producing tissues in the udder, resulting in less than optimal yield and quality during the first and subsequent lactations. The implementation of horn fly control measures such as aerosols, bait, strips, foggers, dust bags, traps, oilers, ear tags, pour-ons, natural predators, and insect growth regulators is instrumental in reducing the new infection rate, while existing mastitis cases can be eliminated with antibiotic therapy. Such management practices will promote animal health and well-being, as well as ensure that heifers calve with low SCC and the potential for maximum milk yield, thereby enhancing producer profits.

Key Words: horn fly, dairy heifer, staph mastitis

0060 Economic trade-offs between replacement rates and improved genetics.
A. De Vries*, *Department of Animal Sciences, University of Florida, Gainesville.*

Genetic progress in sires used for AI is rapidly increasing. This means that replacement heifers are increasingly much better genetically than cows. Economically, this should lead to increased voluntary culling and thereby decrease cow longevity. On the other hand, lower culling rates are often viewed favorably because the costs and environmental impact to maintain herd size are generally lower. Thus, there is an economic trade-off between genetic progress and longevity in dairy cattle. Objective was to investigate these trade-offs. USDA results show that the annual increase in average predicted transmitting ability (PTA) of Net Merit dollars of Holstein sires is accelerating from $20/yr when the sire entered AI in 2000 to 2004, to $52/yr in 2005 to 2009, to $86/yr in 2010 to 2014. We expect that heifers born in 2015 are about $50 more profitable per lactation than heifers born in 2014. An elegant but older study is from Allaire (1981). He found that the economically optimal cull rates were in the range of 25 to 27%, compared with the lowest possible cull rate of 20%. There was only a small effect of using the best surviving dams to generate the replacement heifer calves. Genetic progress from sires also had little effect. Using a spreadsheet model to determine genetic lag in Net Merit PTA between service sires and dams shows that increased cow cull rates reduce the genetic lag only marginally. The ratio of annual genetic trend in sires' PTA for Net Merit and genetic lag was 6.6, 7.7, 8.7, and 9.4% for the annual cull rates of 20, 30, 40, and 50%, independent of the magnitude in sire genetic trend. These results confirm the findings of Allaire (1981) that cow depreciation costs overwhelm the value of the genetic superiority of the replacement heifers. Van Arendonk (1985) showed that the effect of changes in genetic improvement in milk revenue minus feed cost on herd longevity was relatively small. Reduced involuntary cull rates improved profitability, but also increased optimal voluntary culling. Finally, an economic optimal culling model with prices from 2015 confirmed that optimal annual cull rates were insensitive to heifer prices and therefore insensitive to superior genetics in heifers. In conclusion, economic cow longevity depends more on the difference between heifer raising costs and cow cull prices than on genetic progress. This is confirmed by old and new studies.

Key Words: genetics, longevity, economics

ANIMAL BEHAVIOR AND WELL-BEING

0061 Utility of an online learning module for teaching disbudding in dairy calves, including cornual nerve block application.
C. B. Winder*[1], S. J. LeBlanc[2], D. B. Haley[2], K. D. Lissemore[1], M. A. Godkin[3], and T. F. Duffield[2], *[1]University of Guelph, Guelph, ON, Canada, [2]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [3]Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON, Canada.*

Although disbudding or dehorning dairy heifers is necessary for the safety of humans and other cattle, it has been identified as a key animal welfare issue when done without appropriate analgesia. Three-quarters of disbudding or dehorning is done by dairy producers or on-farm staff, the remainder is done by a veterinarian or veterinary technician. Reported use of pain control by dairy producers ranges from 15 to 60%. Cautery disbudding is the most commonly used method; best practices

include administration of a nonsteroidal noninflammatory drug (NSAID) and local anesthetic given as a cornual nerve block (CNB), which requires technical training. Teaching methods may involve one-on-one training with a veterinarian. As well, online training videos exist. To our knowledge, none of these methods have been studied for efficacy. Our objective was to determine if an interactive, online module could teach CNB application and cautery disbudding, as compared with hands-on training. Thirty-four student participants were assigned to either hands-on training or to self-directed online training. Assessments were performed by a blinded evaluator who examined knowledge, handling, CNB technique, disbudding technique, time taken, and self-confidence. Success of CNB was defined as a lack of pain-related behaviors during the first 5 s of disbudding iron application. The hands-on training group had no CNB failures, while online training had 25% CNB failures ($P = 0.13$). Online learners were significantly less confident ($P < 0.01$); had poorer handling ($P = 0.02$), CNB ($P = 0.05$), and disbudding ($P = 0.05$) technical skills; and took more time to perform all tasks ($P = 0.03$). Although online learning alone was surprisingly effective for a psychomotor skill, best practices should include hands-on training. Online learning alone may be appropriate for hard-to-reach populations, or as a preliminary step to hands-on training.

Key Words: calf, dehorn, pain control

0062 WS Grazing behavior and production characteristics among cows differing in residual feed intake while grazing late season Idaho rangeland. J. E. Sprinkle*[1,2], J. B. Taylor[3], P. E. Clark[4], M. C. Roberts-Lew[1], and J. B. Hall[1,2], *[1]University of Idaho Nancy M. Cummings Research, Extension Education Center, Carmen, [2]Department of Animal & Veterinary Sciences, University of Idaho, Moscow, [3]USDA, ARS, U.S. Sheep Experiment Station, Dubois, ID, [4]USDA, ARS, Northwest Watershed Management Research Unit, Boise, ID.*

The objectives were to determine if cows classified as either low- or high-residual feed intake (LRFI or HRFI) differed in BW, BCS, and winter grazing activity over time. Thirty Hereford × Angus (LRFI = 16; HRFI = 14) 2-yr-old cows grazed sagebrush-steppe for 78 d beginning 29 Sept. 2016. Body weight and BCS were collected before and after grazing. Five cows of each RFI classification were fitted with global-positioning-system (GPS) collars on 16 Nov. 2015, with data collection commencing 3 d later and continuing for 25 d in a 323 ha pasture. The GPS units collected location coordinates every 2 min, from which total daily travel was calculated. Visual counts for bite rate were obtained from collared cows over 8 d. Coordinate data, daily bite rate, BW, and BCS were analyzed as repeated measures using a mixed model, which included RFI group, day, and RFI group × day as fixed effects, and cow within RFI group as the random effect. Change in BW and BCS were analyzed by ANOVA, with RFI group as the main effect. Cow BCS and BW differed for both day ($P < 0.0001$) and day × RFI ($P < 0.05$). Body condition was less in LRFI cows at the beginning (5.8 ± 0.13 vs. 6.2 ± 0.14 BCS), but similar to HRFI at the end of the study (4.6 ± 0.13 vs. 4.6 ± 0.14). Body weight for the different RFI cows did not differ ($P = 0.1974$) before going to range. However, BW-change and BCS-change differed ($P = 0.05$) among RFI groups. Not only did the LRFI cows lose less BW (–50.0 ± 5.41 kg vs. –66.6 ± 5.78 kg) over the trial, they also were less variable with respect to BW loss. Cows did not differ ($P > 0.21$) by RFI for distance traveled or bite rate, but day was significant ($P < 0.0001$) with cows increasing bite rate as the season of year progressed (55.2 ± 5.63 bites/min for d 4 vs. 84.8 ± 5.32 bites/min for d 21) and increasing distance traveled as snow storms occurred. Although LRFI cows were leaner than HRFI cows at the commencement of the project, they loss less BW and functioned competitively in a late season rangeland environment.

Key Words: beef cattle, grazing behavior, rangeland, residual feed intake

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0063 Variability in feeding behavior between individual dairy cows fed under different levels of competition. R. E. Crossley*, A. Harlander, and T. J. DeVries. *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to investigate the effects of differing levels of competition for feed access on group-housed dairy cows and on the variation in feeding behavior between individuals within the group. We hypothesized that, as competition increases, (1) cows will consume feed faster and in larger meals, and (2) individuals within the group will experience greater variability in feed consumption patterns. Eighteen lactating Holstein dairy cows with average DIM of 77 ± 20 d and production of 46 ± 7 kg/d at the start of the trial, were divided into groups of three, and fed three times per day. Groups were exposed to each of three competition levels: high (3 cows: 1 feed bin), moderate (3 cows: 2 feed bins), and low (3 cows: 3 feed bins). Treatments were assigned in random order according to a modified Latin Square design and applied for 10 d. DMI and feeding behavior (feeding time, feeding rate, and meal patterns) for each cow were recorded using an automated feed intake system on d 6 to 10 of each period. Data were summarized by group and treatment period, and analyzed in a general linear mixed model. DMI (29.1 kg/d) was found to be similar ($P = 0.63$) across treatments. Increased competition resulted in a reduction in feeding time (low = 202.6, moderate = 194.9, high = 83.6 min/d; SED = 4.49; $P = 0.015$), especially following fresh feed delivery and milking. Rate of feed intake increased with greater competition (low = 0.16; moderate = 0.18; high = 0.20 kg DM/min; SED = 0.01; $P = 0.01$). Meal frequency (8 meals/d) and size (4.0 kg DM/meal) were unaffected by treatment ($P > 0.40$), while meal length increased

Table 0064.

Table 1. Probabilities of being lame for variables measured by precision dairy farming technologies.

Variable	Odds ratio	Standard Error	*P* - value
Lying time (increase by one hour)[1]	1.56	0.14	0.01
Rumination time (decrease by 30 minutes)[2]	1.25	0.04	0.02
Neck activity (decrease by 150 units)[3]	3.87	1.35	0.01
Reticulorumen temperature (increase by one degree)[4]	1.00	0.00	0.01
Milk yield (decrease by five kg)[5]	0.88	0.08	0.16

[1]Lying time was measured by an IceQube (IceRobotics, Edinburgh, Scotland)
[2]Rumination time was measured by an HR tag (SCR Engineers ltd., Netanya, Israel)
[3]Neck activity was measured by an HR tag (SCR Engineers ltd., Netanya, Israel)
[4]Reticulorumen temperature was measured by a DVM bolus (DVM Systems, LLC Boulder, CO)
[5]Milk yield was recorded by the Milkline Milpro P4C (Gariga di Podenzano, Italy) milking system

under high competition (low = 37.0; moderate = 36.6; high = 47.3 min/meal; SED = 3.7; $P = 0.046$). This was due to greater within-meal nonfeeding time, which at the high competition level, was approximately double that of the other treatment levels (low = 10.0; moderate = 10.8; high = 20.3 min/meal; SED = 2.3; $P = 0.008$). Analysis of individual within group variability, calculated as the daily SD of each group averaged across d 6 to 10, revealed treatment differences in variability of meal length (low = 12.0; moderate = 13.9; high = 29.0 min/meal; SED = 5.56; $P = 0.04$) and within-meal nonfeeding time (low = 6.4; moderate = 8.3; high = 21.5 min/meal; SED = 4.57; $P = 0.03$). These results suggest that at elevated competition levels, cows modify their feeding behavior to consume more feed in a shorter period of time and devote a large portion of their meal time toward waiting to gain feed access. Further, there is greater variability in meal patterns within groups at higher levels of competition for feed access.

Key Words: dairy cow, feeding behavior, competition, meal patterns

0064 Identification of lameness using lying time, rumination time, neck activity, reticulorumen temperature, and milk yield. B. A. Wadsworth*, A. Stone, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

Early identification and treatment of lameness can reduce pain and negative performance related to the disease. However, producers frequently misidentify lame cows; therefore, automatic identification of lame cows is needed. The objective of this study was to identify lame cows using precision dairy monitoring technologies. Cows ($n = 98$) were housed at the University of Kentucky Coldstream Dairy from 11 Jan. 2012 to 3 May 2013. Cows were equipped with an IceQube (IceRobotics, Edinburgh, Scotland) on their left rear leg, which measured daily lying time (LT), an HR tag (SCR Engineers ltd., Netanya, Israel) around their neck, which recorded daily rumination time (RUM) and neck activity (ACT), and a DVM bolus (DVM Systems, LLC Boulder, CO) that measured reticulorumen temperature (RETT). Milkline Milpro P4C (Gariga di Podenzano, Italy) milking system recorded daily milk yield (MY). Seasons were categorized as Season 1 (December, January, and February), Season 2 (March, April, and May), Season 3 (June, July, and August), and Season 4 (September, October, and November). Cow gait was assessed weekly using a one (sound cow) to five (severely lame cow) scale. General symmetry, tracking, spine curvature, head bob, speed, and abduction/adduction were scored individually. Final gait score was calculated as a weighted average of general symmetry (24.92%), tracking (20.38%), spine curvature (19.81%), head bob (13.77%), speed (13.12%), and abduction/adduction (8%). Cows that scored ≥ 2 overall were classified as lame. A generalized linear model using the GENMOD procedure in SAS (SAS Institute, Inc., Cary, NC) was used to evaluate the effects of parity, season, LT, RUM, ACT, RETT, and MY on overall gait scores and their two-way interactions. Stepwise backward elimination was used to remove nonsignificant interactions ($P \geq 0.05$). Variables associated with a probability of being lame were an increase in LT by 1 h, a decrease in RUM by 30 min, a

decrease in ACT by 150 units, and an increase in RETT by one degree (Table 1). Milk yield was not associated with a probability of being lame (Table 1). When identifying lameness, using precision dairy monitoring technologies that determine LT, RUM, ACT, or RETT may be useful.

Key Words: lameness, accelerometer, precision dairy farming, technology

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0065 Management and dimensions of footbaths on California dairies. M. Pineda* and N. Silva-del-Rio, *Veterinary Medicine and Research Center, University of California, Tulare.*

Lameness is a common disease found on dairies with important economic and animal welfare implications. Digital dermatitis is one of most common infectious causes of lameness. Footbaths (FB) are commonly used on California dairies to prevent infectious foot diseases. The objective of this study was to describe footbath dimensions and management practices on California. Twenty dairies located in the San Joaquin Valley of California were enrolled in the study. Herds ranged in size from 800 to 10,000 cows. The length, width, and depth of FB was measured. Information on the chemical composition of FB solutions and the frequency that fresh FB solutions were added was obtained through interviews with hoof trimmers and dairy managers. Data collected was entered into spreadsheets for data analysis (Microsoft Office Excel; 2010). Dairies had 1 to 4 FB per dairy (total 39). One dairy applied disinfectant FB solution with front and rear jets. On four dairies, prebaths were placed <30 cm from the FB. No information on frequency of FB use was obtained from one dairy. The frequency of new FB solution application was seven (n = 2), five (n = 6), four (n = 4), three (n = 5), or two (n = 1) days a week. Cows walked through the FB once (n = 12), twice (n = 6), or thrice (n = 1) a day. One dairy walked dry cows through a FB once a week. The maximum FB length was <1.5 (15%), 1.5 to <2.5 m (57%), 2.5 to <3 m (18%), or >3 m (10%). Width measures were <1 m (39%), 1 to <2 m (20%), and ≥2 m (41%). FB solution depth averaged 10 cm (range: 5.4 to 15 cm). Volume of chemical solution in FB averaged 339 L (range: 109 to 1095 L). Most FB (66%) contained between 150 and 500 L of solution. Disinfectant chemical solutions used on dairies were $CuSO_4$ (n = 3), $ZnSO_4$ (n = 2), or formaldehyde (n = 3). However, some dairies combined $CuSO_4$ and formaldehyde (n = 9), $CuSO_4$ and chlorine (n = 1), or $CuSO_4$ and glutaraldehyde (n = 1). On average, 921 cows (range: 185 to 2000 cows) walked through a FB solution before adding fresh solution. Across dairies there was a wide variation on design, dimensions, and management of FB. Further research is needed to establish the implications of various management practices and FB designs on hoof health.

Key Words: lameness, footbath, dairy cow

0066 History of management procedures and hierarchy in dairy cows. A. Butterworth[*1] and L. van Dijk[2], *[1]University of Bristol, Bristol, United Kingdom, [2]HAS Institute, Amsterdam, Amsterdam, the Netherlands.*

This study assessed social interactions between cows in a 186 lactating cow herd, split into high milk yield (<35 wk into milking) and a low milk yield (>35 wk into milking) groups. The shifting hierarchical behaviors of the cows over 20 d was observed through analysis of video. The objective was to determine whether cows with a higher history of management procedures associated with treatment for common mastitis, lameness, and dystokia, would be lower in rank in the social hierarchy, and show more fluctuation in rank, than cows with a low management procedure history. A still-image photo library of the cows in the herd was compiled so that every cow could be identified from video recordings. Cows were identified as being in a high management history group (HMG) or a low management history group (LMG) based on their electronic farm management record. For blind analysis, the categorization into low and high management groups was made after the video analysis had been completed. Cows were filmed at the feed barrier using 1080 p 50 fps GoProHero 4 cameras, each camera supported to give a stable image along the feed barrier. Activity and time budget analysis of individual cow interactions from the video images allowed dominant (+) and submissive (–) interactions between cows to be noted. No significant difference was found in the "average hierarchical rank" between cows in the HMG and the LMG (P = 0.330). Heifers did rank significantly lower than cows, for example, when comparing heifers to cows in their third lactation (P = 0.004). The LMG showed a higher variability (deviation in means score) in rank than the HMG. This pilot study may aid understanding of possible long-term effects of common dairy management procedures. With further development, this method could (a) inform steps to reduce long-term impacts of common procedures, and (b) utilize altered hierarchical behavior as a detection tool for cattle showing long-term deleterious effects of previous management procedures. Cows that had a higher history of management for common dairy cow conditions (lameness, mastitis, or dystokia) did not experience long-term effects on hierarchical behaviors during feeding. However, significant behavioral differences in groups based on age were detected.

Key Words: dairy cows, management, disease, hierarchical, behavior

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0067 Behavioral analysis and performance response of feedlot steers on concrete slats versus rubber slats. D. Wagner*, *Colorado State University, Fort Collins.*

Concrete slats as a flooring substrate pose welfare concerns for feedlot cattle. An alternative system includes overlying rubber mats that fit existing slats. In this series of trials, three

sets of 16 steers were housed on either concrete slats (CONC) or rubber-covered concrete slats (RUBBER) during their finishing period. Each trial had four pens of four steers each, with two pens per treatment. Animals were fed a finishing diet once per day, the room was held at 18.3°C with continuous illumination. Cattle DMI, ADG, G:F, weight, and carpus circumference were tracked for the duration of the finishing period, up to 128 d. Lying and standing duration behavior was also measured on each treatment. Cattle also had their blood sampled at regular intervals for complete blood count analysis. After slaughter, carcass characteristics and front limbs were collected for soft tissue and histological examination. For growth measurements and CBC panel data, with pen as the experimental unit, there were no treatment differences ($P > 0.05$). Carpal circumference was larger on CONC than on RUBBER as each trial progressed, and in particular, the left carpus increased at a faster rate on CONC. Lying and standing behavior differed between treatment groups: on CONC, cattle consistently had fewer lying bouts per day than steers on RUBBER; in Trial 1, the average number per day was 21.2 ± 1.3 on CONC and 25.1 ± 1.3 on RUBBER ($P = 0.0039$). In Trial 2, lying and standing duration behavior did not differ between treatments. The average number of lying bouts per 24 h period was 33.1 ± 2.2 and 39.2 ± 2.2 on CONC and RUBBER, respectively ($P = 0.0068$). In Trial 3, average number of lying bouts per 24 h period was 14.6 ± 1.4 on CONC and 21.3 ± 1.4 on RUBBER ($P < 0.0001$).The behavioral results in conjunction with the joint circumference results, indicate that cattle were experiencing a greater amount of discomfort in lying and standing transition phases. It is concluded that steers on RUBBER have a higher standard of welfare than cattle on CONC.

Key Words: cattle, joint, rubber, lying

0068 Effect of corral modification for humane livestock handling on cattle behavior and cortisol release.

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Most traditional corral facilities are designed and built without the use of animal welfare principles, and can cause stress and fear reactions. This experiment was conducted to evaluate the influence of modifications to transform traditional corral into humane livestock handling system in cattle behavior and serum cortisol. The corral modifications consisted of blocking vision when the worker stands inside the animal's flight zone, eliminating contrast of light and dark or shadows, and keeping the workers calm, not allowing them to scream or hit the animals during handling. Electric cattle prods were not permitted. A total of 382 Nellore steers, from 12 to 20 mo of age, from five different ranches were studied. First, the behavior of the animals in a traditional corral was evaluated. After corral modification and changing for calm handling procedures, the same animals returned (6 d later) for a second behavioral assessment. During restraining, before and after corral modifications, blood samples were collected from the jugular vein for analysis of serum cortisol. The cattle were evaluated using visual scores. Entry behavior (EB) into the restraint device was evaluated by observing whether the bovines walked, trotted, or ran. Chute temperament (CT) was assessed by considering whether the animal was very calm, calm, agitated, very agitated, or struggling to escape; and exit gait (EX) by observing whether the animal walked, trotted, or ran. After corral modification, cattle exhibited lower EB ($P < 0.0001$) and EX ($P < 0.0001$) and a higher proportion of animals was calm (CT-P < 0.0001) during restraining. The proportion of cattle that walked, trotted or ran was, respectively, 61.9, 30.4, and 7.7% for EB and 47.9, 36.9, and 13.4% for EX before corral modification, and 79.3, 16.8, and 3.9% for EB and 74.0, 19.7, and 6.3% for EX after corral modification. For CT, the proportion of very calm, calm, agitated, very agitated, and struggling to escape animals was 26.8, 36.6, 23.4, 12.1, and 4.2% before corral modification, and 48.1, 32.1, 15.1, 3.6, and 1.1% after corral modification, respectively. Serum cortisol levels were significantly lower ($P < 0.0001$) after corral modification. Mean serum cortisol was 47.87 mg/dL before corral modification and 32.49 mg/dL after corral modification. Good handling practices, corral reconstruction, blocking vision in specifics areas, and respecting the natural movement can reduce stress in cattle.

Key Words: cattle stress, good practice, welfare

0069 A preliminary examination of swine caretakers' perspectives for euthanasia technology and training.

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An observational study was performed to better understand swine caretaker attitudes and opinions about euthanasia methods in swine production. A questionnaire was developed for swine caretakers to document the following: (1) psychosocial aspects, such as moral stress and job satisfaction associated with euthanasia, (2) current use of euthanasia techniques, and (3) views on animal welfare. To gain insight on caretakers'

perspectives on the issues listed above, caretakers were asked to rank their personal opinions on these topics. A total of 2104 surveys were mailed between December 2014 and June 2015 to caretakers associated with four swine production companies in eight states. The return rate was 8.3% (n = 175), with 168 completed surveys used for analysis. Respondents included 115 male and 53 female caretakers, whose work experiences with pigs ranged from <1 to 55 yr. Sixty-seven percent of caretakers worked in swine breeding units, while the remainder worked in farrowing, nursery, grow finish units, or a combination of production cycle units. Odds ratio analyses were performed to examine the effects of gender on caretaker opinion and acceptance regarding euthanasia techniques. There were no differences between male and female caretakers regarding the acceptance of different euthanasia methods in suckling pigs ($P > 0.05$). A large percentage of caretakers agreed that it is important to have good skills for euthanasia, that they knew how to euthanize humanely, and that it is more humane to euthanize terminally ill pigs than to let them die (93, 95, and 95%, respectively). Male and female caretakers did not differ in their personal opinions about euthanizing pigs, speaking publicly about their job, or euthanasia preferences ($P > 0.05$). Forty-nine percent of caretakers were trained in euthanasia techniques within the last year, and 30% reported that they would like more training. Caretakers preferred to be trained on-farm, followed by the use of video, classroom setting with a trainer, and reading materials. Caretakers rated carbon dioxide more acceptable than the use of blunt force trauma for suckling pigs (70% and 37%, respectively). The current study suggests that swine caretakers agree that proper euthanasia techniques are important and male and female caretakers do not differ in perspectives concerning euthanasia technology and training.

Key Words: swine caretakers, caretaker attitudes, euthanasia, animal welfare

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0070 Slow doesn't win the race: Reduced energy diets did not improve sow articular cartilage.

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Sow lameness accounts for approximately 15% of culling, resulting in a decrease in productivity and welfare. Previous research in our laboratory has shown a high incidence of osteochondritic lesions in young sows. We hypothesized that decreasing the growth rate of sows would allow for proper formation of articular cartilage. The objectives of this study were to (1) quantify behavioral changes associated with the diet, and (2) prevent the development of osteochondritic lesions. Therefore, 70-d old gilts were placed on either a control diet (CON; n = 23) or a low energy diet (LOW; n = 24). The CON diet contained 3427 Kcal/kg ME. The LOW diet utilized wheat middling and soy hulls, and contained 2643 Kcal/kg ME, targeting 65 to 70% of growth. Both diets were available ad libitum from d 70 to 182. Gilts were fed LOW or CON diets in four 28 d phases, and were weighed at diet changes to calculate ADG and ADFI, which were 0.80 and 0.92 kg, respectively, for CON gilts and 0.61 and 1.06 kg, respectively, for LOW gilts. A G:F of 1.15 resulted for CON and 1.73 for LOW gilts. Behavioral observations were recorded monthly and included posture, activity, agonistic behavior, and vices. Joint samples were taken (CON = 9; LOW = 10) between d 182 to 361 and analyzed for damage. Joints were evaluated for number of lesions, lesion size, and received an articular cartilage score from 0 to 4, with 0 representing healthy cartilage and 4 representing severely lesioned cartilage. The LOW gilts spent more time standing ($P < 0.01$), sitting ($P < 0.01$), and feeding ($P < 0.01$). Overall, diet did not alter sham chewing ($P = 0.76$), nosing ($P = 0.11$), or tail biting ($P = 0.36$). Both LOW and CON gilts did not differ in the number of fights ($P = 0.67$); however, CON gilts spent less time fighting than LOW gilts ($P < 0.01$). Energy restricted feed did not decrease the lesion size or prevalence of lesions ($P > 0.10$). Older gilts had larger lesions on the proximal humerus ($P < 0.01$) and femur ($P < 0.01$) and the distal humerus ($P < 0.03$) and femur ($P < 0.04$) than younger gilts. An energy restricted diet is not a suitable solution to decrease fighting or to improve joint health in young sows.

Key Words: articular cartilage, energy restriction, sow longevity

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0071 WS Use of a human triaxial pedometer for measurement of sheep activity.

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The accuracy of a simple, human triaxial pedometer at measuring sheep steps at a walk was investigated. Adult ewes (n = 10) were subjected to a three week halter-training program, with the end result of ewes being able to walk for 100 m next to a handler with little or no resistant behavior. A triaxial pedometer was attached to the left hind leg. Ewes were led for 100 m and the number of steps reported by the pedometer was recorded. A handheld video camera was used to record each trip, and the visual step count of the ewe was determined from the video recording. Each ewe was led through this pattern twice, and the average of the pedometer and visual step count at 80 m was used for statistical analysis. A Wilcoxon signed rank test was used to compare the means of the pedometer and visual step counts, and a Pearson correlation was drawn. The means of the pedometer and visual step counts were statistically different ($P < 0.001$) and the correlation was negligible ($r = 0.03$). The simple triaxial pedometers overestimated the amount of steps each ewe made, and therefore, cannot be considered accurate at measuring sheep activity.

Key Words: sheep, activity, triaxial pedometer

0072 Cooling cows with soakers: Spray duration affects heat loss in dairy cattle. G. Tresoldi[*1], K. E. Schütz[2], C. B. Tucker[1], [1]*University of California, Davis,* [2]*AgResearch, Hamilton, New Zealand.*

Soakers reduce heat load in cattle. Determining appropriate spraying strategies (e.g., time on and off) may improve the efficiency of heat loss and water use. Our objective was to evaluate the effects of a single cycle of spray on evaporation time, the surrounding air temperature, and heat load responses in dairy cows. In a crossover design, five spray durations (0, 0.5, 1.5, 3, and 13 min; flow rate = 4.9 L/min) were tested in 15 Holstein cows (milk yield 38 ± 3 kg/d) and replicated on 3 d/treatment (15 d total/cow) when air temperature, humidity, and the combined index averaged 31 ± 3°C, 27 ± 10%, and 76 ± 2, respectively. Cows were restrained in shaded head gates at the feed bunk for up to 1.75 h. Respiration rate (RR), skin temperature on the shoulder (received direct spray) and upper leg (remained dry), and the air temperature surrounding the leg were measured immediately before and after the spray application (water temperature 30 ± 3°C), and every 3 min until their coat was dry (a proxy for evaporation time), as measured by water sensitive paper applied to the coat. Data were analyzed with mixed models using SAS. In contrast to 0 min, all treatments reduced skin temperature on the shoulder (range of mean ± SE: –1.1 to –4.4 ± 0.2°C; $P < 0.01$), whereas treatments ≥1.5 min reduced RR (range: –7 to –24 ± 2 breaths/min; $P \leq 0.04$), and the surrounding air temperature (range: –0.3 to –1.8 ± 0.0°C; $P < 0.01$). Only spraying for ≥3 min reduced the upper leg temperature (range: –0.1 to –0.6 ± 0.0°C; $P < 0.01$). In general, the magnitude of the changes described above increased as the longer spray was on ($P < 0.05$). The coat took slightly longer to dry when cows were sprayed for 13 min compared with ≤3 min (mean ± SE = 16 ± 0.6 vs. 14 ± 0.5 min, respectively; $P < 0.01$). Within this period, RR increased by 5 breaths/min regardless of treatment ($P = 0.75$). Cooling benefits, as well as changes in air temperature surrounding the leg, were more pronounced when water was sprayed for longer. Spray duration had a little effect on evaporation time, and no additional cooling was observed in this phase.

Key Words: sprinklers, heat stress, spray length

0073 Association between rumination behavior, milk yield, and milk composition in dairy cows kept on commercial farms. T. Miedema and T. J. DeVries*, *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

Automatic sensors are able to give an accurate indication of the duration of time that dairy cows spend ruminating, allowing for collection of rumination data on cows kept in commercial environments. The objective of this study was to associate rumination behavior with milk yield and milk composition for lactating dairy cows kept in commercial operations. In this study, 8 commercial dairy farms in Eastern Ontario, Canada, were recruited for participation. Selection criteria included: free-stall housing, parlor milking, >90 lactating cows in the herd, primarily have Holstein-Friesian genetics, participated in a DHI program, and fed a TMR. Chosen farms had a mean herd size of 187 cows (range: 95 to 419 cows), mean adjusted 305-d milk yield of 11,228 kg (range: 9787 to 13,006 kg), and a geometric mean annual bulk milk SCC of 162,000 cells/mL (range: 145,000 to 172,000 cells/mL). Rumination time for 30 cows/herd was monitored using an automated rumination monitoring system. In total, the rumination activity of 240 lactating Holstein cows (57 ± 29 DIM) was monitored for 6 d and associated, in a multivariable general linear mixed model, with their production data (as measured by the closest in time DHI test, on average ± 3.5 d from the day of rumination sensor placement), controlling for farm, parity, DIM, body condition score, and dietary (TMR) characteristics (nutrient content and particle size). Across cows, rumination time averaged 506 ± 85 min/d (mean ± SD), milk yield averaged 44.7 ± 10.2 kg/d, milk fat averaged 3.69 ± 0.54%, and milk protein averaged 2.97 ± 0.24%. Rumination time increased with cow parity ($P < 0.001$) and tended ($P = 0.09$) to be positively associated with the percentage of long particles (>19 mm) in the TMR fed to the cows (+10.0 ± 5.5 min/d rumination time per 5% increase in long particles). Milk yield increased with cow parity ($P < 0.001$), milking 3× vs. 2× (+4.5 ± 2.3 kg/d; $P = 0.05$), and was positively associated with rumination time (+0.2 ± 0.07 kg milk per 10 min increase in rumination time per d; $P = 0.01$). Rumination activity was not associated with milk fat content, and tended ($P = 0.08$) to be quadratically associated with milk protein content. In summary, the results of this study demonstrate that rumination time, as measured on lactating cows on commercial dairy farms, could indicative of milk yield; however, it showed less consistent association with milk components.

Key Words: rumination, behavior, dairy cow

0074 Lameness, productivity and cow behavior in dairy herds with automated milking systems. M. T. King[*1], E. A. Pajor[2], S. J. LeBlanc[3], and T. J. DeVries[1], [1]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*University of Calgary, Calgary, AB, Canada,* [3]*Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to evaluate how herd management, barn design, and lameness relate to productivity and cow behavior in herds with automated milking systems (AMS). We visited 41 AMS farms in Canada (Ontario: $n = 26$; Alberta: $n = 15$), averaging 105 ± 56 (mean ± SE) lactating cows and 2.2 ± 1.3 AMS units. Details of barn design, stocking density, and herd management were collected. At each farm, 40 cows

were gait scored (or 30% for herds > 130 cows) using a five-point numerical rating system (NRS; 1 = sound to 5 = lame). Cows were defined as clinically lame with NRS $\geq$ 3 (26.2 ± 13.0%) and severely lame with NRS $\geq$ 4 (2.2 ± 3.1%). For 6 d periods, we collected milking data from AMS units and lying data from electronic data loggers. Data were analyzed in multivariable mixed-effect linear regression models. At the herd level, an increase of 1 percentage point (p.p.) in the prevalence of severe lameness was associated with production losses of 0.6 kg of milk produced/cow/d ($P = 0.05$) and 32 kg milk harvested/AMS/d ($P = 0.03$), while each 10 p.p. increase in clinical lameness prevalence was associated with 0.1 fewer milkings/cow/d ($P = 0.05$). One additional cow/AMS unit was associated with 32 kg more milk harvested/AMS/d ($P < 0.001$), but also decreased milking frequency (–0.2 milkings/cow/d for each 10 additional cows/AMS; $P < 0.001$). Daily lying time was positively associated with the frequency of feed push-ups (+3 min/cow/d/push-up; $P = 0.05$) and negatively associated with the placement of neck rails from the rear curb of lying stalls, such that cows lied down less as neck rails were placed farther forward (–23 min/cow/d/10 cm; $P = 0.03$). Lying bouts (min/bout) were 12 min longer in deep-bedded stalls vs. mattresses ($P = 0.003$), and 5 min longer with each 10 p.p. increase in the prevalence of clinical lameness ($P = 0.001$). In a cow-level comparison (30 cows/farm) of lame (NRS $\geq$ 3: $n = 353$) and sound cows (NRS < 3: $n = 865$), lame cows were fetched more often ($P = 0.002$), produced 1.6 kg/d less milk ($P = 0.002$) in 0.3 fewer milkings/d ($P < 0.001$), and spent more time lying down (+38 min/d; $P < 0.001$) in longer bouts (+3.5 min/bout, $P = 0.03$). In conclusion, lameness is especially problematic for AMS herds, reducing productivity at the cow and herd level. Although few cows in our study were severely lame, producers need to identify and reduce clinical lameness. Widening lying stalls, providing deep-bedded stalls, and scraping alleys more frequently were factors associated with reduced lameness prevalence and are potential ways to optimize productivity in AMS herds.

Key Words: automated milking, dairy cow behavior, lameness

0075 Assessment of biomarkers of pain and daily activity patterns in lactating dairy cows diagnosed with clinical metritis.

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Postpartum uterine diseases such as clinical metritis (MET) are associated with substantial economic losses due to reduced milk yield, delayed time to conception, treatment costs, and increased culling and death rates. Furthermore, MET has been characterized by bovine veterinarians as a painful event and can be regarded as a welfare concern since it can be associated with systemic signs, such as fever, depression, loss of appetite, and visceral pain. The objectives of this study were to: (1) assess the circulating concentrations of substance P, and (2) daily activity patterns (i.e., lying and standing time) in lactating dairy cows diagnosed with MET. Lactating dairy cows ($n = 200$) from two commercial dairy herds were enrolled in the present study. Cows diagnosed with MET ($n = 100$) at 7 ± 3 d in milk (DIM) were matched according to parity and DIM to cows without MET (noMET; $n = 100$). On study d 1, MET was diagnosed (using a metricheck device) by the presence of watery, reddish, or brownish foul-smelling vaginal discharge; blood samples were collected for assessment of circulating concentration of substance P. In addition, on study d 1 activity monitors were placed on the hind leg of cows (MET; $n = 56$; noMET; $n = 56$) and were kept until study d 7. Cows showing any other signs of disease were not included in the study. Data were analyzed using the MIXED procedure of SAS. Cows with MET had higher ($P = 0.0004$) plasmatic concentrations of substance P when compared with noMET cows (MET = 72.44 pg/mL; noMET = 55.73 pg/mL). Furthermore, cows with MET tended to spend more time lying ($P = 0.06$; MET = 635.60 min/d; noMET = 603.02 min/d) and less time standing ($P = 0.06$; MET = 804.08 min/d; noMET = 837.25 min/d) than noMET cows. These findings provide evidence that circulating concentrations of substance P are increased, and activity is affected in lactating dairy cows diagnosed with MET.

Key Words: metritis, substance P, activity

0076 Effect of social feeding environment on the feeding behavior of dairy cows and their willingness to consume a novel feed.

G. Mainardes and T. J. DeVries*, *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

Social contact may improve the willingness of dairy cattle to consume a novel feed. To test the impact of social contact while feeding and the reaction of mature cows toward a novel feed, we compared (1) animals fed individually (Single) and (2) cows fed in side-by-side in social pairs (Pairs). It was hypothesized that animals feeding beside each other would show similar behavioral patterns to each other, and a greater willingness to consume a novel feed product compared with those fed individually. Twelve Holstein cows (parity = 3.3 ± 1.3; mean ± SD) were assigned to four groups of three animals (each with two cows fed beside each other in adjacent feed bins and 1 fed alone on her own feed bin). Two feed types were offered separately: a familiar food made up of a total mixed ration (TMR) and an unfamiliar 5 kg of chopped carrots topped with 6 kg of TMR (as-fed). Each group was observed for 10 d, each consisting of 3 periods: (1) 4 d of adaptation (only TMR); (2) d 5 to 7 the carrots were introduced to the Single cow and to 1 of the 2 cows eating in Pairs; and (3) from d 8 to 10, all three cows were fed carrots and TMR. Dry matter intake (DMI), feeding behavior, rumination time, and sorting activity were

monitored for each animal. Cow behavior was observed for an hour after each feed delivery. Data were summarized by cow and period and analyzed in a repeated measures general linear mixed model. No differences in DMI of TMR (27.1 kg/d) or carrots (0.09 kg/d) and feeding time (193.9 min/d) were found between any animal eating as a Single or in Pairs. However, the DMI of carrots increased from Period 2 to Period 3 (0.04 to 0.12 kg/d; $P = 0.03$). In Period 2, Paired animals (typically heifers or younger animals feeding socially) ate faster than the other cows (0.19 vs. 0.13 and 0.12 kg DM/min; $P = 0.05$). In period 2, Paired cows tended to select more for medium particles (106 vs. 102% of predicted intake; $P = 0.08$) and sorted to a greater extent against short (97 vs. 99%; $P = 0.02$) and fine fractions (89 vs. 97 and 96%; $P = 0.05$). Overall, the intake of carrots was very low in all treatments; however, animals consumed more carrots in the third period. These results suggest that the acceptance of novel food might increase with the length of exposure. It is also concluded that animals showed similar feeding behavioral patterns regardless of feeding situation.

Key Words: novel feed, dairy cow, social feeding

0077 Effects of acute and chronic heat stress on feed sorting behavior of lactating dairy cows.

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The objectives of this study were to assess the effects of acute and chronic exposure to heat stress on feed sorting of dairy cows. Lactating Holstein dairy cows ($n = 32$; parity = 2.8 ± 1.2; mean ± SD) were group-housed in a free stall barn and milked three times per day. Cows were fed individually using Calan gates and offered ad libitum access (target 20% orts) to TMR (containing on DM basis: 3.3% ryegrass hay, 16.5% ryegrass baleage, 24.7% corn silage, 11.1% brewers grains, 19.7% ground corn, 19.8% concentrate, and 4.9% protein/mineral supplement), provided once per day. Cows were divided into two groups (balanced by days in milk and parity) and, beginning at 186 ± 60 DIM, were exposed to either heat stress (HT; $n = 15$) conditions (average temperature-humidity index in barn: 77.6), or evaporative cooling (CL; $n = 17$), consisting of misters and fans over the freestall and feed bunks to alleviate heat stress. Data were collected during a 4 d baseline period (starting 18 d before treatment), and two 4 d experimental periods: starting at 10 d after implementing treatments (during acute heat stress for HT cows), and at 62 d after implementing treatments (chronic heat stress for HT cows). Fresh TMR and orts samples were collected daily from individual cows for particle size analysis. The particle size separator had three screens (19, 8, and 1.18 mm) and a bottom pan, resulting in four fractions (long, medium, short, fine). Sorting was calculated as the actual intake of each particle size fraction expressed as a percentage of the predicted intake of that fraction. Data were analyzed using a repeated measures general linear mixed model, with sorting during the baseline period included as a covariate. During both acute and chronic heat stress, HT cows sorted in favor of the long particle fraction to a greater extent than CL cows (105.0 vs. 100.6%; SE = 1.09, $P = 0.001$). Sorting of medium and short particles were subject to treatment by period interactions ($P < 0.006$): in the period of acute heat stress, HT cows sorted to a greater extent than CL cows against medium (86.5 vs. 93.0%; SE = 0.36; $P = 0.006$) and short particles (94.1 vs. 97.5; SE = 0.64; $P = 0.002$), whereas in the period of chronic heat stress, sorting of HT cows did not differ from CL cows ($P > 0.9$). These results suggest that exposure to heat stress influences feed sorting and that feed sorting may increase in response to acute heat stress.

Key Words: feed sorting, heat stress, lactating dairy cow

0078 In utero exposure to heat stress during late gestation has prolonged negative effects on activity patterns of dairy calves.

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Exposure to heat stress (HS) during the dry period not only negatively affects cow performance, but it also exerts carryover effects on postnatal performance of the calf. The objective of this experiment was to evaluate the health, responsiveness, and activity of heifer calves born to cows exposed to HS (provided only shade, $n = 13$) or cooling (CL, fans, soakers, and shade, $n = 9$) environmental conditions during the entire dry period (~56 d). On the day of calving, calves were fed 3.8 L of maternal (HS or CL) colostrum. Within 2.8 ± 2.6 h of birth, we scored suckling reflex (1–3; 1 = no suckling response, 3 = strong suckling response) and movement (1–3; 1 = not able to stand when prompted, 3 = stands promptly). Calves were housed in individual pens and provided pasteurized milk (6 L/d) and ad libitum access to grain and water, until weaning at 49 d. Activity was assessed during the first week of life (week 1), weaning (week 7), and the first week postweaning (week 8) using electronic data loggers (HOBO Pendant G data Logger, Onset computer corp., Pocasset, MA) attached to the left rear leg of the calf. Heifer health was monitored weekly from birth to weaning (heath score 1–5). Data were analyzed by time period in a general linear mixed model, with day as a repeated measure for activity data. All heifers were healthy through the duration of the experiment. At birth, the suckling reflex (1.8 vs. 2.1; SE = 0.24; $P = 0.33$) and movement score (2.42 vs. 2.33; SE = 0.18; $P = 0.69$) were similar for CL and HS calves, respectively. However, CL calves spent more time standing in the first week of life (303.6 vs. 254.3 min/d; SE = 9.6; $P < 0.001$) as a result of longer standing bouts (14.2 vs. 12.2 min/bout; SE = 0.55; $P = 0.006$). In weeks 7 and 8,

CL calves maintained greater total daily standing time (442.6 vs. 406.8 min/d; SE = 10.7; $P < 0.019$) and spent more time standing/bout (30.7 vs. 24.3 min/bout; SE = 1.2; $P < 0.001$). However, CL calves had less frequent standing bouts than HS calves (15.4 vs. 17.7 bouts/d; SE = 0.6; $P < 0.01$). These results suggest that in utero HS during late gestation can have prolonged negative effects on activity patterns of dairy calves.

Key Words: heat stress, calves, behavior

0079 Factors associated with the occurrence of stillborn calves. M. I. Chavez[*1], M. A. Mellado[2], E. Carrillo[3], and J. E. Garcia[2], *[1]Universidad Autonoma Agraria Antonio Narro, TORREON, Mexico, [2]Universidad Autonoma Agraria Antonio Narro, Saltillo, Mexico, [3]Instituto Tecnologico de Torreon, Torreon, Mexico.*

The aim of this study was to determine the prevalence of stillborns calves in nulliparous and pluriparous cows in the Laguna region, as well as the effect of the type of delivery, duration of pregnancy, occurrence of dystocia, use of sexed semen and sex of calf on the occurrence of stillborns calves. The study was conducted in a large dairy operation in Laguna region (26° N). A data set of both pluriparous and nulliparous Holstein cows (2010–2014) were collected, with a total of 22,996 births. The data were statistically analyzed with descriptive methods for determining the percentage of stillborns. Odds ratios were calculated using logistic regressions (PROC LOGISTIC of SAS) for risk factors that affect the occurrence of stillborns. The results showed that gestations > 279 d decreased the occurrence of stillborns (odd ratio = 0.07, CI = 0.5–0.8; $P < 0.004$). Male calves were six times more likely (95%CI = 4.6–7.9; $P < 0.001$) to be stillborn than females. Calves with birth weight at calving ≥39 kg were less likely to be stillborn (odd ratio = 0.02, 95% CI = 0.1 to 0.2; $P < 0.001$) than lighter calves at birth. Calves derived from sexed semen breedings were twice as likely to be stillborn (95% CI = 1.6–2.7; $P < 0.001$) than calves from conventional semen. Calves coming from dystocic parturition were twice as likely (95% CI = 1.4–2.9; $P < 0.001$) to be stillborn than calves coming from normal deliveries. It was concluded that all variables studied importantly influence the occurrence of stillborns, particularly, sex of the offspring.

Key Words: stillbirth, calves, dystocia

0080 Reducing heat stress in calf hutches using reflective covers: Optical properties and implications. T. H. Friend[*1] and L. Y. Carrillo[2], *[1]Texas A&M University, College Station, [2]NASA Johnson Space Center, Houston, TX.*

Previous research found that reflective hutch covers reduced ceiling, black globe, and air temperatures within polyethylene hutches, reduced panting, and tended to improve weight gain and calf health. This engineering study reports on the optical properties of materials that can be used to improve the comfort of calves housed in polyethylene calf hutches. The opaque materials were tested in the infrared and solar ranges to determine the efficiency of the surface to absorb radiation at the NASA Johnson Space Center's Thermal Design Branch, Materials Laboratory, in Houston, TX (NASA-JSC). A model was also developed by NASA-JSC to assess the relative impact of each material in terms of British Thermal Unit (BTU)/h. The price and longevity in on-farm testing indicated that a custom aluminized low-density 3-mil thick white and black polyethylene (LDPE) was the most promising material for optical testing. Samples were tested in triplicate (unless the first two tests were identical), and the results were averaged. The high absorptivity (83.8%) of solar radiation of the hutch (Table 1) indicates reflective coverings could be very useful in keeping calves cooler. The aluminized side of the white aluminized LDPE had a low solar absorptivity (16.3%), indicating it reflects 83.7% of the incident solar energy. The aluminized black LDPE has characteristics that indicate its potential to be useful during winter, with the aluminized side turned toward the calf. The NASA-JSC model found that the bare hutch absorbed 1959 BTU/h/m^2 while the aluminized white LDPE absorbed 893 BTU/h/m^2 at its surface, indicating its potential to reduce solar heating of the hutch. The black side of the aluminized black LDPE absorbed 5037 BTU/h/m^2, indicating potential to warm hutches during sunny days in the winter. The optical properties of the aluminized polyethylene helps explain the findings from prior hot weather trials and supports further research on its winter applications.

Table 0080.

Table 1. Mean percent absorptivity (range) in the infrared and solar spectrums for the materials tested.

Material tested	Infrared	Solar
Commonly used calf hutch	50.4 (0.6)	83.8 (1.3)
Aluminized side white LDPE	9.3 (2.8)	16.3 (0.8)
White side of Al LDPE	60.1 (3.8)	38.6 (0.9)
Aluminized side black LDPE	9.7 (0.6)	19.8 (0.4)
Black side of Al LDPE	85.5 (1.5)	94.3 (0.0)

Key Words: calf, hutch, heat stress

0081 Sprinkler system in a holding pen: Behavioral responses of dairy cows during the subsequent grazing. S. V. Matarazzo[*1], D. S. Mello[1], L. M. de Toledo[2], I. Arcaro Júnior[2], and S. A. D. A. Fernandes[3], *[1]State University of Santa Cruz, Ilhéus, BA, Brazil, [2]Animal Science Institute, Nova Odessa, SP, Brazil, [3]State University of Southwestern Bahia, Itapetinga, BA, Brazil.*

Our objective was to evaluate the effects of cooling systems in a holding pen and its effects on the behavioral responses of pasture-based dairy cow. The experiment was performed

during February and March, 2014. Thirty-six black and white Holstein cows (BW = 527 ± 49 kg) were used in a crossover design (6 × 3). The cows were divided into groups of two animals (n = 18 groups) and each group was acclimated for 3 d following 6 d of data collection (2 d/treatment). The treatments used were: (1) control: no cooling, (2) sprinkler with media flow (MF): 0.08 L of water/nozzle/min, and (3) Sprinkler with high flow (HF): 1.00 L of water/nozzle/min. The sprinkler cycle included 30 s of water spraying and 60 s turned off. Cows were milked twice daily (0630 h and 1430 h) and treatments were applied during 20 min before each milking. After the milking routine, dairy cows were allowed to graze as a single herd. Environmental variables air temperature (AT), relative humidity (RH), black globe temperature (BGT), temperature humidity index (THI), and heat load (HLI) were recorded in a holding pen, in a pastured area and under the natural shade present at the grazed area. The dairy behavior (posture, location, and activity) was monitored from 0800 to 1230 h and from 1530 to 1800 h every 10 min. Panting score (PS) was evaluated each 15 min. The difference in water flow used in sprinkler systems reduced (P < 0.01) HLI and THI in a holding pen. However, sprinkler systems did not change behavioral patterns of dairy cows on pasture. The lowest PS average occurred at 0800 h (0.04) and highest at 15 h (0.75). PS was positively correlated (ρ = 0.94) with the THI under the shade, and it was negatively associated with the time spend on the paddock (ρ = –0.63). Cows were observed 50% of the time in rest activity, followed by grazing activity (25%), rumination (14%), other activities (9%), and drinking water (2%). The HLI was negatively correlated (ρ = –0.82) with the percentage of time spent on grazing. Cows spent 89% under natural shade during the hottest hours. The results demonstrate which evaporative cooling system used in a holding pen has immediate and short-term effect on dairy cows.

Key Words: welfare, evaporative cooling, pasture-based system

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0082 Evaluation of alternative flooring surfaces for dairy goats. M. A. Sutherland*, G. L. Lowe, C. M. Ross, D. Rapp, and G. A. Zobel, *AgResearch, Hamilton, New Zealand.*

In New Zealand, dairy goats are predominantly housed on sawdust; however, previous studies suggest that goats may prefer alternative surfaces. Therefore, the aim of this study was to evaluate the effect of four different flooring types on goat behavior and cleanliness. At 6 mo of age, 32 female Saanan cross does (45.4 ± 6.10 kg) were restricted to one of four different flooring types for 10 d, then restricted to the other three surfaces (10 d per surface) using a Latin square design consisting of eight replicates (n = 4 goats per replicate). The four flooring types included sawdust (SW), metal slats/grating (MT), plastic slats (PL), and rubber matting (RB). Goats were then given free access to all four flooring types simultaneously for 48 h. Lying behavior and position in the pen were recorded for 24 h at the end of the free access period using camcorders and accelerometers. To assess goat cleanliness, swab samples were collected from the udder of two goats per replicate over the restriction period, and *Escherichia coli* counts were analyzed by the most probable number method. Data were analyzed by ANOVA and results are presented as least square means ± SE. At the end of the study, when given free access to all flooring types simultaneously, goats spent more (P < 0.005) time lying on RB (50 ± 4.5%) than PL (31 ± 4.5%), MT (8.6 ± 4.5%), or SW (9.7 ± 4.5%), and more (P < 0.005) time on PL than MT or SW. The same preference was shown for the standing surface (P < 0.05). The number of *E. coli* recovered from the udder was highest (P < 0.001) after goats were restricted on SW (median: 0.5 Log per cm^2; range: 0.1–1.0 Log per cm^2) than MT (median: 0.1 Log per cm^2; range: 0–1.0 Log), PL (median: 0 per cm^2; range: 0–0.2 Log per cm^2) or RB (median: 0 per cm^2; range: 0–2.1 Log per cm^2). These results suggest that goats had a preference for lying on RB and least preferred lying on MT and SW. In addition, RB appeared to be cleaner than SW. Therefore, it may be advantageous to provide dairy goats with RB lying surfaces, but further investigation into implementing this into commercial dairy goat housing facilities is needed.

Key Words: bacteriology, behavior, welfare

0083 Risk factors associated with lameness severity in feedlot cattle. S. Marti[1,2], E. D. Janzen[1], K. Orsel[1], M. J. Jelinski[3], L. C. Dorin[3], E. Pajor[1], J. K. Shearer[4], S. T. Millman[5], J. F. Coetzee[6], D. U. Thomson[7], and K. S. Schwartzkopf-Genswein*[2], *[1]University of Calgary, Calgary, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]Veterinary Agri-Health Services, Airdrie, AB, Canada, [4]Iowa State University, Ames, [5]Department of Veterinary Diagnostic & Production Animal Medicine, Iowa State University, Ames, [6]Pharmacology Analytical Support Team, Iowa State University College of Veterinary Medicine, Ames, [7]Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan.*

Lameness is of significant health, welfare, and economic concern in feedlot cattle. However, few studies have identified the risk factors associated with becoming lame or the severity of lameness. The objective of this study was to determine the relationship between animal, feedlot management, and environmental risk factors associated with lameness severity in feedlot cattle. Between 2013 and 2015, data on lame cattle was collected weekly from two large feedlots (>10,000 head) in Southern Alberta. Animal variables included sex, breed, days on feed (DOF), type of cattle, source, number of implants/vaccination, body weight (BW), body condition score (BCS),

rectal temperature, hide mud score, location of affected limb, salivary cortisol, and lameness diagnosis. Feedlot management variables included diet composition, frequency and time of feeding, pen and bunk space, group size, and location of the water. Finally, environmental variables included weather (minimum, maximum, average temperature, and temperature differential; relative humidity; THI, and precipitation), pen condition, pen mud depth, and season. Lameness severity was assessed in 1128 cattle using a five-point gait score: (1) Sound; (2) Mild: slightly abnormal gait and arches back when walking; (3) Moderate: stands and walks with arched back, head bob with short strides (4) Severe: (as described for score 3) with the addition of reduced weight bearing on affected limb and slow movement with frequent stops 5) Highly Severe: reluctant to move, bears no weight on affected limb. Animal, management and environmental risk factors were tested for collinearity and data were analyzed using a stepwise multiple logistic regression separately for each group of risk factors. Significant variables remaining in each model were combined and analyzed as described above. The F-to enter and F-to remove were set at 0.15 and 0.10, respectively. Animals lame in the fore limbs had greater ($P = 0.03$) lameness severity than those with hind limb lameness. Lameness severity increased ($P < 0.01$) by 0.4% for every 1 d increase in DOF. In addition, lameness severity increased ($P = 0.001$) with number of implants/vaccinations administered. Finally, cattle housed in pens with a mud depth greater than 5 cm had double ($P < 0.01$) the risk of becoming severely lame as those cattle housed in pens with a mud depth < 5 cm. To successfully reduce lameness in feedlots, interventions should be focused on reducing DOF, handling frequency and pen mud depth.

Key Words: lameness, beef, risk factors

0084 Assessment of acute pain during and after knife and band castration following a single dose of Meloxicam in 1-wk-old beef calves.

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Beef producers are often advised to castrate calves as early as possible to reduce pain associated with tissue damage. However, there has been no research to determine if 1-wk-old calves do not feel pain at the time of castration. The aim of this study was to assess the effects of a single dose of s.c. meloxicam (Metacam®, 0.5 mg/kg BW) immediately before castration on pain mitigation during and after castration in 1-wk-old beef calves. Seventy-two 1-wk-old Angus bull calves were randomly assigned to one of 6 treatments ($n = 12$): control (C), band (B), or surgical castration (S) without meloxicam; and control (CM), band (BM) or surgical castration (SM) with meloxicam. Data were collected on d –1 before castration, immediately before castration, 60, 90, 120 min and 1, 2, 3, and 7 d after castration, except for the visual analog score only obtained during castration. Physiological measures included salivary cortisol (SC), haptoglobin (HP), substance P (SP) and scrotal area temperature (SAT). Behavioral measures consisted of a visual analog score (VAS), hind limb stride length (SL) and daily lying and standing durations. None of the physiological or behavioral parameters assessed differed between calves castrated with or without pain medication. A time × treatment interaction ($P = 0.02$) was observed for SC, S and B calves had greater SC concentrations 60 min after castration compared with C calves, while B calves had greater concentrations compared with C calves 90 min after castration. A time × treatment interaction ($P = 0.01$) for SAT was observed; S calves had lower scrotal temperatures compared with C calves 60 min after castration, while S had lower temperatures compared with B, and S and B had lower temperatures compared with C 90 and 120 min after castration. A time × treatment interaction ($P < 0.01$) was also found where B calves had lower temperatures compared with C and S 1, 2, 3, and 7 d after castration. The VAS was greater ($P < 0.001$) in S than B calves, and in S and B compared with C calves. As expected, knife and band castrated calves exhibited more signs of acute pain compared with noncastrated controls; however, results suggest that subcutaneous Meloxicam administered immediately before band or knife castration did not eliminate behavioral or physiological indicators of acute pain or discomfort in 1-wk-old calves.

Key Words: castration, acute pain, beef, calf, cortisol, behavior

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0085 Effect of castration method and analgesia on inflammation and behavior in feedlot cattle.

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There is little agreement on the best castration method in feedlot cattle; a recent USDA survey reported 52.3 and 41.1% of bulls are surgically and band castrated, respectively, and analgesia may mitigate inflammatory pain associated with either method. Our objective was to determine the effect of castration timing (birth vs. feedlot entry), method (surgical vs. banding) and use of the analgesic meloxicam (MEL) on behavior and inflammation in feedlot cattle. This study was a randomized complete block design conducted over a 3-yr period. Single-source Angus × Hereford steer ($n = 42$) and bull ($n = 152$) calves were randomized at birth to one of five treatments arranged as a 2 × 2 + 1 factorial: (1) steers castrated near birth (CON), (2) bulls surgically castrated without MEL (SUR), (3) bulls surgically castrated with MEL (SUR+MEL), (4) bulls band castrated without MEL (BAN), and (5) bulls

band castrated with MEL (BAN+MEL). Upon feedlot arrival (d –10), animals were blocked by initial BW (224 ± 4.5 kg) and assigned randomly to treatment pens (n = 6). Oral MEL was administered at 1 mg/kg BW concurrent with castration on d 0. Blood samples were collected from a subset of animals (n = 5 animals/pen) on d 0, 0.25, 1, 4, 7, and 14 to determine haptoglobin (Hp) concentration, as a proxy for inflammation. On d –10, accelerometers were placed on the same subset of cattle to determine baseline and postcastration changes in behavior indicative of pain; activity variables (standing, steps, lying bouts, motion index) were continuously logged and averaged by d. There was a treatment × day interaction (P = 0.04), with SUR animals having the greatest (P < 0.01) concentration of Hp on d 1 and 4. Meloxicam administered during surgical castration reduced (P = 0.01) Hp concentration relative to SUR on d 1. Method of castration had contrasting effects on specific behavior variables. Relative to baseline, standing duration for surgical castration increased 113 min (P < 0.01), while banding caused 6.7 more lying bouts (P < 0.01) immediately following castration on d 0. Steps were increased on d 0 for banded (2723), intermediate for CON (2216), and least (1801 steps) for surgical (P < 0.01). Results suggest that MEL mitigated the more pronounced inflammation observed for surgical castration; whereas, behavior was differentially altered for castration method indicative of a divergent pain response.

Key Words: analgesia, beef cattle, castration

0086 A systematic review-meta-analysis of castration and welfare indicators in beef cattle.

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To quantify the effects of castration in male beef cattle on welfare indicators based on cortisol concentration, average daily gain (ADG) and vocalization, a systematic review and meta-analysis were performed. We searched on five electronic databases (CAB Abstracts, ISI Web of Science, PubMed, Agricola, and Scopus) from January 1900 to May 2015 and included conference proceedings and electronically contacted experts, and also checked references of relevant review papers. Inclusion criteria were complete studies using beef cattle until 1 yr of age undergoing castration that analyzed cortisol level, ADG, or vocalization. Data were extracted using predefined protocols. The included documents were written in English, Spanish, Portuguese, or Italian. Random effect meta-analyses were conducted for each indicator separately with the mean of control and treated group. Possible influences of study characteristics and quality were assessed in meta-regression analyses. A total of 18 prospective publications reporting 23 studies and 156 trials were included in the MA involving 1617 animals. Significant between studies heterogeneity was observed for MA results when analyzing cortisol and ADG. Regardless the control group and the castration technique, the comparison analyses showed no changes ($P \geq 0.05$) changes on cortisol levels when castration was performed without drug administration. We found no evidence ($P \geq 0.05$) for multimodal therapy in decrease cortisol concentration 30 min after surgical procedure. Anesthesia tended to decrease cortisol level (MD = 0.411 nmol/L; P = 0.077; 95% CI: –0.868, 0.045) 120 min after surgical castration compared with castrated group without drug administration. Random-effect meta-analysis suggested an increase in ADG in surgical (MD = 0.231 g/d; P = 0.010; 95% CI: 0.056, 0.405) and nonsurgical castration (MD = 0.883 g/d; P < 0.001; 95% CI: 0.313, 1.453) with no pain mitigation in comparison to uncastrated cattle. Publication bias was observed when cortisol was studied as an outcome, indicating that small size studies reporting nonsignificant effect were less likely to be published than similar studies with significant effect. In a meta-regression, only publication type contributed to the total variation (18.52%) when the outcome evaluated was ADG. The vocalization score presented data in a manner that was not suitable to MA. Our MA study demonstrates an inconclusive result to draw recommendations on preferred castration practices to minimize pain in beef cattle.

Key Words: animal welfare, cattle, cortisol, pain, vocalization, weight

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0087 Blocking the steer's view of people during restraint in a squeeze chute results in calmer behavior.

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The aim of this study was to evaluate if facility design influences cattle behavior. Two types of systems were compared: open sides (OP) or solid wall (SW). To meet the objectives of this study, cattle were assessed at nine feedyards, according to the BQA Feedyard Assessment (FA) guidelines for cattle handling in commercial feedlots. Each bovine was observed once during and after vaccination processing. Four-hundred steers, from five feedyards were observed in the OP design, and 380 steers, from four feedyards were observed in SW. The variables recorded were vocalization, miscaught (MH), exit gait (run, trot, or walk) and exit behavior (jump, stumble, and fall). The statistics model for analyses included two factors: facility design (SWxOP), and feedyard. The SW design reduced vocalization (P = 0.0003) and had no effect for MH (P = 0.3158). From observed animals, respectively for OP and SW, 41.5% and 26.3% vocalized and 1.6% and 2.5% MH. There was effect on exit gait (P < 0.001) and on exit behavior

($P = 0.0008$). Steers processed in OP conditions exited faster than steers observed in the SW design, with 56.2 and 36.2% running and trotting for OP, and 23.2 and 66.9% running and trotting for SW, respectively. In conclusion, if the view of cattle is restricted during restraint, the frequency of vocalization will decrease, and exit speed will be reduced.

Key Words: cattle behavior, corral, feedyard

0088 Effect of different hydraulic squeeze chute and cattle breed on behavior of steer during restraining in feedyard facilities.

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The objective of this study was to investigate the relationship between hydraulic squeeze chute brand, breed of steers, and their behavior during processing in feedyard facilities. Two brands of hydraulic squeeze chute (A and B) and three breeds of cattle (Angus, Hereford and Continental cross) were compared. The assessments were made in 11 feedyards, totaling 1083 steers, using the BQA Feedyard Assessment (FA) guidelines for cattle handling in commercial feedlots. Each steer was observed once during and after the vaccination processing. Six feedyards had hydraulic squeeze chute (HSC) brand A (A) and eight feedyards had HSC brand B (B). The behavior variables of interest were vocalization, miscaught (MH), exit gait (run, trot or walk) and exit behavior (jump, stumble and fall). An effect of HSC brand on vocalization ($P < 0.0001$), exit gait ($P < 0.0001$) and exit behavior ($P < 0.0001$) was observed, but no effect on MH ($P = 0.52$) was observed. There was an effect of breed on vocalization ($P < 0.0001$), exit gait ($P < 0.001$) and exit behavior ($P < 0.0001$). The results for vocalization, run, trot, and jump were 25.8, 53.9, 40.4, and 14.4% for HSC A and 63.7, 42.5, 48.7, and 37.6% for HSC B, respectively. The results for vocalization, run, trot and jump were 15.1, 44.4, 47.5, and 29.4% for Angus; 2.7, 66.7, 28.8, and 17.8% for Hereford; and 22.2, 40.8, 50.7, and 31.8% for Continental cross, respectively. Brand of hydraulic squeeze chute and breed of cattle can influence the behavior of steers during and after restraining in feedyard facilities.

Key Words: breed, cattle behavior, feedyard, squeeze

0089 Movement and spatial proximity patterns of rangeland-raised Raramuri Criollo cow-calf pairs.

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The objective of this study was to compare movement patterns of nursing vs. nonnursing mature cows and to characterize cow-calf proximity patterns in two herds of Raramuri Criollo cattle. Herds grazed rangeland pastures in southern New Mexico (4355 ha) and west-central Chihuahua, Mexico (633 ha). At each site, five nursing and four nonnursing adult cows weighing approximately 325 kg were fitted with Lotek 3300 LR GPS collars which recorded animal position at 10-min intervals for 25 d during March to April 2015. Nursing cows and their calves were also fitted with Sirtrack proximity loggers that recorded number and length of dam-calf contact events ($\leq$3m distance). All calves were $\leq$2 wk old at the onset of the study. Collared animals grazed with a herd of 30 and 68 adult cows at the NM and Chihuahua sites, respectively. Distance traveled and path sinuosity of cows and time spent by calves within 3 m of their dam and number of dam-calf contact events during day and nighttime hours were calculated. Movement data were subjected to ANOVA to determine effect of cow state (nursing vs. nonnursing) on distance traveled and path sinuosity. ANOVA was also used to determine if calves spent similar amounts of time within 3 m of their dam during day vs. nighttime hours. PROC MIXED (SAS 9.3) with a randomized complete block design was used for statistical analyses. No differences were detected in distance traveled by nursing and nonnursing cows over a 24-h period (8.43 vs. 8. 56 ± 0.29 km; $P = 0.67$), daytime (5.47 km vs. 5.75 ± 0.24 km; $P = 0.24$), or nighttime hours (2.96 vs. 2.80 ± 0.15 km; $P = 0.32$). However, nighttime/daytime ratio of distance traveled was greater for nursing cows (0.62 vs. 0.55 ± 0.08; $P = 0.05$). Nursing cows exhibited more sinuous 24 h travel trajectories compared with nonnursing counterparts (0.13 vs. 0.18 ± 0.05 km; $P < 0.01$). Calves spent on average 66.9 ± 3.41 min/d within 3 m of their dam, distributed over 86.4 ± 3.7 proximity events/d. Minutes spent by calves within 3 m of their dam were not different for day vs. nighttime periods ($P = 0.07$); however, more contact events occurred during daytime hours (predawn = 13.8; AM = 26.1; PM = 22.0; postsunset = 24.5 ± 2.02 contact events). Physiological state of Criollo cows affected their movement patterns in large rangeland pastures.

Key Words: Raramuri Criollo, beef cattle, maternal behavior

0090 Effects of predation on cortisol and progesterone levels in gestating ewes. M. Ward*[1], A. F. Summers[2], S. Roscano[1], J. Beard[1], S. A. Soto-Navarro[1], and D. M. Hallford[2], *[1]New Mexico State University, Las Cruces, [2]Animal and Range Science Dep., New Mexico State University, Las Cruces.*

Production losses due to predation in range livestock are typically quantified by death loss. However, little is understood concerning the long term impacts chronic exposure to predation may have on surviving animals. Pregnant Dorper and Suffolk × Hampshire ewes (n = 40) located on the main sheep unit of the NMSU campus farm were attacked by two dogs in February 2015. During the attack, four ewes were killed or had to be euthanized and five died later based on complications from injury. Over 75% of the remaining flock sustained injury. To better understand the impacts of predation on surviving animals, blood was collected via jugular venipuncture at 4, 24, 48, and 72 h post attack. Furthermore, a subset of ewes located at the west sheep unit, not exposed to the attack, were only bled at 4 h (CON). Ewes were classified based on injury status and location into three treatments; CON = no exposure, E = exposed to dog attack with no visible injuries, and EI = exposed to dog attack with visible injury. At 4 h, EI had greater cortisol levels than both CON and E ($P < 0.01$). At 24 h, both E and EI had greater circulating cortisol than CON ($P < 0.01$). At 72 h, EI was still greater than CON ($P < 0.01$); however, CON and E cortisol levels were similar ($P > 0.05$). The attack had no effect ($P > 0.05$) on circulating progesterone across treatments. These data demonstrate increased circulating concentrations of cortisol in ewes receiving injury 4 h after attack, whereas blood cortisol concentrations were not greater than CON in the E group until the 24 h sampling. Although dog attack occurred approximately 2 wk before lambing, there was no difference in proportion of ewes experiencing dystocia (P = 0.27) or the level of dystocia (P = 0.15) based on a 3-point scale (0 = no complications, 1 = some complications, 2 = severe complications) for EI and E ewes. These data indicate exposure to predation impacts stress responses at similar levels as those injured. Additional information is needed to determine the length of time cortisol remains elevated within the two treatment groups and at which stage of gestation predation would negatively impact lambing success.

Key Words: sheep, livestock, cortisol

0091 Feeding and watering behavior of Nellore bulls fed with or without calcium, phosphorus and trace minerals supplemental sources. D. Zanetti*[1], L. A. Godoi[2], M. M. Estrada[2], F. A. S. Silva[3], L. F. Prados[2], T. E. Engle[4], and S. C. Valadares Filho[5], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Brazil, [3]Universidade Federal de Vicosa, Vicosa, Brazil, [4]Colorado State University, Fort Collins, [5]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil.*

Forty-two Nellore beef bulls were utilized to investigate the impact of roughage source and mineral supplementation on feed and water intake. Basal diets were formulated with feeds commonly utilized in Brazilian feedlot diets, with or without

Table 0091.

Table 1 – Water and feeding behavior of Nellore bulls fed with or without calcium (Ca), phosphorus (P) and trace minerals (TM)

Item	Treatments						SEM	Contrasts			
	SH100[1]	SH0[2]	SC100[3]	SC0[4]	CS100[5]	CS0[6]		A[7]	B[8]	C[9]	D[10]
Feeding behavior											
kg/d	7.68	7.56	7.55	7.67	7.47	7.32	0.30	0.7718	0.7844	0.7193	0.8315
min/d	97.61	96.79	95.95	91.80	98.58	85.96	6.37	0.9286	0.6481	0.1568	0.2626
# Visit/d	67.02	85.24	68.94	80.80	111.58	99.88	4.17	0.0038	0.0518	0.0478	0.0772
rate, kg/min	0.1629	0.1586	0.1571	0.1700	0.1871	0.2188	0.01	0.817	0.4889	0.0841	0.2104
rate, kg/# visit	0.2286	0.1814	0.2157	0.1957	0.1614	0.1850	0.01	0.0068	0.2315	0.1471	0.1305
min/visit	0.71	0.94	0.73	0.89	1.17	1.18	0.08	0.0589	0.1977	0.9215	0.0577
Watering behavior											
Total water	30.73	23.77	22.90	24.80	29.79	29.34	1.72	0.0069	0.4397	0.8477	0.1950
l/d	23.23	16.29	15.70	17.01	19.31	18.19	1.48	0.0022	0.5398	0.5868	0.0692
min/d	19.97	24.56	19.97	22.29	22.78	20.13	2.57	0.2155	0.5283	0.4573	0.4993
Visit/d	8.12	7.42	6.67	7.22	7.67	7.34	0.51	0.3412	0.4496	0.6418	0.7049
rate, l/min	1.26	0.72	0.89	0.76	1.00	0.94	0.14	0.0150	0.5262	0.7788	0.0504
rate, l/visit	2.90	2.24	2.41	2.40	2.59	2.49	0.22	0.0445	0.9748	0.733	0.1621
min/visit	2.49	3.44	2.99	3.18	3.02	2.72	0.38	0.0909	0.7277	0.5663	0.3789

[1] Diet composed by sugarcane and concentrate based in soybean hulls, with supplementation of Ca, P and TM. [2]Diet composed by sugarcane and concentrate based in soybean hulls, without supplementation of Ca, P and TM. [3] Diet composed by sugarcane and concentrate based in soybean meal and grounded corn, with supplementation of Ca, P and TM. [4] Diet composed by sugarcane and concentrate based in soybean meal and grounded corn, without supplementation of Ca, P and TM. [5] Diet composed by corn silage and concentrate based in soybean meal and grounded corn, with supplementation of Ca, P and TM. [6] Diet composed by corn silage and concentrate based in soybean meal and grounded corn, without supplementation of Ca, P and TM. [7] A = SH100 versus SH0. [8] B = SC100 versus SC0. [9] C = CS100 versus CS0. [10] D = (SH100, SC100 and CS100) versus (SH0, SC0 and CS0).

supplemental Ca, P, and trace minerals. Dietary treatments consisted of: (1) Sugarcane as the roughage source and a concentrate that consisted of soybean hulls with (SH100) and without (SH0) Ca, P, and TM supplementation; (2) Sugarcane as the roughage source and a concentrate base that contained soybean meal and ground corn with (SC100) and without (SC0) Ca, P, and TM supplementation; and (3) corn silage as the roughage source and a concentrate that contained soybean meal and ground corn with (CS100) and without (CS0) Ca, P, and TM supplementation. Supplemental minerals were formulated to meet or exceed the BR Corte (2010) requirements for Nellore bulls. Cattle were housed in a group pen for 125 d. The pen contained electronic feeders and waterers that allowed for individual animal consumption data to be collected. Comparisons between treatment means were made using orthogonal contrasts. The contrasts evaluated were: (A) SH100 vs. SH0; (B) SC100 vs. SC0; (C) CS100 vs. CS0; and (D) (SH100, SC100, and CS100) vs. (SH0, SC0 and CS0). Total DMI and time spent consuming feed (kg/min) were not affected by supplemental Ca, P, and TM. Cattle receiving supplemental minerals tended ($P < 0.08$) to have less visits to the feeder per day when compared with cattle not supplemented with minerals. Cattle consuming sugarcane based diets had more ($P < 0.05$) visits to the feeder per day than cattle consuming corn silage based diets, but DMI was similar across treatments. Cattle receiving diets containing soybean hulls with supplemental minerals consumed more water (total and liters/d) and liters per minute and per visit when compared with cattle receiving diets containing soybean hulls with no supplemental minerals. We concluded that, with absence of Ca, P, and TM in diet, the number of feeding times increased without affecting DMI, and water intake was reduced.

Key Words: corn silage, feeding rate, sugarcane

0092 Effects of ventilation and water misting on the physiological response of pigs kept in a stationary trailer before unloading.

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This study aimed at evaluating the effects of ventilation combined with water-misting on the physiological response of pigs kept in the truck during the waiting time before unloading at the slaughter plant. In the summer 2015 (19.7 ± 4.0°C, ranging from 16.5 to 28.1°C), a total of 2674 pigs were transported from a farm to a slaughter plant (2 h trip) using two pot-belly trailers (seven loads of 191 pigs/trailer). On arrival at the plant, the two trailers were kept stationary during a 30 min waiting period before unloading. During this time, one of the two trailers was exposed to external forced ventilation and misting for 30 and 10 min, respectively, using a fan-mister bank located near the unloading dock, while the other trailer (control) was not exposed to any cooling procedure. A total of 168 pigs (24 per trailer) were equipped with a gastro-intestinal tract temperature (GTT) monitor (High Resolution Thermochron iButton) for real-time recording of GTT data. Blood was collected from these pigs at exsanguination for the analysis of cortisol, lactate and creatine kinase concentrations, and hematocrit. Data were analyzed using the mixed model procedure of SAS. A probability level of $P \leq 0.05$ was chosen as the limit for statistical significance in all tests. A delta GTT (ΔGTT) was calculated as the difference between the measured GTT at a determined event and the GTT measured at rest. Except for the blood hematocrit level that was lower ($P < 0.05$) in pigs being exposed to the cooling procedure while waiting in the trailer, the cooling treatment had no effect on any blood parameter. At the end of the wait period and at unloading, the decrease of GTT was greater (higher-ΔGTT value; $P < 0.05$) in control pigs than in those exposed to the cooling treatment. This result may be explained by the greater heat loss of control pigs due to heat stress. Based on these results, the cooling method applied in this study appears to improve the thermal comfort and reduce dehydration in pigs kept in a stationary truck before unloading at the slaughter plant.

Key Words: pigs, transport, thermal comfort

0093 Increased intake of tannin-rich sainfoin (*Onobrychis viciifolia*) pellets by parasitized and nonparasitized sheep after a period of conditioning.

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Individuals alter their behavior and phenotypic traits in response to environmental challenges. Recent studies suggest that parasitized herbivores are able to select tannin-containing plants with anthelminthic activity. The objective of this study was to determine whether parasitized sheep learn to prefer tannin-rich sainfoin pellets. Forty lambs (4 mo old) were randomly assigned to two groups ($n = 20$). The parasitized group (PG) was infected with 3000 L3 stage larvae of *Haemonchus contortus*, and the other group (nonparasitized; NP) was not infected. Animals were submitted to preference tests by

offering a free choice between sainfoin pellets with high (T+; 4%) or low (T–; 2%) concentration of condensed tannins during three periods of 4 d each: Initial (Test 1), after the group PG developed an infection (Test 2), and after conditioning, when all animals consumed just T+ for 21 d so that parasitized animals experienced the benefits of therapeutic doses of condensed tannins (Test 3). Preference ([intake of T+ or T–] × 100/[total intake]) and fecal egg counts (FEC) were analyzed as a repeated measures design with animals nested within group. The group PG showed a clear increase in FEC after infection (from 0 to 3512 ± 446.34 eggs per gram; $P < 0.05$), but no further increase was observed after animals received T+ during conditioning (3145 ± 401.44 eggs per gram; $P > 0.05$). During Tests 1 and 2 animals preferred T- (Test 1: PG = 71.0 ± 3.9%; NP = 71.2 ± 4.3%; Test 2: PG = 73.9 ± 2.8% NP = 74.7 ± 2.7%; $P < 0.05$). However, preference reversed after conditioning (Test 3): Both groups, PG and NP, preferred T+ (PG = 61.0 ± 3.9%; NP = 62.6 ± 3.4%; $P < 0.05$). These results stand in contrast with previous studies using other types of antiparasitic condensed tannins (e.g., tannins extracted from the quebracho tree) with antinutritional properties. In such studies, only parasitized animals increase preference for a quebracho tannin-containing food relative to nonparasitized individuals. When condensed tannins do not exert negative postingestive effects on consumers, or even provide postingestive benefits (i.e., improved nitrogen utilization) like those observed in sainfoin, both parasitized and nonparasitized animals may display similar levels of acceptability to the tannin-rich feed. These results are consistent with a feed-forward mechanism in which endoparasitic loads are controlled by the frequent ingestion of safe bioactive-containing feeds which are typically preferred by consumers.

Key Words: diet selection, foraging, *Haemonchous contortus*

0094 Mitigation of variability in feeding patterns between competitively-fed dairy cows through increased feed delivery frequency.

ANIMAL BEHAVIOR AND WELL-BEING SYMPOSIUM: METRICS FOR ON-FARM ANIMAL WELFARE ASSESSMENT—CURRENT STATE AND FUTURE NEEDS

0095 Poultry welfare assessments: Where do we go from here. R. Blatchford*, *University of California, Davis.*

Recent attention has been given to developing welfare assessment tools for research purposes and for use directly on poultry farms. Historically, most of these tools have relied on resource- and management-based measures, but it is unclear how well they correlate with outcomes indicative of positive animal welfare. The subjective nature of many of these tools also makes it difficult to generalize across studies and farms without extensive training. More recently, the European Union Welfare Quality® project set out to design assessment tools that were scientifically based and combined resource- and management-based measures with animal-based measures. Adding these measures was especially important for farm-level comparisons where farms may be utilizing different housing systems with inherent differences affecting the utility of resource- and management-based measures. The Welfare Quality® Assessment protocol for poultry offers researchers a tool that has been validated, tested for repeatability, and standardized across farms. This tool has been used in the United States and Canada both at the experimental and farm levels. However, assessment tools were only developed for layer-type hens and broiler chickens. There is a vast need for the development of assessment tools for other poultry species such as ducks, turkeys, quail, and game birds. Tools are continuing to be developed, but many have measures that need validation and benchmarking and creating tools that can be used by producers without needing training to use successfully is important on a go-forward basis. Tools must be designed for North American commercial production with a better understanding of the appropriate sample size, as well as their utility for use in alternative and extensive housing systems. These tools show promise in helping to understand the influence of genetics, housing design, and management factors on the welfare of poultry.

Key Words: assessment tools, poultry, welfare

0096 Metrics for beef cattle welfare. D. Griffin*, *Great Plains Veterinary Educational Center, Clay Center, NE.*

The "Five Freedoms" of livestock is an important concept in the stewardship of beef cattle. These are the backdrop for evaluating the beef cattle welfare husbandry guidelines. The beef cattle care, husbandry, and welfare guidelines for cow-calf, pastured stocker cattle and feeder cattle developed by the National Cattlemen's Beef Association (NCBA) are reviewed. The Canadian and Australian feeder cattle care and welfare guidelines will also be reviewed and compared with the NCBA guidelines. A U.S. packer currently has developed and implemented a Feedlot Cattle Audit. Their audit will be reviewed and the unique items not included on other beef cattle welfare assessments will be discussed. Important differences between site assessments and site audits are listed, and the utility of each approach to improving beef cattle care and husbandry. The major areas included are development of SOPs for; safety of employees and cattle, employee training, living space design and management, feeding and feed stuff selection management (including water), cattle handling, heath

management and pain mitigation, medication management including withdrawal times, timely attention to individual cattle needs such as injury and euthanasia, and transportation.

Key Words: beef, husbandry, welfare, management

0097 Optimizing outcome measures of welfare in dairy cattle assessment. E. Vasseur*, *McGill University, Ste-Anne-de-Bellevue, QC, Canada.*

In most countries producing milk, industry-, government- and/or other stakeholder-driven initiatives are in place to improve welfare and dairy farming sustainability, for example, by enhancing profitability and reducing environmental impact. Those initiatives typically include a system of verification of reaching targets and tracking progress over time. Reliable indicators of welfare are required to provide public assurance and allow improvement on farms. Assessing dairy cattle welfare through outcome measures is done today through visual evaluations, including lameness, injuries, hygiene, and body condition. Numerical scoring charts have been validated, together with the development of training programs, to achieve high repeatability of assessors. Sampling strategies have been validated to determine how many animals and how many days are required to obtain reliable estimates of prevalence. However, visual evaluations require a long period of data collection and multiple visits to farms, along with follow-up checks of assessors to maintain repeatability over time, and in turn, are costly to implement. An attractive alternative is relying on automated measures collected from activity monitors that are becoming common on commercial farms; among those, lying time has gotten the most attention. The use of herd lying time in both free-stall and tie-stall situations has been validated. Current research is looking at relationships between lying time and other outcome measures of welfare, as well as lying time and risk factors for welfare in the environment (e.g., poor stall configuration or hoof trimming routine). We are not yet ready to rely solely on lying time to assess welfare; however, activity monitoring could certainly contribute to early detection of health and welfare issues (e.g., frequency of visits to the robotic milking system or feeders). Another interesting avenue is the development of early outcome measures of welfare and, possibly, remote indicators; for example, performance data (milk production, reproductive success, longevity) collected routinely in DHI databases. The rationale being that a herd with good health and high longevity should be at lower risk of poor welfare. Research is needed to identify predictors and their conditions of use, allowing to discriminate good vs. poor welfare status, both at the individual and herd level. Finally, milk samples are already collected in routine to check quality and safety. It would be extremely convenient to be able to predict cow welfare status directly in the milk using biomarkers; but again, we are not there yet.

Key Words: dairy cattle, welfare, outcome measure

0098 The Common Swine Industry Audit: Future steps to assure positive on-farm animal welfare utilizing validated, repeatable, and feasible animal-based measures. M. Pairis-Garcia[1] and C. J. Rademacher*[2], *[1]The Ohio State University, Columbus, [2]Swine Medicine Education Center, Department of Vet Diagnostic & Production Animal Medicine, Ames, IA.*

The Common Swine Industry Audit (CSIA) was developed in collaboration with pork producers, packers and processors to provide stakeholders with a consistent, reliable and verifiable system to assure on-farm swine welfare and food safety. This audit tool was built from the framework of Pork Quality Assurance®Plus program to develop a single, common audit platform for the U.S. Pork industry. The audit can be broken down into 27 key aspects that cover swine care, husbandry, and preharvest food safety. Of these key areas, animal based measures represent approximately 50% of the total points achievable for the audit and encompass all critical criteria including willful acts of abuse and timely euthanasia. As this tool is designed to provide an objective, science-based platform to facilitate continuous improvement in animal care, the use of validated, repeatable, and feasible animal-based measures is critical. Recognizing this, the CSIA task force and researchers within this field are focusing on the future needs and expectations of the audit by evaluating three questions. (1) How do we determine thresholds for animal based measures? Within the CSIA, each animal based measured has a threshold for what is considered acceptable or unacceptable. For example, farms will receive 10 points if 1% or less of the pigs observed have a body condition score of 1 or 0 points if prevalence is $\geq$2%. Although thresholds provide a more objective manner to validate welfare on farm, these thresholds may often be arbitrary and based more on experience than science. (2) How do we identify, interpret and provide value to animal based measures assessed in the audit? For any assessment and audit, the data we collect must directly relate back to the welfare status of the pigs on the farm. Identifying animal-based measures that cover a broad range of potential welfare problems to provide direct interpretation and value of individual pig welfare is critical. (3) What do these values mean to the U.S. swine industry as a whole? As the goal of the audit it to provide useful feedback for continuous improvement on farm, we must as an industry be committed to utilizing the information attained through on-farm audits to develop the educational tools, resources and support to advance on-farm swine welfare.

Key Words: audit, swine, welfare

ANIMAL HEALTH

0099 In silico identification of natural product inhibitors of *Brucella abortus* threonyl-tRNA synthetase. M. Li[1,2], N. Zheng[1,2,3], F. Wen[1,2], Y. Zhang[1,2], S. Li[1,2], S. Zhao[1,2], and J. Wang[*1,2,3], *[1]Ministry of Agriculture Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture–Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Bovine brucellosis is mainly caused by the bacterium *Brucella abortus*, and represents a major problem to livestock industry development worldwide and is also a threat to human health in many developing and underdeveloped countries. Aminoacyl-tRNA synthetases (aaRSs), the central enzymes in protein translation, catalyze the covalent attachment of correct amino acids to their cognate tRNAs, yielding the aminoacyl tRNAs (aa-tRNA or charged tRNA) used for protein synthesis. Due to the pivotal role in protein synthesis, aaRSs have been considered as some of the most promising targets for antibiotics development in pathogenic species. In this study, a three-dimensional structural model of *Brucella abortus* threonyl-tRNA synthetase (BaThrRS) was constructed using computer-aided molecular modeling technique taking *Escherichia coli* threonyl-tRNA synthetase (EThrRS, PDB ID: 1QF6) as template. The ZINC natural product database including 11247 compounds was subjected for virtual screening based on molecular docking against the ATP binding site of the target using Autodock Vina program. Considering the mode of binding and affinities, seven leads, ZINC67910544 (–12.4 kcal/mol), ZINC72320615 (–12.3 kcal/mol), ZINC72320626 (–12.2 kcal/mol), ZINC27215482 (–12.6 kcal/mol), ZINC35270978 (–12.1 kcal/mol), ZINC35458951 (–12.1 kcal/mol), and ZINC42805205 (–12.4 kcal/mol) were selected on basis of binding energies in comparison to the selective inhibitor borrelidin (free energy of binding: –9.3 kcal/mol). Among them, ZINC27215482 (–12.6 kcal/mol) was best lead because of its highest inhibitory activity. The binding site of ZINC27215482 on BaThrRS was a pocket consisting of 22 residues: TYR316, ASN319, MET341, ASN342, CYS343, GLN374, MET383, ARG384, VAL385, PHE388, GLN390, ASP392, HIS394, TYR476, LYS479, GLN493, GLN498, THR496, GLN498, HIS525, SER531, and ARG534. Therefore, through a high throughput virtual screen we identified seven novel BaThrRS inhibitors that are used against bovine brucellosis with great potential for further development.

Key Words: *Brucella abortus*, threonyl-tRNA synthetase, virtual screening

0100 Evaluation of immune function markers in OmniGen-AF® supplemented steers. S. A. Armstrong[*1,2], D. J. McLean[2], T. H. Schell[1,2], G. Bobe[1], and M. Bionaz[1], *[1]Department of Animal and Rangeland Sciences, Oregon State University, Corvallis, [2]Phibro Animal Health Corporation, Quincy, IL.*

The effect of OmniGen-AF® (OG) supplementation on the expression of immune function markers in circulating whole blood cells was investigated in the first 28 d of feeding healthy Angus steers. Steers were randomly assigned to control (n = 4/group) or OG (n = 5/group; supplemented daily with 56 g/head OG), and fed a diet including grass hay, alfalfa, and ground corn. Steers were housed in a freestall barn and fed via Calan Broadbent system. Blood was collected via jugular puncture before the study (–4 d) and on d 14, 21, and 28 of supplementation. Genes evaluated included *CXCR2*, *CD80*, *CD62L*, *IL10RA*, *IL10RB*, *MAPK8*, *NOD2*, and *TLR1*. Data were analyzed using LinReg software to account for efficiency of amplification and normalized by three internal control genes (*RPL19*, *RPS9*, and *TBP*) and corrected to d –4. The qRT-PCR data were log-transformed and the data points with Studentized residuals $t > 2$ removed (i.e., outliers). The final data set was subjected to ANOVA analysis with treatment, time, and treatment × time as main effect and animal as random effect using Proc GLIMMIX of SAS. Time, treatment, and time × treatment did not have an impact on *CD62L* gene expression. The expression of *CD80*, *CXCR2*, *IL10RA*, *IL10RB*, *MAPK8*, and *NOD2* was different through time ($P < 0.05$), and time had a tendency to influence *TLR1* gene expression ($0.05 < P < 0.10$). Compared with controls, OG supplementation down-regulated *CD80* and *IL10RB* gene expression ($P < 0.05$); OG supplementation had a tendency to down-regulate *CXCR2* and *MAPK8* expression compared with controls ($0.05 < P < 0.10$). A treatment × time effect was detected for *CXCR2* gene expression ($P < 0.05$) with control steers displaying higher *CXCR2* expression by the conclusion of the supplementation period compared with OG supplemented cattle. These results, when considered with previous data on immune function markers and OG supplementation, suggest OG may be regulating antigen presentation and signal transduction. Future studies may also consider using *CD80*, *CXCR2*, *IL10RB*, and *MAPK8* as markers of OG efficacy within the first 28 d of supplementation.

Key Words: OmniGen-AF®, immunity, beef steers

0101 Influence of dietary supplementation with a *Saccharomyces cerevisiae* fermentation product prototype on the pathophysiological response to a combined intranasal bovine herpesvirus-1 and intratracheal *Mannheimia haemolytica* challenge in Holstein steers. K. P. Sharon[*1], Y. Liang[1], R. E. Hudson[1], I. Yoon[2], M. F. Scott[2], N. C. Burdick Sanchez[3], P. R. Broadway[3], J. A. Carroll[3], and M. A. Ballou[1], *[1]Texas Tech University, Lubbock, TX, [2]Diamond V, Cedar Rapids, IA, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to determine the effects of supplementing a *Saccharomyces cerevisiae* fermentation product prototype (Prototype) on the pathophysiological response during a combined viral-bacterial respiratory challenge. Holstein steer calves (126.5 ± 6.11kg; $N = 16$) were completely randomized to treatments including 0 (CON) or 20 g/head/d of Prototype ($n = 8$). Calves were housed in open, dry lot corrals with four calves per pen (2 pens/treatment). Calves were offered ad libitum access to a 50:50 total mixed ration of a commercially available 16% CP pelleted calf grower and 18% CP chopped alfalfa hay. Treatments were top dressed for 30 d. Orts were measured daily and the quantity of feed was adjusted for approximately 10% orts. Calves were moved to individual stanchions (2.13 × 0.76 cm) in an enclosed barn, fitted with rectal temperature monitoring devices, and allowed 24 h adaptation before initiating the respiratory challenge. All calves were challenged with 1.5×10^8 PFU·mL^{-1}·nostril^{-1} of bovine herpesvirus-1 cooper strain at –72 h using a mucosal atomizer and with 10^6 CFU of *M. haemolytica* (MH) intratracheal at 0 h. Blood samples were collected via jugular venipuncture at –96, –72, –48, –24, 0, 6, 24, 48, 72, 120, 168, and 240 h relative to the MH challenge. Total leukocytes counts tended ($P = 0.063$) to be greater at 24 h among CON steers. Neutrophil:lymphocyte also tended to be greater ($P \leq 0.095$) at 24 and 72 h among CON steers. Monocyte phagocytosis of an environmental *Escherichia coli* tended ($P = 0.056$) to be greater in steers fed the Prototype at 24 h. Neutrophil oxidative burst to an environmental *Escherichia coli* tended ($P = 0.071$) to be greater at 6 h and was greater ($P = 0.011$) at 168 h among steers fed the Prototype. However, monocyte oxidative burst tended ($P = 0.052$) to be greater among CON at 72h. Neutrophil L-selectin did not differ between treatments ($P = 0.515$). Neither serum haptoglobin concentrations ($P = 0.773$) nor rectal temperature ($P = 0.985$) differed between treatments. These data demonstrate that the *Saccharomyces cerevisiae* fermentation product prototype may influence some acute leukocyte responses during a viral-bacterial respiratory challenge, but did not have strong influences on measures of inflammation or disease.

Key Words: health, respiratory, *Saccharomyces cerevisiae* fermentation product

0102 Dose response effect of *Saccharomyces cerevisiae* fermentation product prototype on leukocyte functionality and ex vivo cytokine production during a dexamethasone challenge in Holsteins steer calves. K. P. Sharon[*1], Y. Liang[1], R. E. Hudson[1], I. Yoon[2], M. F. Scott[2], N. C. Burdick Sanchez[3], P. R. Broadway[3], J. A. Carroll[3], and M. A. Ballou[1], *[1]Texas Tech University, Lubbock, [2]Diamond V, Cedar Rapids, IA, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to determine the dose response effects of supplementing *Saccharomyces cerevisiae* fermentation product prototype on leukocyte functionality and ex vivo cytokine production during a dexamethasone (DEX) challenge. Holstein steers (125.1 ± 8.16 kg; $N = 32$) were assigned to treatments including 0, 20, 40, or 60 g/head/d of prototype ($n = 8$). Calves were housed for 21 d in dry lot corrals with four calves per pen (2 pens/treatment). Calves were offered ad libitum access to a 50/50 TMR of a commercially available 16% crude protein pelleted grower and 18% CP chopped alfalfa hay. Treatments were top dressed. The quantity of feed offered and orts were measured daily. After the 21 d adjustment to diets, calves were jugularly catheterized and moved into individual stations (2.13 × 0.76 cm) in an environmentally controlled barn and allowed 48 h to adapt before the first DEX injection. Blood samples were collected at –24, –6, 0, 6, 12, 18, 24, 48, and 72 h relative to the first DEX injection. DEX was administered via jugular catheter at 0.1 mg/kg BW at 0, 6, and 12 h. Peripheral blood neutrophil (PMN) concentrations increased ($P < 0.001$) at 6 h and remained elevated through 72 h in all steers. Neutrophil L-selectin and PMN and monocyte (MONO) oxidative burst (OB) and phagocytosis (PHAG) of an environmental *Escherichia coli* decreased ($P < 0.059$) at 6 h in all steers. L-selectin returned to baseline at 72 h while OB and PHAG failed to return to baseline by 72 h. Total leukocyte counts ($P < 0.001$) and PMN concentrations ($P = 0.001$) increased linearly with prototype dose. PMN L-selectin concentrations did not differ ($P = 0.684$) among treatments. Oxidative burst intensity in PMN ($P = 0.025$) and MONO ($P = 0.003$) increased linearly with prototype dose at 72 h, as well as in MONO PHAG intensity ($P = 0.004$) at 6 h. The percentage of PMN ($P = 0.012$) and MONO ($P = 0.013$) that were both PHAG and OB positive increased linearly with prototype at 72 h. Ex vivo whole blood lipopolysaccharide stimulated TNF-α concentrations was greater ($P = 0.026$) in prototype steers than control steers at –24 h. Overall, these data demonstrate that the dexamethasone challenge induced severe leukocyte dysfunction, and prototype supplementation influenced plasma neutrophil concentrations and may have increased recovery of neutrophil and monocyte function.

Key Words: dairy, health, yeast fermentation product

0103 Effects of climatic conditions before and after birth on growth rate of Holstein calves in a hot environment. E. L. Lopez-Rodriguez[*1], A. Martinez[2], and M. Mellado[3], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Mexico, [2]UAAAN, Saltillo, Mexico, [3]Autonomous Agrarian University Antonio Narro, Saltillo, Coahuila, Mexico.*

Birth weight and growth records, representing 5938 Holstein calves from three large commercial dairy herds in northern Mexico (26° N; 24.2°C mean annual temperature) were analyzed to document the effects of environmental factors on growth traits of dairy calves from 2013 to 2015. Climate variables indicative of heat stress [e.g., maximum ambient temperature (MaxT) and temperature-humidity index (THI)] were considered, 1 or 2 mo before calving and at calving. Growth traits were birth body weight (bBW), weaning weight (WW), preweaning daily weight gain (DWG). The effect of season, MaxT, and THI the day of calving and MaxT one and 2 mo before calving were analyzed by the GLM and REG procedures of SAS. The relationship between bBW and MaxT on the day of calving was negative and curvilinear. When MaxT and THI reached 34°C and 80 units, bBW had a noticeable drop ($P < 0.01$) compared with lower ambient temperatures (38.6 ± 3.6 vs. 39.2 ± 3.9 kg for calvings at MaxT < or > 34°C, respectively). Birth body weight was lower ($P < 0.01$) in calves born in spring than the rest of the year (38.3 ± 3.9 vs. 39.1 ± 3.8 kg; mean ± SD). Maximum ambient temperature one or 2 mo before calving did not affect bBW. Body weight at weaning and DWG of calves decreased gradually ($P < 0.01$) when MaxT and THI reached 28°C and 73 units at calving, respectively. A season effect was detected ($P < 0.01$) for DWG and WW. These traits were 403 ± 117 and 450 ± 110 g and 66.0 ± 8.5 and 69.2 ± 8.1 kg for summer and winter, respectively. It was concluded that, in this particular environment (high heat load for most of the year), heat stress markedly affects bBW and growth rate of Holstein calves. Thus, environmental management of the late gestation cow during hot summer months is warranted to optimize calf growth rates.

Key Words: birth body weight, growth traits, heat stress

0104 The hidden cost of a hidden disease: growth performance of calves as affected by bovine respiratory disease diagnosed using ultrasonography. C. Tejero[*1] and A. Bach[2,3], *[1]Rancho Las Nieves, Mallen, Spain, [2]ICREA, Barcelona, Spain, [3]IRTA, Caldes de Montbui, Spain.*

The aim of this study was to assess the consequences of bovine respiratory disease (BRD) during the first 60 d of life on subsequent growth performance. One thousand sixty-six calves (42.5 ± 6.9 kg of BW and 12.4 ± 5.6 d old) were raised, fed, and managed under exactly the same protocols in a contract heifer operation. Five hundred and thirty-three calves were diagnosed with BRD using an ultrasound and a 8–5 MHz linear probe with 12 cm scan depth, and the remaining coetaneous 533 calves were healthy and never diagnosed with BRD (NBRD). Ultrasonographic scans evaluated the right lung from the 10th intercostal space (ICS) cranial to the first ICS, and the left lung from the 10th ICS cranial to the second ICS. Calves were considered BRD positive when ≥1 cm of consolidation was present. Calves diagnosed with BRD were immediately treated with antibiotics. Respiratory disease was classified as lobular pneumonia type I (1 cm consolidation), type II (2 cm consolidation), and type III (3 cm consolidation), or lobar pneumonia (consolidated lobe). The potential impact of BRD and its severity on growth performance was assessed using a mixed effects model. The cranial area of the right cranial lung lobe was most commonly affected, followed by the right middle lung lobe, and the caudal area of the right lung lobe. Most BRD cases were diagnosed between 5 and 56 d of age (average 26.2 ± 12.6 d). Daily growth between 12.4 ± 5.6 and 50.8 ± 5.8 d was greater ($P < 0.001$) in NBRD (742 ± 4.9 g/d) than in BRD Type I (649 ± 8.4 g/d), and the latter had a greater ($P < 0.001$) ADG than BRD Type II calves (604 ± 13.9 g/d). Between 49.7 ± 2.5 and 111.6 ± 3.5 d, NBRD calves also grew (1176 ± 7.6 g/d) more ($P < 0.01$) than BRD calves (1084 ± 12 g/d), independently of the severity of the lung lesion. However, from 113.3 ± 7.3 to 162.8 ± 5.4 d, there were no differences in ADG (1116 ± 18 g/d) between NBRD and BRD calves. Therefore, BW at 50, 113, and 163 d was lower ($P < 0.01$) in BRD (66 ± 0.29, 135 ± 0.56, and 192 ± 0.76 kg, respectively) than in NBRD (70.9 ± 0.3, 143 ± 0.67, and 201 ± 0.98 kg, respectively) calves. It is concluded that having a lobular pneumonia with a lesion of ≥1 cm within the first 2 mo of life induces close to 10 kg of BW lag at 23 wk of age despite the application of antibiotic treatment on BRD diagnosis.

Key Words: health, lung, pneumonia

0105 Serum and colostrum antibody titers in Holstein cows, and the relationship between these titers and serum antibody titers in their calves. D. J. McLean[*1], J. D. Chapman[1], A. Woolums[2], D. J. Hurley[3], and L. O. Ely[3], *[1]Phibro Animal Health Corp., Quincy, IL, [2]Mississippi State University, Starkeville, [3]University of Georgia, Athens.*

Vaccination of cows in late gestation is sometimes used to improve maternal antibody titers in their calves. However, scant published research has reported the relationship between serum antibody titers to specific infectious agents in vaccinated cows, the colostrum of these cows, and the serum of calves consuming their colostrum. As part of a larger study, the relationship between cow serum and colostrum antibody titers and calf titers was evaluated. Fifty-four multiparous Jersey and Jersey-cross cows were vaccinated between dry-off and calving with commercially available vaccines containing bovine herpesvirus-1 (BHV-1), bovine viral diarrhea

virus (BVDV), bovine respiratory syncytial virus (BRSV), rotavirus, coronavirus, *E. coli* J-5, and *Salmonella* siderophore receptor and porin (SRP); blood was collected at dry off, mid-dry, and at calving. Calves born to enrolled cows were fed colostrum from only their dams; calf serum was collected at 7 and 30 d of life. Antibody titers against agents in the vaccine were measured in serum and colostrum of cows by standard neutralizing techniques or ELISA, and correlations between cow serum antibodies at 30 d before calving, cow colostrum, and calf serum antibodies at 7 d of life were evaluated. Correlations between cow serum antibodies and colostrum antibodies for different agents were significant ($P < 0.05$) but only moderately strong (Pearson correlation coefficient [PCC] range: 0.32–0.7), and varied for different agents. Similarly, correlations between cow colostrum antibodies and calf serum antibodies were usually significant, but only moderate (PCC range: 0.36–0.77). The R^2 value for the correlation between colostrum antibodies and calf antibodies ranged from 0.11–0.59, indicating that for most agents, the colostrum antibody titer to a given agent did not explain a majority of variation in the calf serum antibody titer to that agent. Antibody titers to specific agents in cows are significantly, but not strongly, correlated with their colostrum antibody titers, and colostrum antibody titers are significantly but not strongly, related to antibody titers in calves. These data suggest that, in addition to maternal antibody concentration, other factors have an important impact on serum antibody titers to specific infectious agents in young dairy calves.

Key Words: colostrum, antibody transfer, vaccination

0106 Evaluating preweaned calf housing and its impact on calf respiratory parameters on New York dairy farms. K. M. Morrill*, *Cornell University, Ithaca, NY.*

The objectives of this project were to (1) evaluate environmental and air quality parameters across different types of calf housing facilities; (2) evaluate rates of respiratory illness in preweaned calves; and (3) determine the impact of environmental factors, air quality, and housing type on calf health. This was an observational study in which calf facilities were evaluated on a single visit during June 2015. Housing included hutches ($n = 9$), individual pens in a barn ($n = 11$), and group pens in a barn ($n = 9$). Facility and calf pen evaluations included wind speed, temperature, relative humidity, heat stress index, bedding type, bedding composite sample for bacteria counts, nesting score of calf pens, calf health scoring, and airborne bacteria. Data were analyzed using SAS 9.3 to determine the impact of housing type, environmental, and air quality variables on calf respiratory score. A total of 29 facilities and 437 preweaned calves were evaluated. Calf facility temperature averaged 24.2°C (range 15.5 to 30.6°C) with a relative humidity of 21.5% (range 10 to 78%) and a heat index of 21.5°C (range 6 to 30.9°C). Temperature and airborne bacterial counts were greater in hutches as compared with individual and group pens ($P < 0.01$). Humidity was similar for hutches and group pens, but greater than individual pens. Gram negative airborne bacterial counts were lowest in individual pens. No difference in heat index was observed across housing type. Mean calf respiratory scores was 2.5 (range of 0 to 9) on a 12 point scale; 13.33% of calves evaluated scored greater than 5, indicating a respiratory challenge. Prevalence of respiratory illness in preweaned calves ranged from 0 to 50% of calves on a per farm basis (mean = 11.05% of calves/farm), with 44.82% of farms having no respiratory illness and 10.32% of farms having 30 to 50% of evaluated calves exhibiting signs of respiratory illness. There was a negative correlation between respiratory score and pen temperature ($R^2 = 0.90$). There was no influence on respiratory score by housing system, bedding type, ventilation system, relative humidity, airflow, or airborne bacterial counts. Data collected from this study suggests that respiratory illness continues to be a challenge, even when weather is temperate. Additional research is needed to evaluate rates of respiratory illness during cold stress and transitional weather, as well as to evaluate management factors that increase the risk of infection.

Key Words: calves, housing, respiratory

0107 Differential primary and secondary immune responses in calves fed heat-treated or unheated colostrum. S. L. Gelsinger* and A. J. Heinrichs, *The Pennsylvania State University, University Park.*

An experiment was conducted to compare immune responses between calves that received unheated or heat-treated colostrum. Half of a single, pooled batch of colostrum was frozen without heating; the other half was heated and maintained at 60°C for 60 min before freezing. Bull calves ($n = 26$) were randomly assigned to receive 8% of their birth weight as either unheated or heat-treated colostrum. Blood samples were collected at birth and 48 h of age to assess passive transfer. At 14 and 35 d of age, all calves received a subcutaneous injection of 0.2 mg ovalbumin per kg birth weight. Blood was sampled at 0, 4, 8, and 12 h, and daily on days 2 to 10 after each injection. Plasma was collected for analysis of total IgG, ovalbumin-specific IgG, interferon γ (IFNg), tumor necrosis factor α (TNFa), and interleukin 1 β (IL1b). Area under the curve was calculated for plasma cytokine and antibody concentrations, and all data were analyzed using Proc Mixed in SAS. Colostrum treatment, time point, and their interaction were included as fixed effects with calf as a repeated random effect. All calves achieved successful passive transfer of IgG. Calves fed unheated colostrum at birth had greater plasma IL1b and nonovalbumin IgG ($P < 0.05$) during the first challenge and tended to have greater nonovalbumin IgG during the second challenge ($P = 0.08$). Calves fed heat-treated colostrum at birth tended to have greater plasma IFNg during the second challenge ($P = 0.09$). These results imply that calves

fed heat-treated colostrum exhibit improved T-cell mediated but reduced innate and B-cell mediated immune response. Despite changes in cytokine and antibody production, neither body weight, body temperature, weekly feed (milk and starter) intake, nor total IgG concentration were different between groups through 45 d of age.

Key Words: calf, colostrum, immune response

0108 The effect of novel antiseptic compounds on umbilical cord healing and infection rates in the first week of life in dairy calves. A. L. Robinson*, L. L. Timms, K. J. Stalder, and H. D. Tyler, *Iowa State University, Ames.*

The objective of this study was to compare the effect of four umbilical dips on the healing rate and incidence of infection of umbilical cords using newborn Holstein and Jersey calves (n = 76). Calves were alternately assigned by birth order to four treatment groups: 7% iodine, a dry dip created using an antibacterial peptide (nisin) mixed with talc (formulation concentration = 3.105 g nisin per 100 g talc on a weight per weight basis), liquid nisin (64 ug/mL), and chlorhexidine mixed with alcohol in a 50:50 solution. Umbilical cords were dipped 30 min after birth. Before initial dipping, diameter of the umbilical cords (as an indicator of cord drying) were determined using digital calipers. As a potential indicator of umbilical infections, surface temperature of the umbilical stump (along with a reference point at the midpoint of the sternum) was measured using a dual laser infrared thermometer (Model 42570, Extech Instruments Nashua, NH). The IR and caliper measurements were all repeated at 24 ± 1 h, 48 1 h, and 72 1 h of age. Measurements of calf umbilical diameter were continued until the umbilical cord healed to the point of detachment. All data were analyzed using mixed model methods (PROC MIXED, SAS Version 9.2). Age at umbilical cord detachment tended to be different between treatments (P = 0.105); calves dipped with chlorhexidine mixed with alcohol detached at a mean age of 20 d compared with 15.5 d for the other three treatments. No treatment differences were noted (P > 0.05) between dips on drying rate of umbilical cords. Mean umbilical cord diameter was 17.81 ± 5.73 mm at birth and they healed to a mean diameter of 8.10 ± 5.07 mm at 24 h of age. Similarly, there were no treatment effects (P > 0.05) on incidence of umbilical infections (umbilical infection rate for all calves was 18.4%). Mean surface temperature of the umbilical stump was 27.4 ± 4.0°C at birth (0.1 ± 0.2°C lower than the sternal reference temperature). At 24 ± 1 h of age the mean temperature of the umbilical stump was 29.2 ± 4.3°C (0.4 ± 0.1°C lower than the sternal reference temperature). These data suggest that all four dips are effective in preventing umbilical infections and permitting healing of the umbilical cord when used within 30 min of birth.

Key Words: calves, umbilical cord, umbilical dip

0109 Effects of OmiGen-AF® and Provia 6086 on growth, leukocyte, and hematological variables of preweaned and immediately postweaned Holstein calves. Y. Liang*[1], R. E. Hudson[1], T. L. Harris[1], K. P. Sharon[1], J. P. Jarrett[2], D. McLean[2], J. D. Chapman[2], J. A. Carroll[3], and M. A. Ballou[1], *[1]Texas Tech University, Lubbock, TX, [2]Phibro Animal Health Corporation, Quincy, IL, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to determine the effects of OmniGen-AF (OG) and Provia 6086 (PV) on the performance and health of preweaned and immediately postweaned Holstein calves. Holstein calves within 1 d of birth were randomly assigned to one of four dietary treatments (N = 80). The study was conducted in two consecutive periods with 40 calves/period (n = 10 calves/treatment/period). Dietary treatments were given in both the milk replacer and calf starter. Treatments were arranged and analyzed as a 2 × 2 factorial with OG and PV as the main fixed effects. Diets were formulated to supply approximately 10 g/d of OG and 2 billion CFU/d of PV if calves were consuming milk only or 1.36 kg of calf starter only. Calves were housed in an enclosed barn and fed 275 g of a 22% CP and 20% fat milk replacer daily at 0730 and 1630. Calves had ad libitum access to calf starter and water. The quantity of water and starter offered as well as refused was recorded and adjusted daily for approximately 10% orts. Calves were individually housed until they were weaned at 56 d when they were grouped within treatment with four calves/pen for an additional 28 d. There were no treatment or treatment × time differences on starter intake during either the preweaned ($P \geq 0.111$) or postweaned ($P \geq 0.297$) periods. Additionally, there were no treatment or treatment × time differences ($P \geq 0.500$) in ADG during either the preweaned (0.593 ± 0.096 kg/d) or postweaned (0.845 ± 0.096 kg/d) periods. The surface expression of CD14 on peripheral blood monocytes decreased ($P \leq 0.001$) with increased calf age; however, there were no treatment or treatment × time differences ($P \geq 0.339$). Similarly, there were no treatment or treatment × time differences ($P \geq 0.316$) on the surface expression of CD62L on peripheral blood neutrophils. There was an OG × PV × time interaction (P = 0.018) in peripheral blood neutrophil counts, whereas there was a tendency (P = 0.089) for the Control and OG + PV to have reduced neutrophils when compared with OG and PV calves at 21 d. Lastly, there were no treatment × time differences ($P \geq 0.430$) on hematocrit percentages; however, there was a significant time effect (P = 0.001), whereas hematocrits were elevated at 14 and 21 d. These data indicate that OmniGen-AF and Provia 6086 supplementation during the preweaned and immediate postweaned periods did not influence growth performance, leukocyte, or hematological measures in these Holstein calves.

Key Words: calf, growth, immunity

0110 Health status of dairy feeder calves arriving to a veal facility. D. L. Renaud*, T. F. Duffield, D. F. Kelton, S. J. LeBlanc, and D. B. Haley, *Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

There are approximately 959,600 dairy cows producing 479,800 male dairy calves every year in Canada. Based on information gathered from the 2015 Canadian National Dairy Study, less than 7% of male calves are euthanized at birth, leaving a significant number of male calves to enter the red meat industry. In Ontario and Quebec, the majority of male dairy calves flow into the veal industry. In 2015, 213,659 veal cattle from approximately 551 producers were slaughtered in Ontario and Quebec. Currently, there is little information about the fitness of dairy feeder calves (traditionally referred to as veal calves) entering the veal industry in Canada. The objective of this descriptive study was to evaluate the health status of calves arriving at a large veal farm. Using a scoring program (Calf Health Scorer App) developed by McGuirk et al. (2014) and supplemental scoring adapted from Wilson et al. (2000), Holstein and crossbred calves (n = 1356; 1335 male and 14 female) of unknown age were evaluated immediately on arrival at the commercial milk-fed veal facility in Southwestern Ontario. The results from the period of November 2015 until March 2016 were tabulated and confidence intervals (CI) were calculated (Wald's test) using Stata 14 (StataCorp College Station, Texas). Enlarged navels with at least heat or pain or moisture were found in 25.6% (95% CI: 23.3–27.9%) of calves, diarrhea was present in 16.7% (95% CI: 14.7–18.7%), fever (defined as greater than 39.5°C or 103.1°F) was present in 15.1% (95% CI: 13.2–17.0%), lack of subcutaneous fat or emaciated appearance was present in 22.4% (95% CI: 20.1–24.6%), depression or dullness was present in 26.8% (95% CI: 24.6–29.3%), signs of clinical dehydration (defined as >5% dehydration based on skin tent, attitude, presence or absence of suckle reflex and eye recession) were present in 26.5% (95% CI: 24.2–28.9%), and respiratory disease (defined as a combination of abnormal nasal and ocular discharge, ear and head position, cough and temperature) was present in 9.2% (95% CI: 7.6–10.7%). Based on the results gathered thus far, a significant proportion of calves (42.7% [95% CI: 40.0–45.3%]) are entering the facility with at least one identifiable health abnormality. This represents a significant welfare concern and the causes of the abnormalities need to be further understood to motivate a change in the way dairy feeder calves are treated.

Key Words: dairy calf health, health screening, veal production

0111 Acute immunological responses to a combined viral-bacterial respiratory disease challenge in feedlot heifers supplemented with yeast. A. B. Word*[1], P. R. Broadway[2], N. C. Burdick Sanchez[2], Y. L. Liang[3], K. P. Sharon[3], S. L. Roberts[4], J. T. Richeson[4], P. J. Defoor[5], M. D. Cravey[6], J. R. Corley[7], M. A. Ballou[1], and J. A. Carroll[2], *[1]Texas Tech University, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [4]Department of Agricultural Sciences, West Texas A&M University, Canyon, [5]Cactus Feeders, Canyon, TX, [6]Phileo Lesaffre Animal Care, Milwaukee, WI, [7]Phileo Lesaffre Animal Care, Cedar Rapids, IA.*

Two treatments were evaluated in commercial feedlot heifers to determine the effects of a yeast supplement on immune responses to a combined viral-bacterial respiratory challenge. Thirty-two beef heifers (325 ± 19.2 kg BW) were selected and randomly assigned to one of two treatments, and fed for 31 d: (1) Control (CON), receiving a standard feedlot ration without a yeast supplement, or (2) Yeast (YEAST), control ration plus a combination live yeast (2.5 $g \cdot hd^{-1} \cdot d^{-1}$) and yeast cell wall (2.5 $g \cdot hd^{-1} \cdot d^{-1}$) supplement (Phileo-Lesaffre Animal Care, Milwaukee, WI). All cattle were challenged intra-nasally with 1×10^8 PFU bovine herpesvirus-1 (BHV-1) on d –3 and then allowed to rest in outdoor pens for 3 d. On study d 0, each animal was challenged intratracheally with an average dose of 3×10^7 CFU *Mannheimia haemolytica*, was fitted with an indwelling jugular catheter and an indwelling vaginal temperature recording device, and was moved into individual stanchions in an environmentally-controlled barn. Whole blood samples were collected at the time of BHV-1 challenge at 1-h (serum) or 2-h (complete blood cell counts) intervals from 0 to 8 h, and at 12, 24, 36, 48, 60, and 72 h relative to *M. haemolytica* challenge. Data were analyzed using the mixed procedure of SAS specific for repeated measures with fixed effects of treatment, time, and their interaction. Water intake per hour tended (P = 0.06) to be greater in the YEAST group compared with CON. Nasal lesion scores tended (P = 0.07) to be decreased in the YEAST group compared with CON (2.50 ± 0.26 vs. 3.19 ± 0.26, respectively). There was no difference in cortisol concentrations or vaginal temperature between treatment groups ($P \geq 0.37$). There was no treatment difference (P = 0.21) in total white blood cell counts following BHV-1 challenge. There was a trend (P = 0.13) for serum haptoglobin concentration to be reduced in the YEAST (11,757.3 ± 1631.7 μg/dL) group compared with CON (15,396.174 ± 1631.7 μg/dL). Cattle in the CON group tended (P = 0.07) to have greater neutrophils than YEAST (6.39 ± 0.39 vs. 5.37 ± 0.37 K/μL, respectively). In summary, feeding a combination live yeast and cell wall yeast supplement tended to reduce nasal lesion score, inflammatory response, and neutrophil count with no

effect on febrile response in beef heifers. Further research is warranted to determine if other measures of the inflammatory response were influenced by yeast supplementation in this model of respiratory disease challenge.

Key Words: feedlot health, respiratory disease challenge, yeast

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0112 SafmannanTM and ActiSafTM supplementation in milk replacer modulates health and performance in high-risk, preweaned Holstein calves.

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The objectives of the study were to determine if supplementing milk replacer with Safmannan (SM) and ActiSaf (AS) would affect calf growth and health throughout the preweaned and immediate postweaned periods. The study was performed over 67 d, with 39 Holstein bull calves. Calves were housed in individual pens in an environmentally controlled barn, and were provided ad libitum access to a texturized calf starter and water, as well as offered 350 g of milk replacer solids, 22% CP and 20% fat, at 0700 and 1600 from d 0 to 56. Calf starter and water refusals were recorded daily and intakes calculated. Calves were randomly assigned to treatments that included CON, milk replacer with no added supplements; SM, milk replacer with 5 g SM/calf/d; and SM + AS, milk replacer with 2 g SM/calf/d and 3 g AS/calf/d. Individual BW was measured on d 0, 21, 42, 56, and 67. Blood samples were collected and analyzed for hematology on d 10, 28, and 56; while plasma and whole blood were collected and analyzed for plasma haptoglobin concentrations, neutrophil surface expression of CD62L, and neutrophil phagocytosis and oxidative burst capacity to an environmental *E. coli* on d 0, 10, 28, and 56. All data were reported as CON, SM, and SM + AS, respectively. The LSMeans with various superscripts differ ($P \leq 0.05$). Individual calf starter intake did not differ over the entire study, although from 0 d to 21 d, calves receiving the SM + AS supplement consumed more starter (0.025^{a}, 0.034^{ab}, $0.074^{b} \pm 0.018$ kg/d; $P < 0.05$). Neither ADG (0.63, 0.68, 0.69 ± 0.054 kg/d; $P = 0.699$), nor feed:gain (1.74, 1.74, 1.73 ± 0.070 kg/kg; $P = 0.990$) differed among treatments. Total leukocyte counts were greater in the CON calves on d 10 than the other treatments (14.2^{a}, 9.2^{b}, $11.1^{b} \pm 1.2$ 10^{6}/mL; $P < 0.05$) and was lower in the SM calves on d 28 than the CON and SM + AS treatments (10.4^{a}, 7.9^{b}, $10.6^{a} \pm 0.87$ 10^{6}/mL; $P < 0.037$). Neutrophil surface expression of CD62L was greatest in SM calves when compared with CON calves ($92{,}772^{a}$, $110{,}441^{b}$, $94{,}526^{ab} \pm 5334$ mean fluorescence intensity; $P = 0.052$). Additionally, there were treatment × time interactions on neutrophil phagocytosis and oxidative burst $P \leq 0.024$), whereas SM calves had greater percentages of neutrophils phagocytizing and producing an oxidative burst on d 28. These data suggest that both yeast supplementation strategies may influence the health of high-risk, preweaned Holstein calves.

Key Words: calf, growth, yeast

0113 Evaluation of horn bud wound healing following cautery disbudding of preweaned dairy calves treated with aluminum-based aerosol bandage.

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Dehorning pain management has been extensively studied, though few studies have evaluated the effects of cautery disbudding on wound healing. Inflammation and delayed healing are common postdisbudding, with undocumented significance for health. Our objective was to determine healing following disbudding with or without treatment using topical aluminum-based aerosol bandage (ALU). In a prospective study, Holstein heifer calves raised at three commercial dairy farms were disbudded within 3 wk of life. Local anesthesia and analgesia were performed before disbudding, and ALU treatment was randomly allocated to the right or left bud within each calf. Disbudding site (DS) healing was evaluated thereafter on a weekly basis for 3 wk and lesion score (LS) was categorized as: (1) no scab or discharge; (2) dried scabs; and (3) purulent discharge. LS was dichotomized (normal: LS = 1; and abnormal: LS > 2) to facilitate analysis and interpretation of results and logistic regression was used for statistical analysis. Results were considered statistically significant when $P < 0.05$ and tendency was considered when $0.05 < P < 0.10$. In total, 220 calves were enrolled. There was no difference in LS between groups during the first 2 wk postdisbudding, but at the third week postdisbudding, the proportion of LS = 3 was greater for control DS compared with ALU (16.8 vs. 8.1%, respectively; $P = 0.02$). Similarly, the odds of having LS > 2 were only different during the third week postdisbudding with control DS being 1.42 times more likely to have LS > 2 than ALU treated DS (95% CI = 0.964– 2.10; $P = 0.07$). Abnormal healing during week 1 increased the odds of having abnormal healing in week 2 (OR = 5.36; 95% CI = 2.96–9.69; $P < 0.01$). Likewise, abnormal healing during week 2 increased the odds of abnormal healing during week 3 (OR = 4.22; 95% CI = 2.72– 6.54; $P < 0.01$). A reduction in LS at the third week postdisbudding was observed when using ALU. Once abnormal healing started, it increased the likelihood of abnormal healing later. Discharge and/or scabs may be a part of the normal healing process; however, in this study, it was considered abnormal since no cultures were performed to rule out DS infection. Our data indicates that use of ALU may benefit healing after cautery disbudding in preweaned dairy calves.

Key Words: dairy calves, dehorning, wound healing, well-being

0114 Automated milking systems: using productivity and behavioral data to detect illness in dairy cows. M. T. King*[1], E. A. Pajor[2], S. J. LeBlanc[3], and T. J. DeVries[1], [1]*Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada,* [2]*University of Calgary, Calgary, AB, Canada,* [3]*Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

To develop better ways of using milking activity, productivity, and behavioral data to detect illness, we collected longitudinal data throughout the lactation of 57 Holstein dairy cows (19 PP, 38 MP; 3.1 ± 1.1 lactations) housed in a free-stall barn equipped with an automated milking system (AMS). Cases of illness were recorded, including subclinical ketosis (SCK; n = 23), calving-related disease (CRD; n = 14), hoof disorders and severe lameness (n = 16), pneumonia (n = 8), and gastrointestinal issues and displaced abomasum (DA; n = 7). We collected continuous milking activity data from the AMS. Lying, rumination, and activity data were recorded by electronic data loggers. Data were analyzed in repeated measures mixed linear regression models. Days relative to the day of diagnosis/treatment (d 0) were analyzed as a fixed effect for each illness separately, with data extending back to d –14. Analyses were performed between: (a) the day from which each outcome variable deviated significantly from baseline production/behavior (Tukey's tests were used to make day-by-day comparisons), and (b) d –1, since recovery had begun following treatment on d 0. Outcome variables tested were milk yield (3-d rolling average), daily rumination time, activity (unit-less measure of head and neck motion), and lying behavior (lying time, bout frequency, bout length). Mean milk production declined by 4.3 and 4.1 kg/d from d –4 to diagnosis of DA ($P < 0.001$) and pneumonia ($P = 0.01$), respectively. From d –14 to diagnosis of hoof disorders, production steadily declined by 0.6 kg/d ($P < 0.001$). Mean rumination time declined by 54 and 55 min/d from d –5 to diagnosis of DA ($P < 0.001$) and pneumonia ($P = 0.03$), respectively. Before SCK diagnosis (2 tests/fresh cow ~1 wk apart), rumination decreased by 13 min/d from d –6 to diagnosis ($P = 0.05$); this was most drastic d –3 to –1 (–34 min/d; $P = 0.001$). Activity levels declined by 40 units/d from d –4 to diagnosis of DA ($P < 0.001$), but decreased gradually from d –14 to diagnosis of SCK (–15 units/d; $P < 0.001$) and CRD (–23 units/d; $P < 0.001$). Lying behavior was less predictive of illness, as it did not vary until the day of diagnosis of any illness. These results suggest that the effects of illness on rumination, activity, and productivity are apparent several days before diagnosis and could be used to earlier identify illness in AMS herds. Since behavior and productivity appear to respond differently to various types of illness, it is possible that certain parameters may be illness-specific.

Key Words: automated milking, dairy cow behavior, illness

0115 Occurrence of mycotoxins in the 2015 U.S. corn crop. P. N. Gott*[1], B. G. Miller[1], R. Beltran[2], and G. R. Murugesan, *BIOMIN America Inc., San Antonio, TX.*

Mycotoxins are toxic metabolites produced by filamentous fungi which commonly contaminate feedstuffs harvested for both human and livestock consumption. Although the different types of mycotoxins have variable effects on different livestock species, exposure to mycotoxins can impair health and adversely affect animal performance. The objective of the current study was to determine the occurrence of mycotoxins in the 2015 corn crop in the United States and to assess the potential risk to livestock species. From September 2015 to January 2016, 381 corn samples were collected from 20 states as part of the annual Biomin Mycotoxin Survey. Samples were analyzed either by high performance liquid chromatography (HPLC) or liquid chromatography tandem mass spectrometry (LC-MS/MS) techniques, which are highly sensitive in detecting very low mycotoxin concentrations. The major mycotoxin groups analyzed were aflatoxins (Afla), zearalenone (ZEN), trichothecenes including deoxynivalenol (DON) and T-2 toxin (T-2), fumonisins (FUM), and ochratoxin A (OTA). Mycotoxins were detected in 94% of the corn samples tested and 50% of the positive samples contained more than one mycotoxin. Co-occurrence of mycotoxins may lead to synergism and enhanced toxicity in animals which consume contaminated feed. The percentage of positive samples, mean of positives (ppb), maximum of positives (ppb), and risk threshold (ppb) for the six major mycotoxins are presented in Table 1. The occurrence of Afla, T-2, and OTA were minimal in relation to ZEN, DON, and FUM in these samples. The highest threat in these corn samples was posed by DON due to its high prevalence and number of samples above the FDA recommended level. As a result of their common co-occurrence, ZEN also presents a major threat. In terms of occurrence, FUM ranks second among the six major mycotoxins analyzed in these samples. With the increased occurrence and co-occurrence levels in 2015 compared with the previous year, DON, FUM, and ZEN pose a higher risk to livestock production in 2016.

Key Words: mycotoxins, deoxynivalenol, fumonisin

0116 Associations of hygiene and lying behavior with the risk of elevated somatic cell count and lameness. I. Robles*[1], D. F. Kelton[2], H. Barkema[3], G. P. Keefe[4], J. P. Roy[5], M. A. von Keyserlingk[6], and T. J. DeVries[1], *[1]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [2]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [3]University of Calgary, Calgary, AL, Canada, [4]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada, [5]Faculté de Médecine Vétérinaire, University of Montreal, St. Hyacinthe, QC, Canada, [6]Animal Welfare Program–University of British Columbia, Vancouver, BC, Canada.*

The objective of this study was to identify how cow-level factors and housing management affect the risk of elevated SCC (eSCC) and lameness in lactating dairy cows. Cows from six commercial free-stall dairy herds in Ontario, Canada, were enrolled in a longitudinal study. Ten Holstein cows/herd were randomly selected based on days in milk (DIM; <120 d), absence of mastitis treatment in the last 3 mo, and somatic cell count (SCC < 100,000 cells/mL). Data on SCC were collected through DHI testing (~5 wk intervals). The study began within 7 d after a DHI-milk test, continued until three tests were completed (~105d), for a total of three observation periods/cow. Elevated SCC was used to indicate subclinical mastitis. An incident of eSCC was defined as a cow having a SCC > 200,000 cells/mL at the end of a period when SCC was <100,000 cells/mL at the beginning of that period. Lying behavior was recorded for 6 d after each milk sampling using data loggers. On d 1 of each recording period, a trained observer scored cows for lameness (5-point numerical rating scale, NRS $\geq$ 3 = lame). Hygiene scoring (four-point scale), also done by a trained observer, occurred on each visit. Cows were categorized as clean (1, 2) or dirty (3, 4). Stall cleanliness was assessed with a 1 m^2 metal grid, containing 88 squares, centered between stall partitions of every 10th stall, and then counting the squares containing visible urine and/or fecal matter. Data were analyzed using multivariable logistic regression models. Cows averaged (mean ± SD) 627 ± 107.7min/d lying, 9 ± 2.8 lying bouts/d, and 72 ± 19.9 min/bout. Over the study period, 13 eSCC were detected, resulting in an incidence rate of 0.73 eSCC/cow-year at risk. The risk of experiencing an eSCC increased 1.4× ($P < 0.01$) with every 20,000 cells/mL SCC increment at the beginning of the study. Mean proportion of soiled squares/stall was 27%. Each SD (18.8%) increment in proportion of dirty squares/stall was associated with lameness (NRS $\geq$ 3; OR = 1.5; $P = 0.05$) and increased the odds of having a dirty udder (DU; OR = 2.4; $P = 0.02$). Each SD (108min/d) increment in lying time/d increased the risk of having dirty upper legs and flank (DULF; OR = 2.1; $P < 0.01$), and tended to increase the risk of having a DU (OR = 1.44; $P < 0.08$). For each 9.6% increase above mean (100%) cow/stall stocking density, the risk of having DULF increased by 1.7× ($P = 0.03$). These results indicate that lower stocking density and management practices that improved stall hygiene and should be encouraged to reduce the risk of poor hygiene and clinical lameness in dairy cows housed in free-stall barns.

Key Words: subclinical mastitis, lameness, cleanliness

0117 Using milk fat-to-protein ratio to evaluate dairy cows energy balance status. T. Schcolnik*, *Afimilk, Afikim, Israel.*

The objective of the present study was to establish the association of negative energy balance status of the calving cow with the duration of high daily fat-to-protein ratio (FPR). Such an association could be utilized to evaluate fresh cow's energy balance status. A dairy cow's physiological condition is reflected in the composition of its milk. AfiLab™ is a real-time milk analyzer measuring individual cows' milk fat, protein and lactose contents during each milking. Fat-to-protein ratio is a combination of milk protein production rate with body fat mobilization rate; that is, it reflects energy availability to a cow's body needs of maintenance and production. Negative energy balance (NEB), ketosis, and body condition score losses are related to reduced conception rate and decreased milk yield. Utilizing FPR for evaluation of cows energy status provides valuable indications, which enable prompt intervention and increase economic profit. Daily milk component data, extracted from the ICBA Israeli HerdBook, included 117,846 observations (days in milk [DIM] periods) of 23,192 cows at first lactation or more, calving through 2014, in 44 Israeli Holstein herds using Afilab. Analysis was done by SAS®PROC GLIMMIX. Means of FPR up to 50 DIM were calculated for 3 periods: 1–15, 16–35, and 36–50 DIM. Four categories were defined by FPR threshold of 1.4: (1) means of all periods < 1.4, (19,181 cows); (2) mean of any one period $\geq$ 1.4 (2979 cows); (3) means of any two periods $\geq$ 1.4 (779 cows); and (4) means of all three periods $\geq$ 1.4 (253 cows). The results establish valid associations between production and fertility traits and the duration of NEB after calving. Least squares means of conception to first AI service were 35.34, 31.62, 30.17, and 33.0% for groups 1, 2, 3, and 4, respectively. Differences between groups 2 and 3 vs. group 1 were statistically significant. The least squares means of days open for the same groups were 122, 125, 129, and 128 d, respectively. The least squares means for 180 d milk yield were 7621, 7685, 7636, and 7468 kg, respectively. Differences between groups 1, 2, and 3 vs. group 4 were statistically significant. We concluded that the intensity of the negative effects of NEB on fertility and production variables examined, relates to the duration of NEB after calving. Therefore, real-time detection of NEB per individual cow allows for specific and prompt treatment.

Key Words: energy status, fat-to-protein ratio, production

0118 Evaluation of three lameness detection strategies on the odds of cure in dairy cows. E. M. Wynands*, D. Moe, and G. Cramer, *Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul.*

The high prevalence of lameness in U.S. freestall dairy herds is both an animal welfare and an economic concern. To achieve a low prevalence of lameness, strategies to lower incidence need to be combined with methods to decrease duration. This requires methods to detect and treat lameness. The objective of this study was to evaluate the impact of three lameness detection strategies on the odds of cure. A trial was conducted from June to August 2015 on a dairy farm in Minnesota. Three pens of cows were randomized to different lameness detection strategies. The strategies were: (1) locomotion scoring using a 3-point scale (VLS), (2) headlock scoring by observing leg posture and weight-bearing while cows were restrained (HS), and (3) casual observation at unspecified times (farm's current strategy), serving as the control group (C). Cows newly detected as lame by the different strategies were evaluated in a hoof trimming chute and treated for the cause of lameness. All groups were locomotion scored for lameness once per week (LS) as cows exited the parlor. The weekly LS were used as the outcome measure to assess odds of cure. Cows that began nonlame as defined by LS and who were subsequently diagnosed as lame by LS were included in the analysis. The scores from the LS system showed a high degree of week-to-week variability. Logistic regression models were constructed for the odds of cure at 3 wk (n = 486) and 6 wk (n = 290) following lame diagnosis. At the 3 wk follow-up, 176 individuals (36.2%) remained lame. Primiparous cows had higher odds of recovering than multiparous cows (OR, 1.79; CI, 1.20–2.67). Days in milk at enrollment were negatively associated with odds of cure (P = 0.03). There was no significant association between detection strategy and odds of cure at 3 wk. At the 6 wk follow-up, 125 individuals (43.1%) remained lame. Primiparous cows had higher odds of recovering than multiparous cows (OR, 2.71; CI, 1.62–4.53). The odds of cure were higher in the VLS group compared with the C group (OR, 2.15; CI, 1.12–4.12). The week-to-week variability in individual cow LS identified a limitation of the LS system, as this variation is inconsistent with the pathology of lameness. These results show that the odds of cure improved when the VLS active detection protocol was implemented.

Key Words: dairy, lameness, locomotion scoring

0119 Risk factors for subclinical ketosis in grazing dairy herds in Brazil. R. R. Daros*[1], M. J. Hötzel[2], S. J. LeBlanc[3], J. A. Bran[2], A. J. Thompson[1], and M. A. von Keyserlingk[1], *[1]Animal Welfare Program, University of British Columbia, Vancouver, BC, Canada, [2]Universidade Federal de Santa Catarina, Florianopolis, Brazil, [3]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

Minimizing disease, including subclinical ketosis (SCK), continues to be a challenge for the dairy industry. Work on SCK has focused on confinement systems, with little work on pasture-based dairies. The aim of this study was to determine the prevalence and herd-level risk factors for SCK in cows housed on pasture. We visited 48 pasture-based farms in southern Brazil between February and September 2015. All farms used a rotational grazing system (2 to 3 paddocks per day). Cows (n = 13 per farm) between 3 and 21 d in milk were assessed for SCK based on blood β hydroxybutyrate ≥ 1.2 mmol/L. Data regarding number of recumbent cows up to 3 d after partum (a crude measure of milk fever) over the course of 1 yr, supplemental feeding, and transition cow management were collected using a questionnaire by interview and environmental inspection. Herds were categorized either as Holstein or crossbred (crossbred Holstein and Jersey, or a mix of Holstein and Jersey). Herd-level prevalence of down cows was categorized into low (0–5%), medium (5–10%), and high (>10%). Herd prevalence of SCK was log transformed. Univariable linear regression models were used to select variables associated with SCK (P < 0.2). Variables from the final multivariable model were back transformed for interpretation. The overall prevalence of ketosis was 21%. Breed, down cow prevalence, and access to water (free versus limited access), were retained in the final model. Referent herds had 8% (95% confidence interval [CI]: 5–11%) SCK prevalence and consisted of Holsteins with free access to water and low prevalence of down cows. Compared with referent herds: Crossbred herds had 1.7 times higher predicted prevalence of SCK (95% CI: 1.14–2.55; P = 0.01); limited access to water increased herd level predicted prevalence of SCK by 1.5 times (95% CI: 1.05– 2.31; P = 0.03) and herds with high predicted prevalence of down cows had three times higher prevalence of SCK (95% CI: 1.75–5.09; P < 0.01). Pasture-based dairies appear to have similar point prevalence of SCK to confinement systems, but the risk factors are different. This work indicates that crossbred herds have higher levels of SCK, so prevention methods for SCK in these herds is especially important. Improved feeding and management that would prevent down cows and allowing cows to have free access to water should decrease the prevalence of SCK in grazing dairy herds.

Key Words: health, hyperketonemia, transition period

0120 Mortality risk factors for calves entering a multilocation white veal farm in Ontario.
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Mortality in preweaned dairy breed calves of both sexes represents a potential welfare issue and a source of economic loss for the industries involved. While morbidity and mortality in veal production has been described, this work reflects a wide range of management practices and requirements throughout the world. In preweaned dairy heifers, rates of morbidity and mortality can also range dramatically, due in large part to differing management strategies. It has been over two decades since mortality in veal calves in Ontario was last described. The objective of this retrospective cohort study was to determine if recorded on-arrival data collected from a large white veal farm could be used as predictors of mortality. Data was collected from 10,910 calves entering seven barns of a single white veal farm, all locations of barns within Ontario, from 1 Jan. to 31 Dec. 2014. Calves were followed until death or marketing; no calves were culled during the year. Three logistic regression models were used to determine the effects of weight on arrival, season of arrival, supplier, sex, barn, and standardized purchase price on the risk of overall mortality, mortality in the first 21 d after arrival, and mortality after the first 21 d. In the overall mortality model, significant associations ($P < 0.05$) were seen with season, barn, supplier and weight, with lighter weight calves arriving in winter being at increased odds of mortality. The early mortality model contained significant ($P < 0.05$) associations with weight, season, barn, supplier and tended ($P < 0.10$) to have an association with standardized price; lighter weight calves arriving in winter at lower prices were at increased odds of mortality. The late mortality model had significant ($P < 0.05$) associations with season of arrival, barn and supplier. While not a proxy for body condition, increased weight on arrival being protective for early mortality may have somewhat reflected this, as the distribution of weights was fairly tight and likely represented calves at a week of age or less. Although failure of passive transfer is a significant risk factor for mortality, the seasonal association we saw could reflect early life nutrition stress as opposed to seasonal variation in passive transfer. A further exploration of dairy farm of origin risk factors for veal calf mortality may serve to improve the productivity and welfare of dairy calves of both sexes.

Key Words: calf, mortality, veal

0121 Assessment of tubal patency by hysterosalpingo-contrast sonography in cow.
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Recently, several studies have reported the use of ultrasound contrast media to assess tubal patency during transvaginal ultrasound in the imaging of infertile women. However, in the field of veterinary medicine, there is little information regarding the use of hysterosalpingo-contrast sonography to test for tubal patency. The present study aimed to estimate the clinical usefulness of hysterosalpingo-contract sonography for tubal patency in cows. Five nonlactating Holstein cows were used, and four of them were treated twice. Sixteen microliters of perflubutane (Sonazoid® for injection, Daiichi-Sankyo) was diluted with 60 mL of saline as echo-contrast medium. At the luteal phase (around 10 d after ovulation), a 16 Fr balloon catheter was gently inserted into one uterine horn, the balloon was placed approximately 5 cm cranial to the uterine bifurcation. The linear probe of the ultrasound (5.0 MHz) was inserted rectally and 30 mL of echo-contrast medium was injected slowly into the uterine horn through the catheter. After the injection, the flow of contrast medium in the uterus, uterotubal junction, and oviduct was monitored with the ultrasound for 20 min. The opposite oviduct was tested in the same way. Tubal patency was diagnosed if the contrast medium was visualized at the infundibulum of the oviduct. Twelve of 18 cases were diagnosed as tubal patency. Contrast medium was first observed within the uterus and then immediately moved toward the oviduct. In the case of tubal patency, it was visualized as a funnel-like appearance adjacent to the ovary at the infundibulum of the oviduct. The transit time of the contrast medium to reach the infundibulum of the oviduct after injection was 6.5 ± 3.3 min ($n = 12$). Two cases were diagnosed as tubal obstruction. Although the contrast medium was clearly visualized in the uterus and the isthmus of the oviduct, an accumulation of contrast medium was found at the position of the ampulla of the oviduct in one of them. The other four cases were inconclusive because of poor image quality due to posterior echo enhancement and technical artifact. The present study demonstrated that the flow of the contrast medium injected to the uterus was visualized at the infundibulum of the oviduct, suggesting that hysterosalpingo-contrast sonography is useful as a diagnostic tool for tubal patency in cows. However, further technical improvement is required to reduce inconclusive cases for accurate diagnosis.

Key Words: tubal patency, hysterosalpingo-contrast sonography, cow

0122 Retained placenta and subclinical endometritis: Prevalence and relation with reproductive performance in crossbred dairy cows. R. R. Buso, C. C. Campos, T. R. Santos, J. P. E. Saut, and R. M. Santos*, *FAMEV-UFU, Uberlândia, Brazil.*

Our objective was to determine the effects of type of calving (eutocic vs. dystocic) and season of the year (rainy vs. dry) on retained placenta (RP) and subclinical endometritis (SE) prevalences verify the relationship between these two diseases, and effects of RP and SE on culling rate, calving to conception interval, and number of AI/conception in crossbred dairy cows. The study was conducted in nine different dairy farms located in Minas Gerais state, Brazil. Retention of fetal membranes was recorded on the first day postpartum. Endometrial cytology was performed between 30 and 80 d in milk (DIM) and the threshold used for SE diagnosis was ≥5% neutrophils. Data were analyzed by logistic regression and ANOVA on Minitab program. The prevalence of RP was 14.93% (69/462) and of SE was 27.49% (127/462). A tendency of effect of RP on SE prevalence was detected (35.82 vs. 26.07%; $P = 0.10$). Dystocia increased RP prevalence (68.42 vs. 12.19%; $P < 0.05$). Cows, which calved during rainy season, had greater SE prevalence (35.48 vs. 20.41%; $P < 0.05$). RP increased culling rate (19.40 vs. 6.08%; $P < 0.05$), calving to conception interval (177.46 vs. 131.19 d; $P < 0.05$) and number of AI/conception (3.30 vs. 2.46; $P < 0.05$), although SE occurrence did not affect these variables ($P > 0.05$). In conclusion, RP showed to be a risk factor for SE, dystocia is a predisposing factor for RP and cows calving during the rainy season had an increase in SE prevalence. There is a negative impact of retained placenta on reproductive efficiency of crossbred dairy cows. Supported by FAPEMIG e CnPQ.

Key Words: cytological endometritis, reproductive efficiency, dairy cows

0123 Association of rumination time and health status with milk production in early lactation dairy cows. V. H. Asselstine[1], E. I. Kaufman[1], S. J. LeBlanc[2], B. W. McBride[1], T. F. Duffield[2], and T. J. DeVries*[1], *[1]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [2]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

The objective of this study was to characterize the associations of rumination time (RT) and health status with milk yield (MY) and milk composition in early lactation dairy cows. A total of 339 dairy cows (first lactation, $n = 107$; second lactation, $n = 112$; ≥ third lactation, $n = 120$) on 4 commercial dairy farms in Ontario, Canada, were monitored from 1 to 28 d in milk (DIM) for rumination behavior (24h/d using an automated system), milk composition (fat, protein, somatic cell count, and milk urea N 1×/wk), and hyperketonemia (HYK; blood β hydroxybutyrate ≥ 1.2 mmol/L, measured 1×/wk). Cows were milked 3 times/d at each farm; Two farms recorded milk weights at each milking to determine daily MY ($n = 170$). Cases of retained placenta, metritis, milk fever, or mastitis during the study period were recorded. Cows were categorized into 1 of 3 groups: healthy (HLT) cows had no HYK or any other recorded disease ($n = 139$); HYK cows with no other health problems during transition ($n = 97$); or hyperketonemic plus (HYK+) cows that had HYK and ≥1 other health problems ($n = 53$). Data were summarized by week and analyzed in repeated measures general linear mixed models. A positive association was found between weekly summarized RT and MY in first (+0.006 ± 0.003 kg milk/min RT, $P = 0.04$) and second lactation (+0.01 ± 0.004 kg milk/min RT, $P < 0.01$) cows from 4 to 28 DIM. A positive association was also seen in parity 3+ cows, however, the relationship between RT and MY differed ($P < 0.01$) across weeks (wk +1: +0.05 ± 0.007 kg/min RT; wk +2: +0.06 ± 0.008 kg/min RT; wk +3: +0.05 ± 0.011 kg/min RT; wk +4: +0.04 ± 0.014 kg/min RT). During wk +2 and +3, second lactation HYK cows had lower milk protein percentage compared with HLT cows (0.08 ± 0.043w/w% and 0.12 ± 0.041w/w%, respectively; $P \leq 0.05$). Hyperketonemia+, second lactation cows also had lower milk protein content compared with HLT cows in wk +1, and +2, (0.14 ± 0.068w/w% and 0.20 ± 0.089w/w%, respectively; $P \leq 0.05$). Over the 4 wk observation period, first lactation HYK+ cows tended to have lower protein compared with HLT cows ($P = 0.1$) and ≥ third lactation HYK and HYK+ cows produced less protein than HLT cows ($P \leq 0.03$). Second lactation cows in HYK+ produced less milk than HLT cows during wk +1 (7.1 ± 2.9 kg/d, $P = 0.02$), +2 (14.2 ± 4.0 kg/d, $P < 0.001$), +3 (13.8 ± 4.5 kg/d, $P = 0.003$), and +4 (10.6 ± 5.3 kg/d, $P = 0.05$). Ketosis decreased MY and protein percentage variably with parity. Rumination time was shown to have a positive association with MY in early lactation dairy cows.

Key Words: hyperketonemia, milk production, rumination behavior

0124 Associations of cow-level factors with the risk of poor hygiene. I. Robles[*1], D. F. Kelton[2], H. Barkema[3], G. P. Keefe[4], J. P. Roy[5], M. A. von Keyserlingk[6], and T. J. DeVries[1], *[1]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [2]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [3]University of Calgary, Calgary, AL, Canada, [4]Atlantic Veterinary College, University of Prince Edward Island, Charlottetown, PE, Canada, [5]Faculté de médecine vétérinaire, University of Montreal, St. Hyacinthe, QC, Canada, [6]Animal Welfare Program, University of British Columbia, Vancouver, Canada.*

The objective of this study was to identify how cow-level factors affect the risk of having poor hygiene. Cows from 68 commercial dairy herds in Ontario, Canada, were enrolled in a cross-sectional study. Cows were housed in free-stall (FS, n = 43) or tie-stall (TS, n = 25) barns. Twenty-five percent of the cows in each lactating pen (FS) or row of stalls (TS) in herds with > 160 cows, or a minimum of 40 cows per herds with <160 cows were randomly selected for hygiene scoring (n = 2594 cows). Cows were scored for cleanliness on each of three visits (7d apart), on a scale of 1 (clean) to 4 (dirty), in each of three zones (lower leg, udder, and upper leg and flank); scores were categorized as: clean $\leq$ 2 or dirty $\geq$ 3. DHI data from the test closest to the first visit and another test closest to the last visit were obtained. Data were analyzed using multivariable logistic regression models. DIM (mean ± SD) was 171.6 ± 106.1 for cows housed in FS barns and 177.4 ± 114.0 for those in TS barns. In FS barns, first and second parity cows were at 1.5× and 1.4×, respectively, greater risk ($P < 0.01$) of having dirty lower legs (DLL) compared with $\geq$ 3 parity cows. Also in FS barns, first parity cows had a lower risk of having a dirty udder (OR = 0.40; $P < 0.05$), as well as dirty upper legs and flank (DULF; OR = 0.84; $P = 0.01$), when compared with $\geq$3 parity cows. In TS barns, first lactation cows had a 2.3× greater risk ($P < 0.01$) of having DLL compared with $\geq$3 parity cows. First and second parity cows in TS barns had greater risk (OR = 1.9 and 1.3, respectively) of having DULF ($P < 0.01$). Each SD (114.0) increment in DIM was associated with lower risk of having DLL (OR = 0.41; $P < 0.01$) and dirty upper legs and flank (DULF; OR = 0.60; $P < 0.01$) for cows in TS barns. Each SD (106.1) increment in DIM was associated with lower risk of having a dirty udder (OR = 0.90; $P = 0.03$) and DULF (OR = 0.84; $P < 0.01$) for cows housed in FS barns. The results suggest that cow hygiene varies by parity and stage of lactation in both free-stall and tie-stall barns.

Key Words: hygiene, housing, parity

0125 Genomic markers associated with hyperketonemia in Jersey cows. R. S. Pralle[*1], H. A. Adams[2], T. L. Chandler[1], and H. M. White[1], *[1]Department of Dairy Science University of Wisconsin, Madison, [2]CRI International Center for Biotechnology, Mount Horeb, WI.*

Hyperketonemia is a metabolic disorder in dairy cattle commonly attributed to a parturition-induced negative energy balance. Prevalence of this disorder is variable among dairy operations with similar management strategies, as well as among dairy breeds. This suggests differences in genetic selection practices among farms and breeds that may alter a cow's predisposition to hyperketonemia. Identification of genomic markers for hyperketonemia could assist dairy producers in identifying transition cows requiring intensive management. The objective of our study was to identify genetic markers associated with the hyperketonemia phenotype. Genomic marker association was performed on 387 Jersey cows genotyped with the *GeneSeek* Genomic Profiler LD v3 chip. Blood and hair samples were collected at a single time-point from Wisconsin (5–21 d in milk [DIM], five herds) and New England (2–30 DIM, five herds) Jersey cows. Serum β-hydroxybutyrate (BHBA) concentration was determined by a colorimetric assay. Samples were diagnosed into categorical phenotypes for threshold and gap analysis, generating two case-control phenotype sets based on serum BHBA concentrations. Threshold hyperketonemia cases were defined as BHBA concentration $\geq$ 1.2 mM, and remaining cows were controls; gap cases were BHBA concentrations $\geq$ 1.2 mM, and controls were BHBA concentrations $\leq$ 1.0 mM. A log-additive model that accounted for parity group was applied to the data, using the SNPassoc package in R, to identify markers significantly associated with hyperketonemia status. Means ± standard error are reported. Markers were considered significant at a false discovery rate-corrected $P \leq 1 \times 10^{-6}$. The mean DIM at sample collection was 15.0 ± 0.73. The prevalence of hyperketonemia within the dataset was 22.0%. Blood BHBA was 0.68 ± 0.01 mM for controls and 2.08 ± 0.13 mM for cases. Thirteen markers were found to be significant in the gap and/or threshold analyses. Six markers were significant across both analyses. Of the significant markers identified in threshold or gap comparisons, markers were identified within exonic regions of eight genes: periphilin 1, multimerin 2, alkB homolog 1 histone H2A dioxygenase, Parkinson disease protein 2 co-regulated-like, ataxin 1, protein phosphatase 1, β-γ crystallin domain containing 3, and 2,3-cyclic nucleotide 3 phosphodiesterase. Although gene functions are not exclusive to energy metabolism, the research objective was to identify markers consistently associated with hyperketonemia, which may serve as valuable genetic markers. Identification of these markers can aid in establishing a marker-assisted management program for Jersey dairy producers striving to effectively

manage hyperketonemia.

Key Words: Jersey, hyperketonemia, genome association study

0126 Meta-analysis of factors influencing new intramammary infection rate in experimental challenge teat dip efficacy trials. B. D. Enger[*1], R. R. White[1], S. C. Nickerson[2], L. K. Fox[3], *[1]Virginia Tech, Blacksburg, [2]University of Georgia, Athens, [3]Washington State University, Pullman.*

Using an effective teat dip before and after milking reduces the incidence of new intramammary infection (IMI) on dairies. Many factors influence a teat dip's efficacy, and this is why all teat dips should be confirmed efficacious before commercial circulation. To date, many teat dip efficacy trials have been conducted and are published in peer-reviewed journals. The objective of the present study was to conduct a meta-analysis of data from peer-reviewed teat dip efficacy trials that used an experimental challenge study design to identify factors influencing the new IMI rate. A dataset of 21 studies (148 observations) was created. The new IMI rate, based on percentage of new quarter infections/month (PNQI/mo), was calculated for each recorded observation and used as the dependent variable for model derivation. A linear, mixed-effects model with a random study effect, weighted for the standard error of the measurement was derived in a stepwise manner where parameters were sequentially eliminated for nonsignificance. The final mixed model included the terms for the causative mastitis pathogen ($n = 2$; $P = 0.55$), postmilking treatment ($n = 4$; $P < 0.01$), geographic region where the trial was conducted ($n = 3$; $P = 0.02$), and interaction between study region and pathogen group ($P < 0.01$) and postmilking treatment and pathogen group ($P < 0.01$). Overall, the new IMI rate between the causative mastitis pathogens, *Staphylococcus aureus*, 0.0409 ± 0.0097 PNQI/mo and *Streptococcus agalactiae*, 0.0344 ± 0.0096 PNQI/mo, were similar. Quarters not dipped with a postmilking teat dip, 0.0859 ± 0.0087 PNQI/mo, had a greater new IMI rate than those dipped with a postmilking teat dip containing either iodine, 0.0127 ± 0.0099 PNQI/mo, a chlorine compound, 0.0258 ± 0.0095 PNQI/mo, or an "other" active ingredient, 0.0263 ± 0.0106 PNQI/mo ($P < 0.05$). Quarters dipped with postmilking teat dips had similar new IMI rates ($P > 0.05$). Studies conducted in the southern United States, 0.0531 ± 0.0040 PNQI/mo, had a higher new IMI rate than those conducted in the Pacific Northwest, 0.0072 ± 0.0141 PNQI/mo ($P < 0.05$), but not those in the eastern United States, 0.0527 ± 0.0206 PNQI/mo ($P > 0.05$). The results of this meta-analysis indicate that using an efficacious postmilking teat dip has a greater impact on the new *Staphylococcus aureus* and *Streptococcus agalactiae* IMI rate than the active germicidal ingredients present in the postmilking teat dip itself.

Key Words: active ingredient; mastitis; teat disinfectant

0127 The effects of short-term feeding of tocopherol mix (α-, β-, γ-, and δ) on blood neutrophil function and immunometabolic-related gene expression in lactating dairy cows. Y. Qu[*1], T. H. Elsasser[2], M. Garcia[1], C. M. Scholte[1], E. E. Connor[3], J. R. Newbold[4], and K. M. Moyes[1], *[1]Department of Animal and Avian Sciences, University of Maryland, College Park, [2]USDA-ARS, Animal Biosciences and Biotechnology Laboratory, Beltsville, MD, [3]USDA-ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD, [4]Cargill Innovation Center, Velddriel, the Netherlands.*

Alpha-tocopherol has been well-studied regarding improving neutrophil function, especially its involvement in respiratory burst. However, no studies have identified the effect of feeding a tocopherol mix, which contains additional isoforms, on immune cell function. The objective of this study was to investigate how short-term feeding of tocopherol mix alters bovine blood neutrophil (BBN) function and immunometabolic-related gene expression. Twelve healthy, multiparous Holstein cows (DIM: 179 ± 17d) were fed a vegetable-derived tocopherol oil supplement (Tmix) enriched with γ- and δ-isoforms (9% α-, 1% β-, 24% δ-, and 62% γ-tocopherol) at ~620 g Tmix·cow^{-1}·d^{-1} top dressed for seven consecutive days. Jugular blood (~200 mL) was collected from all cows on d 0 before feeding and on d 7 postfeeding of Tmix. Whole blood was then used to measure respiratory burst response via chemiluminescence analysis. Isolated BBN (3×10^6 cells/mL) were used for chemotaxis and immunometabolic-regulated gene expression analysis by quantitative real-time PCR. For gene expression analysis, cells were incubated with lipopolysaccharide (LPS) at a final concentration either of 0.0 or 1.5µg/mL for 2 h at 37°C, 95% humidity, and 5% CO_2. Data were analyzed as a complete randomized design. Significance was declared at $P \leq 0.05$. With regard to function, Tmix improved ($P = 0.04$) BBN chemotaxis function but did not alter ($P = 0.9$) the respiratory burst response in whole blood. For gene expression analysis, LPS challenge increased the expression of proinflammatory genes tumor necrosis factor-α and interleukin-6. However, Tmix did not alter the expression of genes associated with the immune or metabolic response. In conclusion, short-term feeding of Tmix did not impair BBN function of respiratory burst but improved chemotaxis, and Tmix did not alter the immunometabolic response of genes in BBN. Additional evaluations of the effect of individual tocopherol isoforms will offer valuable information regarding their specific roles on bovine immune cell function and gene expression.

Key Words: bovine, neutrophil, tocopherol

0128 Predicting hyperketonemia prevalence in Jersey herds from milk composition and cow test-day information using multiple linear regression.

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Multiple linear regression models have been validated to predict hyperketonemia in Holstein herds; however, potential differences in milk composition and hyperketonemia prevalence warranted further sampling and distinct models for Jersey herds. The objective of this study was to validate the use of multiple linear regression models to predict β-hydroxybutyrate (BHBA) from milk composition and continuous test-day variables in Jersey cows to serve as a diagnostic tool for determining herd-level ketosis prevalence. Blood samples were collected on the same day as milk sampling from 468 Jersey cows 5 to 20 DIM on six dairy farms. Serum BHBA concentration was quantified by colorimetric assay (Stanbio, Boerne, TX). Milk samples were analyzed for concentrations of milk BHBA, acetone, and fatty acid (FA) groups (saturated, unsaturated, trans, short, medium, and long chain FA) by fourier transform infrared (FTIR) spectrometry from MilkoScan FT+ (FOSS Analytical A/S, Hillerød, Denmark), in addition to standard milk analysis variables. Continuous test-day variables were exported from DairyComp305 (Valley Ag Software, Tulare, CA) records. Models were built in the REG procedure of SAS 9.4 (SAS Institute Inc., Cary, NC) using forward stepwise selection by excluding variables with a P-value > 0.15 and using selection criterion of sequential sums of squares, error sums of squares, and Akaike's information criterion. Statistical parameters (R^2, adjusted R^2, root mean square error) were calculated to evaluate model performance. Hyperketonemia, defined as a serum BHBA $\geq$ 1.2 mM, prevalence within the sample set was 20%. Data interrogation justified development of separate models for primiparous and multiparous groups, as well as 5 to 11 and 12 to 20 DIM groups. Significant variables were BHBA, acetone, fat %, protein %, somatic cell count, FA groups, pervious days carried calf, age at calving, previous ME305 milk production, test-day DIM and milk production. Overall, model accuracies were 91% for multiparous cows 5 to 11 DIM (R^2 = 0.85), 86% for multiparous cows 12 to 20 DIM (R^2 = 0.64), 90% for primiparous cows 5 to 11 DIM (R^2 = 0.64), and 90% for primiparous cows 12 to 20 DIM (R^2 = 0.83). Collectively, models predicted animals with hyperketonemia at the 1.2 mM threshold with 86% accuracy. Results suggest that modeling blood BHBA based on milk composition data and cow-test day information provides a practical tool for monitoring hyperketonemia prevalence in Jersey herds.

Key Words: *ketosis, linear regression, Jersey*

0129 Liver transcriptome modifications by nutrient restriction in early lactation Holstein cows challenged with intramammary lipopolysaccharide.

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The objective was to test effects of nutrient restriction on liver transcriptome 24 h after an intramammary lipopolysaccharide (LPS) challenge in early lactation cows. At 24 ± 3 d in milk, multiparous cows were either allowed to continue ad libitum intake of a lactation diet (CON, n = 6), or the ration was diluted with barley straw (48% DM) for 4 d (RES, n = 6). On d 3, one healthy rear mammary quarter was infused with 50 µg of LPS (*E. coli* 0111:B4). Blood and liver biopsies were collected on d 4, corresponding to 24 h after LPS challenge. Liver transcriptome was analyzed with 44K bovine microarrays (Agilent Technologies). Blood and transcriptomic data were analyzed using SAS mixed models and GeneSpring (moderated t test with Westfall-Young correction, $P < 0.05$), respectively, and data mining was performed using Panther and Pathway Studio software. Energy balance did not differ before diet change. By experimental design, energy intake was limited to 41 and 97 ± 15% of NE_L requirements in RES and CON, respectively (mean ± SD; $P < 0.001$). Plasma NEFA and BHBA were greater, and glucose was lower for RES compared with CON (1221 vs. 382 µM, 2.67 vs. 0.70 mM, 56 vs. 69 mg/dL respectively, $P \leq 0.05$, before biopsy), which is consistent with 4 d of nutrient deficit in REST. We detected 77 differently expressed genes (DEG) between CON and RES, with 29 down-regulated and 48 up-regulated in RES. Genes involved in fatty acid synthesis (*ACAT2*, *FASN*, *SCD*), lactate metabolism (*LDHC*), and cortisol binding (*SERPINA6*) were down-regulated in RES, whereas those involved in fatty acid oxidation, detoxification, cholesterol synthesis, lipoprotein lipid secretion, and gluconeogenesis (*ACADVL*, *CPT1A*, *CPT1B*, *ANGPTL4*, *CYP4A11*, *HMGCSA*, *APOA1*, *APOA4*, *GK*, *PC*, and *PCK2*) were up-regulated in RES. Overall, DEG were in agreement with negative energy balance and plasma metabolite profile, and reflect a state intense lipomobilization, glucose deficit and ketogenesis in RES. Preliminary results suggest that nutrient restriction did not change liver expression of genes directly involved in immune function 24 h after

an intramammary LPS challenge.

Key Words: inflammation, liver transcriptome, undernutrition

0130 Growth and transcriptional profile analysis following oral probiotic supplementation in dairy cows.

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The objective of this study was to assess the impact of probiotic administration on growth and global gene expression profile in dairy cow. Use of probiotic supplements is a nonchemical approach to promote animal health. Understanding the mechanism of action of probiotics in cows may aid in sustainable dairy production. Lactating Holstein-Friesian cows (n = 10) received daily oral doses (50ml) of a commercial probiotic FASTtrak microbial pack (Conklin Company, Kansas City, MO) (containing *Lactobacillus acidophilus, Saccharomyces cerevisiae, Enterococcus faecium*, *Aspergillus oryza*, and *Bacillus subtilis*) over a 60-d period. Body weight was recorded weekly. Whole blood was collected at the beginning (d 0) and end of the study (d 60). Blood samples were analyzed for total and viable cell count, packed cell volume (PCV), white blood cell differential counts (WBC), and total protein concentration in plasma. Daily supplementation of probiotics had no effect on BW, PCV, and total protein concentration in plasma at the end of the study ($P > 0.05$). Percentage lymphocyte count increased ($P < 0.05$), and percentage neutrophil count ($P < 0.05$) decreased in probiotic-treated animals. Gene expression analysis identified 10,859 differentially expressed genes, 1168 up-regulated and 9691 down-regulated genes respectively following probiotic administration. Pathway analysis identified 87 bovine pathways impacted by probiotic treatment. These pathways included the Toll-like receptor signaling pathway, inflammation response and Wnt signaling pathways. Oral administration of probiotic to dairy cows has a systemic effect on global gene expression, including genes involved in immunity and homeostasis (Wnt). The results of this study show that the utilization of probiotics in animal agriculture impacts genes important to dairy cow health and production. Further definition of the interaction between the pathways involved may aid in the design of the most effective probiotics for optimum dairy production and health.

Key Words: dairy cows, innate immunity, microarray, probiotic

0131 Mammary gland transcriptome and proteome modifications by nutrient restriction in early lactation Holstein cows challenged with intramammary lipopolysaccharide.

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The objective was to evaluate the effect of nutrient restriction and intramammary lipopolysaccharide (LPS) challenge on mammary gland (MG) gene expression in early lactation cows. At 24 ± 3 d in milk, multiparous cows were either allowed to continue ad libitum intake of a lactation diet (CON, n = 6), or the ration was diluted with barley straw (48% DM) for 4 d (RES, n = 6). On d 3, one healthy rear mammary quarter was infused with 50 µg of LPS. Mammary biopsies were performed 24 h after LPS challenge. RNA and proteins analyzed using bovine 44 K microarrays (Agilent Technologies) and micro-LC-MS/MS, respectively. Transcriptomic data were analyzed using GeneSpring (moderated-t test with Westfall-Young correction, $P < 0.05$). Proteins were analyzed with Progenesis LC-MS software v.4.1 (Nonlinear Dynamics). Production and energy balance did not differ before diet change. Negative energy balance was aggravated in RES (41 vs. 97 ± 15% of requirements, mean ± SD; $P < 0.001$). A total of 87 differentially expressed genes (DEG) were highlighted through the comparison of RES vs. CON group. Among the 33 DEG identified in the transcriptomic analyses, 11 and 22 were down- and up-regulated by restriction, respectively. Among the up-regulated DEG, there were *PDK4* and *CPT1A* which are involved in the regulation of fatty acid, ketone, and glucose metabolism. *CPT1A* is the key enzyme in the carnitine dependent fatty acid transport, promoting fatty acid oxidation. Genes involved in immune response such as *PGLYRP3* and *TRIB2* were up-regulated, suggesting a higher inflammatory response in RES than CON. Proteomic analysis identified 54 proteins with 14 up- and 40 down-regulated in RES cows. Up-regulated proteins were mostly involved in gene expression mechanisms such as translation, RNA splicing and cellular protein modification. The down-regulated proteins (*e.g.*, EIF3H, RS27A, RS15) take part in protein metabolism. This is coherent with transcriptomic results, namely the down-regulation of *RPL 37A*, a component of ribosomal complex, which catalyzes protein synthesis and may partially explain the lower milk protein yield in RES (834 vs. 1163 g/d; P = 0.02). Proteins involved in antigen processing and presentation were down-regulated in RES compared with CON, suggesting an impaired ability to counteract inflammation in RES MG. Preliminary transcriptomics and proteomics analyses show that undernutrition may influence the MG response

to inflammation at each level of gene expression.

Key Words: mammary omics, undernutrition, inflammation

0132 Methionine supplementation modulates the inflammatory response of dairy cow blood neutrophils in response to lipopolysaccharide.

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Methionine (Met) is among the two most-limiting amino acids for milk production in dairy cow diets. The accepted optimal ratio when formulating diets is a Lys:Met of 3:1. However, blood from cows fed corn silage-based diets without supplemental rumen-protected Met averages ~3.6:1. Our recent in vivo research on immunonutrition revealed the immune system could benefit from additional Met. To study the effect of different Lys:Met ratios, blood neutrophils were isolated from five mid-lactating pluriparous Holstein cows (238 ± 20 DIM, 33.8 ± 3.9 kg/d average milk production) to obtain a homogenous pool. Neutrophils were then incubated at a concentration of 6 × 10^6 cells/mL for 2 h in a sterile incubator at 37°C and 5% atmospheric CO_2. A 3 × 2 factorial arrangement of treatments including three Lys:Met ratios (3.6:1, 2.9:1, 2.4:1) and two levels of lipopolysaccharide (LPS, 0 and 50 μg/mL) were evaluated in triplicate. After incubation, cellular RNA was used to measure expression of genes related to immune function and oxidative stress. Data were $\log_2$ normalized and subjected to ANOVA using the Proc MIXED procedure of SAS. As expected, LPS increased ($P < 0.05$) the expression of pro- and noninflammatory cytokines (*IL1B*, *IL10*, *IL6*, *TNF*) and immune-related nuclear receptors (*NFKB1*, *NR3C1*). However, LPS decreased ($P < 0.05$) the expression of chemokine *CXCR1* and antimicrobial enzyme *LYZ*, the latter only when cells were incubated with higher Met (2.9:1 or 2.4:1), and had no effect ($P < 0.05$) on other pathogen killing mechanisms (*MPO, SOD1*). Among genes related to Met metabolism, LPS increased ($P < 0.05$) expression of *MAT1A*, while reducing expression of *GPX1* and *GSR*, suggesting a greater use of Met and a reduced antioxidant system during the inflammatory response. Compared with the lowest level of supplemental Met (3.6:1 Lys:Met) the highest level (2.4:1 Lys:Met) decreased ($P < 0.05$) expression of *NFKB1*, *NR3C1*, and *GSR*, while it increased ($P < 0.05$) *IL6* independently of the LPS level. Furthermore, expression of the noninflammatory cytokine *IL10* was greatest ($P < 0.05$) at 2.4:1 Lys:Met and in non-LPS challenged cells, indicating that supplemental Met improved the oxidative status and the noninflammatory conditions of neutrophils. Overall, data support the idea that Met supplementation could improve the inflammatory and oxidative status of bovine neutrophils.

Key Words: LPS, methionine, neutrophils

0133 Feasibility and safety of nitric oxide releasing solution as a treatment for bovine mastitis.

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Nitric oxide releasing solution (NORS) is a liquid formulation that releases nitric oxide (NO). NO is a broad, nonspecies-specific nonmicrobial nanomolecule, endogenously produced during the innate response in mammals. The objective of this study was to explore the feasibility of NORS as a potential treatment for bovine mastitis (BM). Two common pathogens found in BM (10^6 CFU/mL of *Escherichia coli* and *Staphylococcus aureus*) were added to raw milk from healthy cows, as an in vitro model, to determine the antimicrobial efficacy of NORS at different concentrations (100–400 mM) and at two different NORS:milk ratios (2:1 and 1:1). Next, 10 ex vivo samples of milk from dairy cows presenting with clinical mastitis were obtained and treated with NORS to confirm efficacy. A dose escalating safety study was then performed using three dairy cows, where 40 mL of increasing concentrations of NORS (50–400 mM) were infused into the teat. Nitrite and methemoglobin levels were measured 5, 30, and 460 min posttreatment and nitrites in milk were measured 8 and 24 h posttreatment. Nitrite was measured by chemiluminescence, while methemoglobin was measured using a CO-Oximeter. Results show that NORS could eradicate, in vitro, both bacteria, and was dilution and time dependent. In the 2:1 ratio, NORS significantly ($P < 0.05$) reduced bacterial concentration in milk both in vitro and ex vivo within 2 min, and had no detectable bacteria after 5 min of exposure. In the 1:1 ratio, a significant bacterial load reduction ($P < 0.01$) occurred within 10 min and no detectable bacteria within 20 to 30 min. In the safety study we found an increase in blood nitrites ($P < 0.05$) within 5 min of the NORS treatment at all concentrations. After 8 h, the blood values at all concentrations returned to baseline ($P = 0.27$). Blood methemoglobin changes were nominally increased in the 5 and 30 min samples post 400 mM NORS and no detectable change was seen after 8 h. Eight hours posttreatment, before the evening milking, milk nitrites were 18 times higher than baseline, while 24 h posttreatment nitrites returned to baseline level ($P = 0.36$). NORS was found to eradicate bacteria in milk and, clinically, the treatment was well tolerated. This suggests that NORS has a potential to be a safe and effective nonmicrobial treatment for BM and may allow salable milk during antimicrobial treatment of mastitis. Further, it would provide an alternative to antibiotics, thus contributing to the reduction of antibiotic drug resistance. Further studies are justified.

Key Words: mastitis, nitric oxide, safety study, treatment

0134 Methionine coupled with choline supplementation alters inflammation and oxidative stress gene network expression of dairy cow blood neutrophils. M. Vailati Riboni[*1], A. Bellingeri[2], I. Khan[3], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*Università Cattolica del Sacro Cuore, Piacenza, Italy,* [3]*University of Agriculture, Peshawar, Pakistan.*

The nutritional status of dairy cows is tightly-correlated to the maintenance of proper immune function and health. Methionine (Met), besides being one of the first-limiting amino acids, has stimulatory effects on immune cells both directly and indirectly as a source of antioxidants. The objective of this study was to investigate the effect of supplementing Met or choline as its potential precursor on neutrophil gene expression. Blood neutrophils were isolated from five lactating multiparous Holstein cows (153 ± 5 DIM, 34.6 ± 2.7 kg/d average milk production) to obtain a homogenous pool. Cells were then incubated at a concentration of 6×10^6 cells/mL for 4 h in a sterile incubator at 37°C and 5% atmospheric CO_2. A 3 × 3 factorial arrangement of treatments, including three Lys:Met ratios (3.6:1, 2.9:1, 2.4:1) and three levels of choline chloride (3, 400, 800 μg/mL), were evaluated in triplicate cultures. Cellular RNA was used to measure expression of genes related to inflammation, antioxidant status, and the Met cycle. Data were $\log_2$ normalized and subjected to ANOVA using the Proc MIXED procedure of SAS. The greater expression ($P < 0.05$) of *MTR* at 2.9:1 and 2.4:1 Lys:Met indicated greater flux through the Met cycle compared with 3.6:1 Lys:Met. Both *BHMT* and *CHDH* were undetectable, indicating that neutrophils cannot generate Met from choline through the betaine pathway. Compared with the lowest level of supplementation (3 μg/mL), at the highest level of choline (800 μg/mL) there was lower expression ($P < 0.05$) of pro- (*IL6*, *IL1B*) and noninflammatory (*IL10*) cytokines, and antimicrobial mechanisms (*MPO*, *SOD1*), coupled with lower expression ($P < 0.05$) of genes related to the antioxidant system (*CDO1*, *CSAD*, *CTH*, *GSR*, *GSS*). These indicated a degree of inflammation, together with oxidative stress in neutrophils at the low choline level. In contrast, the interaction among treatments revealed that at higher (2.9:1 and 2.4:1 Lys:Met) Met and low choline (3 μg/mL) supplementation level the expression of *GSS*, *GSR*, *IL1B*, and *IL6* was lower ($P < 0.05$), hence, limiting the negative effect of a low choline level. Furthermore, higher Met supplementation increased ($P < 0.05$) neutrophil recognition capacity (*TLR4*, *SELL*) when incubated together with 400 μg/mL of choline. Overall, data indicate a choline requirement in bovine neutrophils that could potentially be overcome by Met supplementation. Despite this, neutrophil function appeared to be enhanced at high Met together with adequate choline supplementation.

Key Words: methionine, choline, neutrophils

0135 Impact of a BRDC vaccine with a MLV or KV IBR component on the innate inflammatory profile of nulliparous heifers. C. L. Widener*, D. J. Hurley, W. M. Graves, A. H. Nelson, D. A. L. Lourenco, and J. F. Bohlen, *University of Georgia, Athens.*

To investigate the difference in the inflammatory response between bovine respiratory disease complex (BRDC) vaccines containing either a modified live vaccine (MLV) or a killed component for infectious bovine rhinotracheitis (IBR), 28 Holstein heifers (mean ± SD; 12.4 ± 0.5 mo) in two replicates (spring $n = 12$ and fall $n = 16$) were synchronized for estrus using a 7-d CIDR protocol. This protocol included two injections of $PGF_{2\alpha}$, one at CIDR removal and a follow-up injection 16 h later. All animals were calf-hood vaccinated with an available BRDC vaccine with a modified live IBR component. At approximately Heat 2, heifers were vaccinated with either the calf-hood MLV ($n = 14$) or a BRDC vaccine with a killed ($n = 14$) IBR component. Heifers were vaccination blocked according to prevaccination bovine viral diarrhea virus (BVDV) serum neutralizing (SN) titers. On d –7, relative to vaccination, a complete blood count (CBC) and an assay to measure neutrophil activity, as indicated by the relative presence of reactive oxygen species (ROS) were performed to establish a baseline immune profile. Two heifers were removed from the trial for preexisting immunological challenge. These assays were repeated on d 1 postvaccination, d 3 postvaccination, and then weekly until the heifer was bred (Heat 4). Data were analyzed with the PROC MIXED procedure of SAS. The fixed effects for the model were: season, vaccine type, and week relative to vaccination. There was no difference ($P > 0.05$) in postvaccination SN titers. Vaccine type had no significant effect ($P > 0.05$) on any of the cell types measured by the CBC. Season did have a significant effect ($P = 0.0008$) on the circulating lymphocytes, with the fall heifers exhibiting higher average lymphocytes on d 1 and wk 2, 3, 4, 5, and 6 postvaccination. The ROS response ratio was not impacted by vaccine ($P > 0.05$) but was influenced ($P < 0.0001$) by both season and the season × week interaction. When comparing seasons, spring heifers maintained a higher average response ratio when compared with the fall heifers on d 3 and wk 1, 2, 3, 5, and 6 postvaccination, which is substantiated by their higher average circulating granulocytes ($P < 0.05$). These seasonal differences may be a consequence the severe immunological challenge experienced by the fall group shortly after vaccination, which may have obscured their true vaccine response.

Key Words: neutrophil, ROS, IBR MLV

0136 Association between bovine milk infrared temperature and bacteriological results from CHROMagar Mastitis Plates and PathoProof Mastitis Complete-16 Kit. M. G. Marrero-Pérez*, J. Curbelo-Rodríguez[2], G. Ortiz-Colón, H. L. Sánchez-Rodríguez, and Y. R. Vélez-Robles, *University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico.*

Pathogen identification is an important tool for dairy farmers to treat mastitis infections properly. Alternative tools for early identification of mastitis cases should help farmers to increase milk quality and animal health. Infrared thermography (IRT) was used to determine the milk's temperature profile through the short milking tube, and its association with CHROMagar Mastitis plates (CHROM) and the PathoProof Mastitis Complete-16 Kit (PtoPrf-16) bacteriological results were evaluated. Individual mammary quarters (n = 23) with subclinical mastitis (determined by the California Mastitis Test) from two dairy herds in Puerto Rico were evaluated. Milk samples (10 mL in duplicates) were collected and stored in ice for subsequent evaluation. During the morning milking (from 0300 to 0600 h), IRT images were collected 2 min postmilking unit attachment in 30s intervals using an IRT camera (FLIR-E8). Temperature and relative humidity were also recorded using HOBO-U23Prov2Data Loggers. Somatic cell count (SCC) and bacterial identification were determined using a DeLaval Cell counter and CHROM, respectively. Additional samples were sent to the Dairy Herd Improvement Association (Manheim, PA) for bacterial identification using the PtoPrf-16, to be compared with CHROM results. A PROC GLIMMIX in SAS (University Edition version) was used to determine differences in IRT and logSCC by bacteriological results (CHROM vs. PtoPrf-16). The two herds had no difference in logSCC and IRT (P = 0.10); therefore, quarters were analyzed collectively. No differences in IRT or logSCC were found when mastitis pathogens were or not isolated in quarter milk samples using the PtoPrf-16 (P = 0.29 and P = 0.07) and CHROM (P = 0.80 and P = 0.67), respectively. No differences in IRT were observed when PtoPrf-16 (P = 0.69) and CHROM results (P = 0.91) were further categorized by Gram-positive, Gram-negative, mixed isolation, and no-detection, with mean IRT and standard error values of 33.61 ± 0.05 and 33.11 ± 0.36, 33.26 ± 0.62 and 33.75 ± 0.45, 33.86 ± 0.55 and 32.67 ± 0.57, and 32.98 ± 0.43 and 33.36 ± 0.72, respectively. The CHROM and PtoPrf-16 tests can identify 10 and 15 different mastitis pathogens, respectively. However, only 34.78% of bacteriological results concurred among them. The IRT was affected by relative humidity (P < 0.05) but not by ambient temperature (P = 0.16). More data is required to characterize the use of IRT as a tool to discriminate quarters with mastitis. The lack of association among IRT and mastitis pathogens could be attributed to environmental factors such as relative humidity. The discrepancies among bacteriological results among CHROM vs. PtoPrf-16 suggest that additional studies are required to further characterize these differences.

Key Words: CHROMagar, infrared thermography, PathoProof Mastitis

0137 The endometrial microbiome in transition cows fed an energy-restricted diet. G. Esposito*[1,2], J. J. Lim[3], T. Tasara[4], P. C. Irons[2,5], E. C. Webb[2], and A. Chapwanya[3], *[1]Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Pretoria, South Africa, [2]Institute of Food, Nutrition and Well-being, University of Pretoria, Pretoria, South Africa, [3]Ross University School of Veterinary Medicine, Basseterre, Saint Kitts and Nevis, [4]3Institute for Food Safety and Hygiene, Vetsuisse Faculty University of Zurich, Zurich, Switzerland, [5]Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Onderstepoort, South Africa.*

The objective of this study was to evaluate the effect of negative energy balance (NEB) on the endometrial microbiome of transition cows. Ten Holstein cows blocked by parity, BW, and BCS were randomly assigned to two groups: control (CTL) and NEB (80% of the net energy required). Endometrial cytobrush samples were collected at 14 and 35 d postpartum (DPP) and DNA was extracted using a QIAamp DNA Micro Kit. Based on next generation sequencing of 16S rRNA genes, 403 operational taxonomic units (OTUs) were detected. All continuous variables were analyzed by ANOVA. A comparison of the alpha diversity, based on the number of OTUs present, revealed no significant differences in uterine microbiome diversity between 14 and 35 DPP in the CTL group, but significantly (P < 0.05) lower diversity 14 and 35 DPP within the NEB group. The CTL group microbiome on 14 DPP showed significantly (P < 0.05) higher diversity compared with the NEB group. At genus level, the majority of OTUs detected were shared between 14 and 35 DPP (CTL, 47/68 [69%]; NEB, 40/65 [61.5%]) within both groups. However, in the CTL group, there were 16 OTUs detected at 14 DPP that were not present at 35 DPP, while 5 OTUs found at 35 DPP were not detected at 14 DPP; in the NEB group, 4 OTUs at 14 DPP were not detected at 35 DPP, whereas 21 OTUs detected at 35 DPP were not present on 14 DPP. At phylum level, on 14 DPP, Proteobacteria (39.2 vs. 0.46%) and Firmicutes (44.3 vs. 33.7%) were higher in CTL compared with the NEB uterine microbiome; Bacteroidetes (29.9 vs. 8.9%), Fusobacteria (14.3 vs. 3.4%), and unassigned (20.1 vs. 1.4%) phyla predominated in NEB compared with CTL. On 35 DPP, the CTL microbiome was predominated by Cyanobacteria and Proteobacteria sequences, while the NEB microbiome was predominated by Firmicutes and Bacteroidetes. Differences in Proteobacteria and Bacteroidetes levels at 14 and 35 DPP, respectively, were statistically significant (P < 0.05). Relative

abundances of Actinobacteria, Cyanobacteria, and Proteobacteria were significantly higher at 35 DPP compared with 14 in NEB cows. No significant differences were detected in CTL. Our preliminary data although inconclusive due to small sample size and individual animal microbiome variations suggest that there might be some microbiome composition differences between the CTL and NEB at 14 and 35 dpp.

Key Words: NEB, endometrial microbiome, next generation sequencing

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0138 Fecal microbial shifts of the German Holstein dairy cows with left-sided displacement of the abomasum.

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One of the most common diseases in high-performance German Holstein dairy cows is left-sided displacement of the abomasum (LDA). Hypomotility of the abomasum is detrimental during the pathogenesis of LDA. Also, it is known that the improper interactions between the gut microbiota and the enteric nervous system contribute to dysfunctions of gastrointestinal motility. Therefore, we hypothesized that the gut microbial composition will be different between German Holstein dairy cows with and without LDA. We compared the fecal microbiota between cows with and without LDA using 16S ribosomal RNA (rRNA) gene analysis. A total of 20 German Holstein dairy cows at one dairy farm in South Korea, including eight cows without LDA (control group) and 12 cows with LDA (LDA Group), were enrolled in this study. All cows were housed under the same conditions and were fed the same feed without any antibiotics or supplementary additives. Right after LDA was diagnosed, fecal samples were collected immediately from the rectum. Total DNA representing the fecal microbial communities was extracted from individual fecal samples using the stool DNA extraction kit, and the 16S universal primers 27F (5′ GAGTTTGATCMTGGCTCAG 3′) and 800R (5′ TACCAGGGTATCTAATCC 3′) were used to amplify 16S rRNA genes (V1-V4 hyper variable regions). The composition and relative abundance of each member of the microbiota in feces from the control group were different from the LDA group. The proportion of Spirochaetes was significantly different between groups at the phylum level ($P <$ 0.001). An average of 1.5% of the microbiota was members of Spirochaetes in the feces of the control group. On the other hand, there were no Spirochaetes detected in the feces of the LDA group. At the genus level, relative abundance of five genera was significantly different between groups. The proportion of the genus *Enterohabdus* (a member of Actinobacteria), the proportions of members of Firmicutes including *Cellulosilyticum*, *Streptococcus*, and *Turicibacter*, and the proportion of *Treponema* (a member of Spirochaetes) were all significantly higher in the control group than in the LDA group. However, further studies will be needed to elucidate the roles of these genera in the pathogenesis of LDA. Overall, results from this study show that the fecal microbial compositions of German Holstein dairy cows with LDA shifted and were less diverse than those in normal cows.

Key Words: German Holstein dairy cow, microbiome, LDA

0139 Genetic parameters and impact of postpartum diseases on lactation curves in dairy cattle.

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Genetic improvement for milk yield in dairy cattle has impacted the shape of the lactation curve, in addition to the total production. Likewise, incidence of diseases early in the lactation can affect the lactation curve. The objective of this study was to investigate simultaneously health and genetic factors influencing the lactation curve. Test-day milk records on more than 6000 Holstein cows across four states (California, Florida, Minnesota, Texas) and nine herds were evaluated. The trajectory of the lactation curve was modeled using nonlinear mixed effects models including Wood's and Wilmink's functions. The effects of environmental and health indicators on the level of milk yield, increase in milk production early in lactation (Wood's) or milk yield at peak (Wilmink's), and persistency thereafter were evaluated. These effects included: season (summer or winter), state, parity, vaginal mucus score at 7 d postpartum, metritis at 7 d postpartum, mastitis cases within the first 60 d postpartum, blood β-hydroxybutyrate (BHBA) indicating subclinical ketosis, body condition score at 35 d (BCS35), displaced abomasum (DA) by 60 d postpartum, respiratory illness by 60 d postpartum (Resp), and lameness at 35 d. Sire of cow was included in the model as random effect. Estimates from the Wood's model indicated that multiparous cows have significantly higher levels of milk yield immediately after calving and lower persistency than primiparous cows. Lactation curves in winter had higher yield immediately after calving and lower persistency than in summer. Metritis had a negative effect on milk yield level immediately

after calving as well as on persistency. Mucus score and DA had a negative impact on milk yield immediately after calving. Consistent with Wood's estimates, Wilmink's estimates indicated that multiparous cows have higher milk production and lower persistency than primiparous cows. Number of mastitis cases and DA were associated with lower overall milk production and higher persistency. Beta hydroxybutyrate was associated with a higher level of milk yield and lower persistency. The ratio of sire to residual variance estimates from Wood's and Wilmink's functions were consistent and approximately 0.4. Wood's model offered a better fit for the lactation curves considered. Our findings demonstrate the need to incorporate disease indicators on the assessment of the genetic component influencing the trajectory of the lactation curve. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: lactation curves, metritis, nonlinear mixed models

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0140 Genetic and environmental components of disease traits in dairy cattle.

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Diseases in U.S. Holstein are responsible for losses of approximately $ 1 billion annually in dairy production due to reduced milk production and increased costs. The objective was to assess the impact of environmental factors and magnitude of genetic parameters on the incidence of diseases in dairy cows early (<10 d) and late (35 to 60 d) postpartum. Binary and multinomial disease records on approximately 6000 Holstein cows from farms in Texas, Minnesota, California, and Florida were evaluated using mixed effects logistic and Poisson models. Early postpartum binary diseases included: dystocia, retained placenta, subclinical ketosis (blood β-hydroxybutyrate BHBA > 1), and metritis. Late postpartum binary diseases included: displacement of abomasum, mastitis, respiratory problems, and clinical endometritis. Mucus score at 7 d, number of mastitis cases up to 60 d, and lameness at 35 d (five levels) were analyzed assuming a Poisson model. Fixed effects in all models included: lactation number (3 levels), season (summer and winter), U.S. region, and farm. Other fixed effects evaluated depending on the disease included: twins, body condition score, BHBA level, calf gender, stillbirth, first test-day milk production record, and other diseases. The cow's sire was included as a random effect in the models. Overall lactation, region, and season had a significant effect on the incidence of all diseases, except for lactation on respiratory problems, and season on mastitis and displacement of abomasum. First lactation cows exhibited the highest incidence of dystocia, metritis, and clinical endometritis and lowest incidence of mastitis, retained placenta, lameness, and displacement of abomasum. Clinical endometritis, metritis, lameness, and respiratory problems were lower in summer than winter. Dystocia, retained placenta, and subclinical ketosis were positively and significantly associated with clinical endometritis and metritis. Subclinical ketosis and dystocia were positively and significantly associated with displacement of abomasum. Mastitis was negatively and significantly associated with milk yield at first test-day. Heritability estimates for the diseases ranged from 0.06 (retained placenta) to 0.4 (respiratory problems). The differences in genetic parameter estimates among alternative disease descriptors offer insights into effective approaches to lower the incidence of disease through genetic selection. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: metritis, postpartum, production

0141 Undernutrition alters metabolic responses to acute inflammation in early lactation cows.

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The objective was to test effects of nutrient restriction on responses to an intramammary lipopolysaccharide (LPS) challenge in early lactation cows. Multiparous Holstein cows were either allowed ad libitum intake of a lactation diet throughout the study (CON, n = 9, 7.1 MJ/kg DM NE_L, 17.4% CP), or the ration was diluted with barley straw (48% DM) for 4 d (RES, n = 8, 5.2 MJ/kg DM NE_L, 12.2% CP) starting at 24 ± 3 d in milk. After 72 h, one healthy rear mammary quarter was infused with 50 µg of LPS (*E. coli* 0111:B4). Blood samples were collected at –1.5, –0.5, 1, 2, 4, 6, and 10 h relative to LPS. Data were analyzed using SAS mixed models. Intake, milk, and protein yields and NE_L balance did not differ before diet change (21.8, 39.0, 1.15 kg/d, and –5.6 MJ/d, respectively, on d –1), but were significantly affected in RES (9.8, 28.3, 0.79 kg/d and –74 MJ/d, respectively, on d 3 of restriction and before LPS), as were plasma indicators (Table 1). Insulin response (area under the curve, AUC) to LPS was lower

Table 0141.

Table 1. Plasma insulin and metabolite concentration at 72 h of dietary treatments and response to LPS challenge. $P < 0.01$ for all variables.

	Treatments	
	CON	RES
Insulin (μIU/mL)		
72 h	17	11
AUC_{10h} [1]	174	42
NEFA (μM)		
72 h	370	1672
AUC_{10h}	-1,957	-9,047
BHBA (mM)		
72 h	0.69	2.98
AUC_{10h}	3.68	-6.05
Glucose (mg/dL)		
72 h	69	50
AUC_{10h}	-17	64

[1] Incremental area under the curve during 10 h post-LPS, concentration units per 10 h.

in RES compared with CON, but it was greater for NEFA, BHBA, and glucose. The NEFA nadir post LPS was 599 and 101 μM at 4 h for RES and CON ($P \leq 0.001$), respectively, and it preceded insulin change in RES. The BHBA decrease in RES was consistent with NEFA response to LPS, but BHBA increased from a low baseline in CON (treatment × time interactions, $P \leq 0.05$). The negative glucose AUC in CON could be related to the insulin increase post LPS. Rectal temperature increase did not differ between treatments (+2.1 ± 0.15°C at 6 h). Nutrient restriction altered peripheral metabolic responses to an intramammary LPS challenge.

Key Words: inflammation, undernutrition, dairy cow

0142 Potential modulation of the toxic effects of *Escherichia coli* in bovine endometrium by lactic acid bacteria. S. Genís[*1], A. Sánchez-Chardi[2], A. Bach[3,4], and A. Arís[1]. [1]*Department of Ruminant Production, IRTA, Caldes de Montbui, Spain,* [2]*Servei de Microscopia, UAB, Cerdanyola del Valles, Spain,* [3]*ICREA, Barcelona, Spain,* [4]*IRTA, Caldes de Montbui, Spain.*

The ultrastructural assessment of toxic effects using field emission scanning electron microscopy (FESEM) and transmission electron microscopy (TEM) can provide important information to elucidate the mechanisms of infection and to develop preventive strategies. The aim of this study was to evaluate the effects of a lactic acid bacteria (LAB) combination, based on *L. rhamnosus* MOI 25, *P. acidilactici* MOI 25, and *L. reuteri* MOI 2, at preventing *Escherichia coli* infection and maintaining bovine endometrial tissue health. Triplicate samples of epithelial cell cultures were studied in a 2 × 2 factorial design in the presence or absence of an *E. coli* infection and with or without LAB. Samples were mounted in FESEM stubs and observed without coating in a Zeiss Merlin microscope. A qualitative assessment of general structure of the epithelium (size and shape of cells, ultrastructure, and amounts of ultrastructure of microvilli), presence of *E. coli* and LAB in cell surface, cell debris, presence of mucus in the cell surface, mitochondrial damage, and cell death was performed by the analysis of 10 random selected areas for each treatment. For TEM, contrasted ultrathin sections were observed in a Jeol 1400 operating at 80kV. A semiquantitative approach was performed by the analysis of 10 random selected sections in three areas for each treatment and data were analyzed using a Fisher exact test. *Escherichia coli* alone or with LAB appeared in low numbers in epithelial cells surface and in no case formed biofilms or interactions between each other. *Escherichia coli* abundance was lower ($P < 0.05$) in samples treated with LAB than in those infected with *E. coli* alone. Healthy epithelium was observed in cells treated with LAB (epithelial cells with normal size and shape and normal aspect of microvilli), whereas in cultures infected with *E. coli*, abundant areas with cell debris and bacilli in epithelial cell surface were observed. The incidence of necrosis (as assessed by TEM) in *E. coli* samples tended ($P = 0.07$) to be greater than in noninfected cultures. Control or LAB preincubated cells showed less mitochondrial damage ($P = 0.01$) than nontreated cells, a parameter strongly related to cell death. Overall, LAB appear to offer protection against *E. coli*, by mechanism different than the formation of biofilms, and thus, LAB combinations could be used as a preventive strategy for metritis.

Key Words: endometrium, FESEM, TEM

0143 **Meta-analysis of factors influencing new intramammary infection rate in natural exposure teat dip efficacy trials.**

0144 Effects of lactic acid bacteria on metritis prevalence and endometrium inflammation in dairy cows. S. Genís*[1], R. L. A. Cerri[2], A. Bach[3,4], B. F. Silper[2], J. Denis-Robichaud[5], and A. Arís[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada, [3]ICREA, Barcelona, Spain, [4]IRTA, Caldes de Montbui, Spain, [5]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada.*

The aim of this study was to evaluate the effects of a treatment with *Lactobacillus rhamnosus*, *Pediococcus acidilactici*, and *Lactobacillus reuteri* (LAB) on the prevalence of metritis and the modulation of endometrial inflammation in dairy cows. In Experiment 1, 135 cows were enrolled 3 wk before calving and randomly assigned to treatments to ensure similar frequencies for parity and previous illness in all treatment groups. The treatment groups were: (1) two intravaginal doses of lactic acid bacteria (LAB) per wk during 3 wk precalving (vaginal); (2) 1 intrauterine dose 1 d after calving (endometrial); and (3) no intervention (control). Metritis was diagnosed at d 6 when body temperature > 39.5°C and purulent vaginal discharge (>50% pus or worse) was observed. Data were analyzed using a chi-square. Vaginal treatment reduced ($P < 0.05$) metritis prevalence up to 62% compared with the Control group. However, prevalence of metritis did not differ between the endometrial and control groups. In Experiment 2, a combination of in vivo and ex vivo assays to evaluate whether LAB exerted some effects on the endometrium was designed. Twenty healthy do-not-breed cows were enrolled in Experiment 2, and 3 wk before culling were randomly distributed into two treatment groups: (1) 2 doses of vaginal LAB per wk during 3 wk (LAB); and (2) two vaginal doses of carrier (sterile sodium chloride 0.9%) per wk during 3 wk (CTRL). Endometrium was recovered at slaughterhouse and cut in the laboratory in 0.8 cm^2 explants that were incubated by sixtiplicate in 24 well-plates and either infected with *Escherichia coli* or maintained in medium for evaluating the basal expression of proinflammatory genes in the endometrium. Supernatant was collected for IL-8, IL-1β, and IL-6 analysis by ELISA. Explants were recovered for the quantification of proinflammatory gene expression by qPCR. Data were analyzed using an ANOVA, considering treatment and infection as fixed effects and animal as a random effect. Neither the expression of proinflammatory genes nor the direct quantification of IL-8, IL-1b, or Il-6 differed between infected and noninfected explants. In conclusion, when an intravaginal treatment of LAB is applied there is an important reduction on metritis prevalence although this reduction is not mediated by a direct effect the probiotic on the endometrium neither by increasing the protection against *E. coli* nor by reducing basal inflammation.

Key Words: *Escherichia coli*, LAB, metritis.

0145 Metritis severity score misclassification underpredicts consequence cost of disease. M. M. McCarthy* and M. W. Overton, *Elanco Animal Health, Greenfield, IN.*

The objective of this research was to determine the impact of disease misclassification on the estimated impact of metritis on milk production and time to pregnancy. Differential misclassification introduces bias that usually results in underestimating the true association. A convenience sample of DairyComp305 data representing 1 yr of calvings ($n = 3485$) from one midwestern Holstein herd was used. This herd was chosen because it had good recorded incidence of both mild and severe metritis cases. The original dataset included metritis recorded as mild or severe, or not recorded (NR) where no metritis was observed, and was considered to contain the metritis true severity (TS). First, to evaluate the impact of misclassification bias, we retrospectively randomized 40% of mild metritis to be classified as NR to represent inconsistent disease recording (IR); then, all mild metritis cases were changed to NR to represent poor disease recording (PR). The TS, IR, and PR datasets were analyzed separately in JMP. ANOVA was conducted for second test 305 d mature equivalent (2nd305ME), and a multivariate Cox proportional hazards model was conducted for time to pregnancy, censoring at 300 d in milk. Nonsignificant variables were removed when $P > 0.10$, but the variable metritis was forced into all models. Based on the TS model, adjusting for effects of lactation group, month fresh, early lactation mastitis and displaced abomasum, a case of mild metritis was associated with 405 kg less 2nd305ME and a case of severe metritis was associated with 1106 kg less 2nd305ME compared with no metritis. For the IR model, a case of mild metritis was associated with 376 kg less 2nd305ME and a case of severe metritis was associated with 1050 kg less 2nd305ME compared with no metritis. For the PR model, severe metritis was associated with 990 kg less 2nd305ME compared with NR. The IR and PR models underestimated 2nd305ME loss for severe metritis cases by 56 and 116 kg/cow, resulting in 8721 and 18,007 kg of milk loss unaccounted for at the herd level, respectively, compared with TS. For the TS model, cows that did not have metritis were 1.31 times more likely to get pregnant than cows with severe metritis ($P = 0.01$). The risk ratio difference in IR and PR models were 0.03 and 0.08, respectively. Overall, misclassification of metritis cases results in greater bias and largely underestimates the true association between metritis

and consequence costs of the disease.

Key Words: disease consequence, metritis severity, misclassification bias

0146 Subacute ruminal acidosis negatively affects conception rate in Holstein heifers. H. Khalouei*[1], A. A. Alamouti[2], A. Mohammadi-Sangcheshmeh[2], N. Farzaneh[3], J. C. Plaizier[1], and E. Khafipour[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, Canada, [2]Department of Animal and Poultry Sciences, Aburaihan Campus, University of Tehran, Pakdasht, Tehran, Iran, [3]Faculty of Veterinary Medicine, Ferdowsi University, Mashhad, Iran.*

Symptoms of subacute ruminal acidosis (SARA) have been studied at length, but its effects on reproductive performance are not fully understood. Our objective was, therefore, to determine if experimentally induced SARA reduces conception rates of Holstein heifers. One hundred and ten heifers were synchronized for artificial insemination by two injections of $PGF_{2\alpha}$ in a 13 d interval, and assigned randomly to two treatments. The control heifers received a diet containing 32% (DM basis) barley-based concentrate, while the SARA challenge group received a diet containing 68% of this concentrate. The remainder of the diet consisted of corn silage, alfalfa hay, wheat straw, soybean meal, wheat bran, and a vitamin-mineral supplement. Diets were fed ad libitum. The SARA challenge diet started 3 d after the second $PGF_{2\alpha}$ injection, and continued for 7 d. Forty one heifers from the SARA group and 39 heifers from the control group showed visible signs of heat and were inseminated. Heifers in SARA group had higher DMI (10.4 vs. 9.0 kg d^{-1}, $P < 0.01$) and lower rumen pH (6.02 vs. 6.45, $P < 0.01$) and fecal pH (6.71 vs. 6.97, $P < 0.01$) at 6 h post feeding compared with control heifers. The SARA challenge increased rumen concentrations of ruminal lactate, propionate, and valerate, but did not affect the concentrations of acetate, butyrate, and isovalerate. The challenge did not affect glucose, urea nitrogen, aspartate aminotransferase, calcium, and cortisol concentrations in blood, but it lowered blood β-hydroxybutyrate ($P < 0.01$). Induction of SARA markedly reduced first service conception rate tested by ultrasonography 28 d after insemination (53.7 vs. 71.8%, $P < 0.05$). Additionally, 100% of control heifers that were confirmed as pregnant in the 28 d test were also pregnant at 60 d test, whereas this ratio was only 73.9% ($P < 0.01$) in SARA-challenged heifers, suggesting that SARA had a persistent effect on reproduction that lasted at least 60 d after insemination. Results suggest a negative effect of SARA on fertility of dairy heifers. Further studies are required to investigate the possible effects of lipopolysaccharide translocation and systemic immune response that is associated with SARA on embryo survivability to fully elucidate the mode of action of SARA on reproductive performance.

Key Words: conception rate, fertility, subacute ruminal acidosis

0147 Evaluating milk fat to protein ratio and milk fat to lactose ratio as indicators for early lactation disease. S. Paudyal*[1,2], F. P. Maunsell[3], C. A. Risco[3], A. Donovan[3], A. De Vries[4], D. Manriquez[1], and P. J. Pinedo[1,5], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]West Texas A&M, Canyon, [3]College of Veterinary Medicine, University of Florida, Gainesville, [4]Department of Animal Sciences, University of Florida, Gainesville, [5]Texas A&M AgriLife Research, Amarillo.*

The objective was to evaluate the potential of milk fat to protein (FP) and milk fat to lactose (FL) ratios for detection of clinical disease before evident clinical signs. Milk component data from 198 Holstein cows were recorded until 60 days in milk (DIM), using the AfiLab® milk analysis system at the University of Florida (UF) Dairy Unit. Milk components were recorded as an average of AM and PM milkings. Occurrence of health disorders (mastitis [MAS], metritis [MET], clinical hypocalcemia [HYC], digestive disorders [DIG], lameness [LAM], and ketosis [KET]) were assessed by UF veterinarians and farm personnel. Two indices were developed: (i) Cow index (CI) = measurement on the day of diagnosis (d 0) minus –3 to –5 d average relative to d 0, divided by the –3 to –5 d average; and (ii) mates index (MI) = (–3 to –5 d average minus pen mates –3 to –5 d average value)/pen mates d 0 value. Cow alert value (CAV) and mates alert value (MAV) were set when the respective index value was less than –0.1 or more than +0.1.The correlation between FP and FL was intermediate for both sick and healthy cows ($r = 0.50$ and 0.56, respectively). The odds (95% CI) of MAS multiplied by 1.16 (1.01–1.34) and 1.36 (1.26–1.47), for each decimal unit increment in FP and FL, respectively. For each decimal unit increment in FP and FL, the odds of MET multiplied by 1.38 (1.25–1.54) and 1.36 (1.25–1.47), respectively; the odds of KET multiplied by 1.43 (1.31–1.57) and 1.34 (1.24–1.44); the odds of HYC multiplied by 0.40 (0.22–0.73) and 1.39 (1.14–1.69); and the odds of DIG multiplied by 1.31 (1.22–1.39) and 1.35 (1.24–1.47). The odds of LAM were only significant for changes in FL [1.28 (1.12–1.45)]. Sensitivity and specificity calculations (Table 1) suggested that changes in both FP and FL may be used as indicators of disease; MAS and KET were better detected using FL, whereas FP was more effective for HYC detection. Overall, MAV was more effective than CAV on disease detection.

Key Words: disease, fat/lactose, fat/protein

Table 0147.

Table 1: Sensitivity and specificity of alarms by disease condition

	CAV[1]		MAV[2]	
Disease[3]	Sensitivity (%)	Specificity (%)	Sensitivity (%)	Specificity (%)
Fat/Protein ratio				
MAS	54.1	65.9	59.5	66.9
MET	54.8	65.9	54.8	66.8
HYC	100	65.9	100	66.8
DIG	44.1	65.9	55.9	66.9
LAM	52.6	65.9	42.1	66.8
KET	48.8	65.9	53.5	66.8
Fat/Lactose ratio				
MAS	65.7	67.2	74.3	68.6
MET	54.8	67.1	74.2	68.6
HYC	50.0	67.1	50.0	68.5
DIG	53.5	67.2	56.9	68.6
LAM	50.0	67.1	50.0	68.5
KET	57.1	67.1	66.7	68.6

[1]Cow alert value; [2]Mates alert value; [3]MAS = mastitis; MET = metritis; HYC = clinical hypocalcemia; DIG = digestive disorders; LAM = lameness; KET = ketosis

0148 Associations between multiple activity and physiological parameters around the time of disease diagnosis and calving in Holstein cows.

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Our objective was to describe the associations between multiple activity and physiological parameters around the time of disease diagnosis and calving in Holstein cows. Health disorders included mastitis (MAS), metritis (MET), milk fever (MF), depression-dehydration-fever (DDF), digestive problems (DIG), lameness (LAM), and clinical ketosis (KET). Behavioral activity included general activity index (HEAD, activity units), rumination time (RUM, min/d), steps (STEP, *n*/d), steps per hour (SH, *n*/h), and lying bouts (LB; *n*/d) from –15 to 15 d relative to disease diagnosis and calving. Data were collected from 198 Holstein cows from –15d from due date to 60 d in milk, at the University of Florida Dairy Unit. HEAD and RUM data were recorded using a neck collar containing rumination loggers (Hr-Tag®, SCR Engineers Ltd., Netanya, Israel), and STEP, SH, and LB data were recorded by a device attached on one hind leg (Pedometer plus®, Afikim, Israel). Data were log transformed and analyzed using MIXED procedures of SAS. To assess associations between activity variables, Spearman's *P* correlations and *P*-values were calculated using JMP12 (Table 1). The only significant negative correlation was found between SH and LB (–0.60) in cows diagnosed with MAS, showing reduced SH from –9d to –4d and an increased LB activity from –8 to –2 d. Correlations between HEAD and RUM were positive and significant for all the diseases, showing a marked decrease from –6 to –5 d to the time of diagnosis with a subsequent increase until 10 d after diagnosis. In addition, significant positive correlations were determined in MAS cows (RUM/STEP, $r = 0.41$); MET cows [RUM/SH ($r = 0.46$); RUM/LB ($r = 0.53$); and SH/LB ($r = 0.59$)]; MF cows [RUM/STEP ($r = 0.63$); and HEAD/SH ($r = 0.54$)]; DDF cows [RUM/LB ($r = 0.52$); and STEP/LB ($r = 0.43$)]; DIG cows (HEAD/RUM, $r = 0.65$); LAM cows [HEAD/STEP ($r = 0.44$); HEAD/LB ($r = 0.40$); and RUM/LB ($r = 0.62$); KET cows [HEAD/STEP ($r = 0.40$); HEAD/SH ($r = 0.57$); HEAD/LB ($r = 0.51$); RUM/SH ($r = 0.52$); and RUM/LB ($r = 0.39$)]. Significant positive correlations at calving included HEAD/SH ($r = 0.93$), RUM/STEP ($r = 0.91$), RUM/LB ($r = 0.93$) and STEP/SH ($r = 0.94$). Correlation patterns between activity and physiological parameters were dependent on specific diseases, suggesting differential potentials as indicators for early disease that could be used in dairy health monitoring programs.

Key Words: activity, rumination, disease

Table 0148.

Table 1. Spearman's p Coefficients by disease and Activity and Physiological Parameters.

		Mastitis (n=31)		Metritis (n=31)		Milk Fever (n=6)	
Variable	by Variable	Spearman *p*	*P-value*	Spearman *p*	*P-value*	Spearman *p*	*P-value*
HEAD	RUM	0.57	<0.01*	0.80	<0.0001*	0.66	<0.0001*
HEAD	STEP	0.17	0.38	0.21	0.29	0.09	0.73
HEAD	SH	0.20	0.31	0.38	0.053	0.54	0.04*
HEAD	LB	-0.01	0.94	0.28	0.16	-0.01	0.97
RUM	STEP	0.41	0.03*	0.22	0.27	0.63	<0.01*
RUM	SH	0.21	0.28	0.46	0.02*	0.03	0.9
RUM	LB	0.14	0.46	0.53	<0.005*	-0.17	0.53
STEP	SH	0.23	0.22	0.20	0.33	0.45	0.1
STEP	LB	-0.10	0.62	0.03	0.87	0.13	0.64
SH	LB	-0.60	<0.001*	0.59	<0.01*	0.26	0.35

		DDF (n=27)		Digestive (n=51)		Lameness (n=15)	
Variable	by Variable	Spearman *p*	*P-value*	Spearman *p*	*P-value*	Spearman *p*	*P-value*
HEAD	RUM	0.41	0.03*	0.65	0.0001*	0.57	<0.01*
HEAD	STEP	-0.04	0.84	-0.07	0.74	0.44	0.02*
HEAD	SH	0.17	0.39	0.00	0.99	0.05	0.78
HEAD	LB	0.07	0.74	0.04	0.82	0.40	0.03*
RUM	STEP	0.25	0.19	-0.05	0.79	0.27	0.16
RUM	SH	-0.01	0.94	0.09	0.65	-0.13	0.49
RUM	LB	0.52	<0.01*	0.26	0.17	0.62	<0.001*
STEP	SH	-0.13	0.50	-0.01	0.97	0.17	0.37
STEP	LB	0.43	0.02*	-0.17	0.37	-0.02	0.9
SH	LB	-0.20	0.30	0.25	0.2	0.11	0.57

		Ketosis (n=37)		Calving (n=190)	
Variable	by Variable	Spearman *p*	*P-value*	Spearman *p*	*P-value*
HEAD	RUM	0.78	<0.0001*	0.04	0.85
HEAD	STEP	0.40	0.03*	-0.39	0.16
HEAD	SH	0.57	0.001*	0.93	<0.0001*
HEAD	LB	0.51	0.004*	-0.35	0.21
RUM	STEP	0.36	0.054	0.91	<0.0001*
RUM	SH	0.52	0.004*	-0.45	0.1
RUM	LB	0.39	0.03*	0.93	<0.0001*
STEP	SH	0.25	0.19	-0.44	0.1
STEP	LB	0.35	0.06	0.94	<0.0001*
SH	LB	0.25	0.19	-0.44	0.1

* Significant correlations at 0.05 alpha level. HEAD: Activity units/d; RUM: Rumination min/d; STEP: Daily steps; SH: steps per hour/d; LB: Lying bouts/d.

0149 DI/LC-MS/MS-based metabolomics identifies early predictive serum biomarkers for ketosis in dairy cows. B. N. Ametaj*[1], G. Zhang[1], E. Dervishi[1], S. M. Dunn[1], R. Mandal[2], D. S. Wishart[2], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada,* [2]*University of Alberta, Edmonton, Canada.*

Subclinical ketosis is a prevalent metabolic disease in transition dairy cows that affects 30 to 40% of the cows during early lactation. Cows with ketosis have lower milk yield and reproductive performance, greater risk of other periparturient diseases, and higher culling rate. The objectives of this study were to retrospectively evaluate alterations of metabolites in the serum of dairy cows with ketosis before, during, and after

the diagnosis of disease and identify monitoring and diagnostic serum metabolite biomarkers for ketosis. One hundred transition dairy cows, 20 healthy cows (CON), and six cows with ketosis were sampled during d –8, –4, at disease diagnosis, and wk +4 and +8 relative to parturition. One hundred and twenty-eight serum metabolites were quantitatively profiled in CON and ketosis cows using a targeted metabolomics approach based on DI/LC-MS/MS at all time points. Univariate and multivariate data analyses were conducted at each time point to examine alterations of serum metabolites throughout the progress of ketosis. Significant changes were detected in the concentrations of several molecular species of amino acids, glycerophospholipids, sphingolipids, acylcarnitines, biogenic amines, and hexose in the serum of cows with ketosis during the entire experimental period. Multivariate analysis (i.e., PCA and PLS-DA) also showed clear distinctions between the two groups on the basis of the measured 128 serum metabolites at five time points. Furthermore, several metabolic pathways including Lys degradation, biotin metabolism, Try metabolism, urea cycle, Arg-Pro metabolism, protein biosynthesis, Met metabolism, phospholipid biosynthesis, Val-Leu-Ile degradation, betaine metabolism, Asp metabolism, His metabolism, and β-Ala metabolism were perturbed in cows with ketosis during the onset and progression of disease. These new findings give insights into further understanding of the pathobiology of ketosis in dairy cows. Biomarker analysis showed that AUCs for ROC curves were 0.996 (95% CI, 0.969–1) at –8 wks, 0.995 (95% CI, 0.938–1) at –4 wks, 0.99 (95% CI, 0.882–1) at disease wk, 1 (95% CI: 1–1) at +4 wks and 0.985 (95% CI: 0.806–1) at +8 wks, respectively, which suggest that serum biomarkers identified have pretty accurate predictive, diagnostic, and prognostic abilities for ketosis in transition dairy cows.

Key Words: amino acid, biomarkers, dairy cows, ketosis, lipid profiles

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0150 Targeted metabolomics reveals multiple metabolite alterations in the urine of transition dairy cows preceding the incidence of lameness.

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Lameness (Lam) is a major issue of transition dairy cows consuming high grain diets affecting 25–35% of the herd. It is associated with decreased milk production, fertility problems, and high culling rates and treatment costs. Various hypotheses have been forwarded during the years with regards to the causes of lameness including rumen histamine, endotoxin, or biogenic amines. Although much is known about non-mechanical lameness, the precise pathobiology is not known. The objectives of this study were to evaluate weekly metabolite composition of urine in dairy cows starting from the beginning of dry off until 8 wks postpartum. Urine samples were collected from 100 cows at −8, −4, disease week, +4, and +8 wk around calving and stored at −80 C until analyzes. DI/LC-MS/MS analyzes were conducted on samples collected from 20 healthy control cows (CON) and 6 cows diagnosed only with lameness (no other periparturient diseases). A total of 154 metabolites including 41 carnitines, 9 lysophosphatidylcholines, 74 phosphatidylcholines, 15 sphingomyelines, 11 amino acids, 2 biogenic amines, hexose, and carnosine were identified and quantified. Data were processed statistically by MetaboAnalyst and univariate analyses. Results showed that 41, 29, 59, 26, and 40 metabolites were identified and measured to be different between the two groups on −8, −4, disease week, +4, and +8 wks around calving, respectively. The highest number of altered metabolites was identified during the week of diagnosis of Lam. Several metabolic pathways were found to be associated with the disease including amino acid metabolism, catecholamine biosynthesis, protein biosynthesis and urea cycle at −8 wks precalving; cysteine, glutamate, tyrosine, and glutathione metabolism at −4 wks precalving; and β-alanine metabolism during the week of disease. ROC analyses, for determination of specificity and sensitivity of potential biomarkers, identified several metabolites with AUCs for ROC curves 0.96 (95% CI, 075–1.0) at −8 wks; 0.971 (95% CI, 0.905–1.0) at −4wks; 1.0 (95% CI, 1.0–1.0) at disease week; 1.0 (95% CI, 1.0–1.0) at +4wks; and 1.0 (95% CI, 1.0–1.0) at +8wks postpartum. PLS-DA analysis also showed clear separation between the two groups of cows with regards to altered metabolites. In conclusion, targeted metabolomics can be used to identify metabolic alterations in the urine of dairy cows before, during, and after diagnosis of Lam; it can also help to better understand the pathobiology of disease, identify cows more susceptible to Lam, and develop new preventive strategies.

Key Words: dairy cows, DI-/LC-MS/MS, lameness, targeted metabolomics, urine

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0151 Elevated serum amyloid A concentrations in the first days after calving are an early disease indicator in dairy cows.

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Early disease detection is critical for maintaining cow health and productivity. Serum amyloid A (SAA) is an acute phase protein that is primarily produced in the liver and is elevated in response to infections and tissue damage in dairy cows. To evaluate whether serum concentrations of SAA may assist in early disease detection, blood samples were taken from 57 Holstein cows at d −21, −14, −7, −3, −1, 0, 1, 3, 7, 14, 21, and 28 relative to calving and analyzed for SAA concentrations. Cows were grouped based on severity of diseases

(no disease, subclinical, mild clinical, and moderate clinical), class of diseases (no disease, metabolic, infectious, both types), time of diagnosis (no disease, 0–3 d, 4–7 d, 8–28 d after calving), and birth complications (yes, no) in early lactation and examined for group differences. Serum amyloid A concentrations in the first days after calving were higher and elevated longer in cows that developed diseases in early lactation. Observed group differences reflected the severity of disease and preceded clinical disease diagnosis irrespective of disease class. Group differences were strongest 1 d after calving, when 0% (healthy), 43% (subclinical disease), 57% (mild clinical disease), and 72% (moderate clinical disease) of cows had SAA above 125 mg/L (sensitivity for any disease: 66%; specificity: 100%). Cows with birth complications had higher SAA concentrations 2 wk before calving than cows without birth complications. Our results support our hypothesis that greater tissue damage and disproportionate inflammatory responses after calving are gateway disorders that increase disease risk in early lactation. Serum amyloid A can detect those risk factors 1 d after calving and thereby opens opportunities for prevention and early treatment.

Key Words: biomarker, dairy cows, diseases, serum amyloid A

0152 The effect of dry period length and antibiotic treatment at drying off on somatic cell counts across the dry period. R. J. Vanhoeij[*1], A. van Knegsel[2], B. Kemp[2], and T. J. G. M. Lam[3,4], *[1]Wageningen University, Netherlands, [2]Adaptation Physiology Group, Wageningen University, [3]Animal Health Service, Deventer, Netherlands, [4]University of Utrecht, Department of Farm Animal Health, Netherlands.*

Management measures to reduce the risk of new intramammary infections (IMI) during the precalving period include use of dry cow antibiotics. Blanket dry cow therapy is not allowed in several European countries, among which is the Netherlands. Moreover, shorter dry periods are of interest because of beneficial effects on the energy balance and metabolic status in the subsequent lactation. The aim was to study the effect of dry period (DP) length on SCC in the subsequent lactation and occurrence of IMI, based on SCC, across the dry period. This aim was approached in 2 separate experiments: Experiment 1 was conducted with use of dry cow antibiotics and experiment 2 without use of dry cow antibiotics. In experiment 1 Holstein-Friesian cows (n = 167) were randomly assigned to three DP lengths (0, 30, 60 d). Cows with a 30-d or 60-d DP were treated with dry cow antibiotics (Supermastidol®, Virbac Animal Health, Barneveld, Netherlands) at drying off. In experiment 2, Holstein-Friesian cows (n = 127) were randomly assigned to two DP lengths (0 or 30 d) and were not treated with dry cow antibiotics. Data were analyzed using a logistic regression model (SAS Institute Inc., 2011), including DP length as fixed effect. Somatic cell count was log transformed before statistical analysis (LnSCC). Data are expressed as LMEANS ± SE. In experiment 1, cows with a 0-d DP had a greater average SCC in the subsequent lactation (LnSCC 5.01 ± 0.06) than cows with a 30-d (LnSCC 4.68 ± 0.06) or 60-d DP (LnSCC 4.52 ± 0.06) ($P < 0.01$). The proportion of cows with a chronic IMI (SCC ≥ 200,000 both pre- and postpartum) was greater in cows with a 0-d DP (5/10), than in cows with a 30-d DP (1/13) or a 60-d DP (1/12) ($P = 0.04$). In experiment 2, cows with a 0-d DP had a greater postpartum average SCC (LnSCC 4.51 ± 0.04), than cows with a 30-d DP (LnSCC 4.24 ± 0.04) ($P < 0.01$). The proportion of cows with a chronic IMI during the precalving period was not different between cows with a 0-d DP (6/11) or a 30-d DP (2/6) ($P = 0.47$). Postpartum average SCC for lactation is greater in cows with a 0-d DP, than in cows with a 30-d DP, regardless of use of dry cow antibiotics. Studies are ongoing to evaluate whether the greater SCC in early lactation in cows with a 0-d DP is actually correlated with intramammary bacterial infections.

Key Words: continuous milking, mastitis, somatic cell count

0153 Enhancement of the dry-off process by intramammary infusion of metalloproteinase 9 nanoparticles. S. Parés[*1], O. Cano-Garrido[2], E. Garcia-Fruitós[1], F. Fàbregas[1], A. Bach[3,4], N. Ferrer-Miralles[2], M. Terré[3], A. Villaverde[2], and A. Arís[1], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]Departament de Genetica i de Microbiologia, UAB, Cerdanyola del Valles, Spain, [3]IRTA, Caldes de Montbui, Spain, [4]ICREA, Barcelona, Spain.*

The dry-off of dairy cows is associated to welfare and high risk of intramammary infections that could be improved by fostering involution and immune system during early dry period. Metalloproteinase 9 (MMP-9) is a tissue-remodeling enzyme physiologically released in the mammary gland during the dry period. The objective of this study was to explore the role of the infusion of MMP-9 at dry-off. MMP-9 was produced in *Lactococcus lactis* as a soluble protein and nanoparticulated (NP) format. Twelve cows with Somatic Cell Count (SCC) < 200.000 and > 15 kg of milk/d at dry-off were enrolled in the study. Treatments were randomly assigned to the front or rear quarters, thus 24 quarters were distributed in 2 treatments: 1 mg of soluble MMP-9 and 100 mg of NP MMP-9, providing both the equivalent metalloproteinase activity measured by zymography. Saline solution was infused in the contralateral quarters as a negative control for each treatment. Samples of mammary secretion were collected at 0, 1, 2, 3, and 7 d relative to dry-off and processed for SCC determination or kept frozen for subsequent determination of MMP-9 activity, and bovine serum albumin (BSA), lactoferrin, sodium, and potassium concentrations. SCC was analyzed with a Scepter

cell counter, MMP-9 activity by zymography, lactoferrin by ELISA, BSA using a colorimetric assay, and sodium and potassium by ICP–OES. All data were analyzed by ANOVA. As expected, both the soluble and NP forms increased ($P < 0.0001$) the metalloproteinase activity in mammary gland compared with controls. However, only the NP form was able to modulate some involution and immune markers. The NP form increased immunity markers including SCC up to 400 fold ($P < 0.001$) at d 1–7, and lactoferrin concentration up to 1.8-folds ($P < 0.05$) at d 1 and 2 after dry-off, compared with saline controls. Also, there was an increase ($P < 0001$) in involution markers. Concentration of BSA in mammary secretion raised up to eightfold at 1, 2, and 3 d and the sodium/potassium ratio ($P < 0.001$) by 4.5-fold at D1 after dry-off, compared with controls. In conclusion, infusions of either soluble or NP forms of MMP-9 at dry-off, increased the metalloproteinase activity in mammary gland, but only the NP form enhanced the of the involution process and immune system.

Key Words: dry period, nanoparticles, metalloproteinase 9

0154 Effects of inhibiting prolactin production with cabergoline on the physiology of the cow-dry period. S. Parés[1], A. Arís*[1], M. Terré[2], F. Fàbregas[1], E. Garcia-Fruitós[1], J. Ruberte[3], V. Nacher[3], A. De-Prado[4], and A. Bach[2,5], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]IRTA, Caldes de Montbui, Spain, [3]CBATEG Universitat Autònoma de Barcelona, Bellaterra, Spain, [4]Ceva Santé Animale, Libourne, France, [5]ICREA, Barcelona, Spain.*

Cabergoline is an ergot derivative with a high affinity for the D2 dopamine receptor whose dopaminergic effects cause inhibition of prolactin (PRL) secretion, and has been recently released as a dry-off facilitator (Velactis®, Ceva, France). A deep study of its effects along the dry period can help to understand the physiology of the mammary involution. Twenty-four Holstein cows (6 primiparous and 18 multiparous) were distributed in 2 treatments: i.m. injection of either 5 mL providing 5.6 mg of cabergolin (CAB) or 5 mL of saline solution (CTR) at the moment of dry-off. Mammary gland biopsies of posterior quarters and tail blood samples were taken at −10, 9, and 23 d relative to dry-off and −9 and 21 d relative to calving to evaluate the effects of PRL inhibition on hormonal and tissue involution markers along the dry period and onset of the subsequent lactation. Blood concentrations of insulin, PRL, IGF1, IGFBP5, GH, and progesterone were determined using immunoassays. Expression of genes coding for *p16, ki67, igf, igfbp5, upa, mmp9, prlr, occludin, and caspase 3* was determined by qPRC. Lastly, immunohistochemical detection of Ki67, SIRT1 and P16 was performed and quantified by light microscopy. As expected, cows on CAB tended ($P = 0.07$) to have lower serum PLR concentrations (23.5 ± 0.29 ng/mL) than cows on CTRL (36.4 ± 0.25 ng/mL), and had a lesser ($P < 0.001$) expression of PRL receptor (*prlr*) in the mammary tissue (2.09 ± 0.455 vs. 1.77 ± 0.423 relative expression units, respectively). Cabergolin increased ($P < 0.05$) blood insulin concentration (14.3 ± 1.28 μU/mL) compared with CTR (10.7 ± 1.14 μU/mL), but blood concentration of the remaining hormones were not affected although decreased ($P < 0.05$) as the dry period progressed. The expression of *igf1* in the mammary gland increased ($P < 0.05$) in CAB cows in the dry period and decreased at the beginning of next lactation. Also, CAB cows had greater ($P < 0.05$) expression of *mmp9* and *occludin*, which indicates a greater tissue involution and remodeling ($P < 0.05$). Also, immunohistochemical analyses showed an increase ($P < 0.05$) in sirt1 (a gene related with cell proliferation and insulin sensitivity) in CAB animals (75.9 ± 12.02 relative units) compared with CTR (56.9 ± 12.31 relative units) at the onset of the subsequent lactation. In conclusion, this study demonstrates that PRL inhibition by cabergoline at dry-off induces an increased proliferation and tissue remodeling of the mammary gland.

Key Words: dry period, prolactin, tissue remodeling

Table 0155.

Table 1. Antibiotic use, clinical and bacteriological outcomes for two clinical mastitis treatment programs.

Outcome	Culture Based	Positive Control	Treatment Effect		
			Estimate	95% CI	*P*-val
Primary IMM Therapy [% (n)]	28.21 (117)	100 (159)	OR_{PC}=<0.01	<0.01 to 0.02	<0.01
Primary or Secondary IMM Therapy [% (n)]	35.90 (117)	100 (159)	OR_{PC}=<0.01	<0.01 to 0.02	<0.01
IMM Tubes per Quarter Case [mean (n)]	1.13 (117)	3.29 (159)	$Diff_{PC}$=-2.16	-2.49 to -1.83	<0.01
Days of Non-Saleable Milk [mean (n)]	5.72 (98)	6.73 (125)	$Diff_{PC}$=-1.02	-1.44 to -0.56	<0.01
Days to Clinical Cure (Normal Milk) [mean (n)]	3.45 (117)	3.12 (159)	$Diff_{PC}$=0.32	-0.17 to 0.82	0.21
Bacteriological Cure [% (n)]	76.92 (52)	77.08 (48)	OR_{PC}=1.00	0.49 to 2.06	0.98
New Intramammary Infection Risk [% (n)]	20.20 (99)	24.58 (118)	OR_{PC}=0.78	0.41 to 1.48	0.74
Recurrence (14 to 60 Days after CM) [% (n)]	12.82 (117)	25.16 (159)	OR_{PC}=0.44	0.23 to 0.84	0.01
Removal from Herd (Within 21 Days after CM) [% (n)]	7.14 (98)	14.40 (125)	OR_{PC}=0.48	0.18 to 1.14	0.09

0155 The treatment of only environmental Streptococci clinical mastitis cases reduced antibiotic use, days out of the tank, recurrence of clinical mastitis and a tendency to reduce culling. A. Lago*, C. Tovar, J. Zaragoza, D. Luiz, and D. Pearce, *DairyExperts Inc., Tulare, CA.*

This study objective was to compare antibiotic use, clinical and bacteriological outcomes for selective treatment of only clinical cases where environmental streptococci were isolated versus blanket therapy. Cows with mild or moderate clinical mastitis (CM) from a California Central Valley dairy herd were assigned to either a) a positive-control treatment group (PC) or b) a laboratory-culture-based treatment group (CB). Quarter cases assigned to PC received immediate intramammary (IMM) treatment with ceftiofur (Spectramast LC; Zoetis Inc., New York, NY) and repeated once a day for a total of 3 d. Quarters assigned to CB underwent culture over a 24 h period at DairyExperts Laboratory (DairyExperts Inc., Tulare, CA). Only quarters showing environmental streptococci growth were treated the next day with the same therapy as cases assigned to PC. Mixed Models were used with cow included as a random effect. A total of 276 quarter cases of clinical mastitis from 223 cows were enrolled into the study. Results are summarized on Table 1. The selective treatment of only CM cases from which environmental streptococci were isolated resulted in about a two-thirds reduction both in the number of cases treated and in the number of IMM tubes used, as well as a reduction of 1 d out of the tank. Interestingly, CM recurrence was significantly lower and removal from herd tended to be lower when only environmental streptococci were treated with IMM antibiotics.

Key Words: clinical mastitis, selective treatment, streptococcus

0156 Effect of the selective treatment of gram-positive clinical mastitis cases versus blanket therapy. A. Lago*, D. Luiz, D. Pearce, C. Tovar, and J. Zaragoza, *DairyExperts Inc., Tulare, CA*.

This study objective was to compare antibiotic use, clinical and bacteriological outcomes for selective treatment of only Gram-positive clinical cases versus blanket therapy. Cows with mild or moderate clinical mastitis (CM) from a California Central Valley dairy herd were assigned to either a) a positive-control treatment group (PC) or b) a laboratory-culture-based treatment group (CB). Quarter cases assigned to PC received immediate intramammary (IMM) treatment with ceftiofur (Spectramast LC; Zoetis Inc., New York, NY) and repeated once a day for a total of 3 d. Quarters assigned to CB underwent culture over a 24 h period at DairyExperts Laboratory (DairyExperts Inc., Tulare, CA). Only quarters showing Gram-positive growth were treated the next day with the same therapy as cases assigned to PC. Mixed Models were used with cow included as a random effect. A total of 473 quarter cases of clinical mastitis from 425 cows were enrolled into the study. Results are summarized on Table 1. The selective treatment of only CM cases from which Gram-positive bacteria was isolated resulted in about half reduction both in the number of cases treated and in the number of IMM tubes used. Furthermore, the withholding of antibiotic treatment did not have any deleterious effect on time for milk to return visibly normal, bacteriological cure, new infection risk, CM recurrence or removal from the herd.

Key Words: clinical mastitis, selective treatment, gram-positives

0157 Comparison of PCR and culture methods for detecting mastitis causing mycoplasma in bulk tank milk from commercial dairy herds. A. M. Britten, E. D. Tretter*, and M. Gurajala, *Udder Health Systems Inc., Meridian, ID*,

In this study we compared the mycoplasma detection of direct culture, broth enhanced culture and PCR from 1299 bulk tank

Table 0156.

Table 1. Antibiotic use, clinical and bacteriological outcomes for two clinical mastitis treatment programs.

Outcome	Culture Based	Positive Control	Treatment Effect		
			Estimate	95% CI	*P*-val
Primary IMM Therapy [% (n)]	46.45 (211)	100 (262)	OR_{PC}=0.02	<0.00 to 0.04	<0.01
Primary or Secondary IMM Therapy [% (n)]	56.87 (211)	100 (262)	OR_{PC}=0.03	0.01 to 0.06	<0.01
IMM Tubes per Quarter Case [mean (n)]	1.52 (211)	3.33 (262)	$Diff_{PC}$=-1.80	-2.06 to -1.54	<0.01
Days of Non-Saleable Milk [mean (n)]	7.08 (191)	6.70 (234)	$Diff_{PC}$=0.37	-0.12 to 0.85	0.14
Days to Clinical Cure (Normal Milk) [mean (n)]	3.97 (211)	3.56 (262)	$Diff_{PC}$=0.38	0.32 to 0.74	0.06
Bacteriological Cure [% (n)]	68.57 (105)	66.42 (134)	OR_{PC}=1.10	0.64 to 1.90	0.72
New Intramammary Infection Risk [% (n)]	22.35 (170)	20.93 (215)	OR_{PC}=1.08	0.67 to 1.77	0.74
Recurrence (14 to 60 Days after CM) [% (n)]	19.91 (211)	22.90 (262)	OR_{PC}=0.84	0.54 to 1.30	0.43
Removal from Herd (Within 21 Days after CM) [% (n)]	14.66 (191)	14.53 (234)	OR_{PC}=1.01	0.59 to 1.74	0.97

and composite pen milk samples collected from 62 commercial dairies in 11 states. Culture of bulk tank milk directly onto specialized mycoplasma culture media (such as modified Hayflick agar) has proven effective in detection of mycoplasma mastitis outbreaks. Many laboratory methods also incorporate a mycoplasma broth enhancement protocol to increase sensitivity. This routine, direct and broth enhanced mycoplasma culture protocol, of bulk tank milk samples and pooled pen samples is widely practiced as a primary screening method for detection of mycoplasma infection status of a herd. However disease detection can be delayed up to 10 d due to slow colony formation with culture. Direct mycoplasma detection in enriched broth by the use of PCR may have the advantage of detecting the pathogen much sooner, if it is shown to detect the pathogen in bulk tank milk at least as well as culture. All samples in the study were cultured by plating 10 μL of the milk sample directly onto commercial mycoplasma isolation agar. All samples also were enriched by inoculating a 100-μL aliquot into 3 mL of mycoplasma broth and then incubated for 48 h, before plating a 10-μL aliquot of this enriched broth onto mycoplasma agar. Any sample where one or more colonies were detected by either direct or broth enrichment were deemed culture positive. A 2-μL aliquot of the same enriched broth from the culture method was used for the PCR detection method. The PCR method used was a four-way multiplex real time assay including primers for general *Mycoplasma* spp., *Mycoplasma bovis*, *Mycoplasma bovigenitalium*, and an internal positive control. When an organism was detected by any of the mycoplasma primers, the sample was deemed to be PCR positive. Of the 58 PCR detection events 35 (60.3%) were classified as Mycoplasma *bovis*, 16 (27.6%) as *Mycoplasma bovigenitalium*, and 7 (12.1%) were only detected by the *Mycoplasma* spp. primers. The comparison summary presented below shows a high level (98.6%) of agreement between the two methods. Direct PCR amplification of a broth enriched milk sample can rapidly detect *Mycoplasma* spp. in bulk tank and pen samples, and can give results comparable to conventional culture methods. PCR also offers the possibility of providing species differentiation of positive samples.

Key Words: mastitis, mycoplasma, PCR

0158 Effects of antibiotic dry cow therapy and internal teat sealant (Teatseal) on milk somatic cell counts, clinical, and subclinical mastitis in early lactation.

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A randomized multi-site clinical trial was performed to determine the efficacy of an internal teat sealant (TS; Teatseal; Zoetis Australia, Silverwater, NSW, Australia), when used in combination with antibiotic dry cow therapy (ADCT), on milk individual cow cell count (ICCC), milk production and components, and the incidence of clinical and subclinical mastitis in cows up to 60 d in milk (DIM), and when compared with ADCT only. Multiparous Holstein, Jersey, or Holstein cross cows (n = 2200) from 8 farms in Southern and Eastern Australia were randomly assigned to treatment in all 4 quarters with an ADCT alone or with ADCT + TS at dry-off. Individual milk yield, fat and protein percentage, and ICCC were measured at 14 ± 3 d intervals for the first 60 DIM for cows that calved 40 to 100 d after dry-off. The first measurement occurred between 10 and 24 DIM. Clinical mastitis and health events were recorded from dry-off to 60 DIM. Milk yield, ICCC weighted by milk yield, and fat and protein percentage were not affected by treatment or time or their interaction in a generalized linear model. Treatment with ADCT + TS decreased geometric mean ICCC (P = 0.021), compared with treatment with ADCT alone. Geometric mean ICCC (x1000 cells/mL) was 32.0 (95% CI: 26.8 to 38.3) and 43.5 (95% CI: 36.2 to 52.1), respectively. The odds of at least 1 case of subclinical mastitis (ICCC $\geq$ 250,000 cells/mL) were 1.9 times higher (95% CI: 1.4 to 2.6) with ADCT alone, compared with ADCT + TS. Four cows had a first case of clinical mastitis in the dry period; while, 5% of cows had a first case of clinical mastitis between 0 and 60 DIM. Of the 1528 cows included in this analysis, 43 cases (5.7%) and 33 (4.3%) were from the ADCT and ADCT + TS groups, respectively (P = 0.194). Proportional hazards estimates of survival showed no difference in the number of d post-calving to detection of first cases of clinical mastitis between treatments over the first 60 DIM (P = 0.153). The estimated hazard ratio for clinical mastitis over this period in the ADCT + TS cows (relative to ADCT alone) was 0.70 (95% CI: 0.43 to 1.14). The combination of ADCT and TS provides benefits over ADCT alone through improved prevention of subclinical mastitis and reduced ICCC in the first 60 DIM.

Key Words: intra-mammary infection, survival analysis

0159 A new protocol for the isolation of key recombinant proteins in livestock production using lactic acid bacteria as a cell factory.

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Escherichia coli is one of the most widely used expression hosts for the production of recombinant proteins. However,

obtaining pure and active proteins is not an easy task, especially considering difficult-to-express proteins, such as membrane or aggregation-prone proteins. Besides, *E. coli* contains lipopolysaccharide (LPS) that must be removed, which involves costly and time-consuming purification processes. Interestingly, *Lactococcus lactis*, which does not produce LPS, is able to form protein nanoclusters (aggregates) rich in the recombinant protein produced. The objective of this study was to develop an economically-affordable protocol to extract functional proteins from protein nanoclusters of *L. lactis*. For that, interleukin-8 (IL-8) stimulating protein (IL8SP), a difficult-to-express protein, and metalloproteinase 9 (MMP-9), an aggregation-prone protein, were used as model proteins. These proteins, that play important roles during the dry period of cows and have important economical potential, were recombinantly produced in *L. lactis* in the form nanoclusters. Next, IL8SP and MMP-9 nanoclusters were isolated and solubilized followed by some washing steps. Solubilized proteins were further purified following standard procedures for His-tagged proteins. Purified IL8SP and MMP-9 were quantified by Bradford assay and Western blot. The biological activity of IL8SP was measured in vitro by determining the expression of *interleukin-8 (IL-8*) in bovine mammary gland epithelial cell cultures. Specifically, cells were treated with 2 doses of IL8SP (9 and 90 μg). MMP-9 activity was determined by zymography. Data were analyzed using ANOVA. High aggregation ratios in nanoclusters were obtained for MMP-9 (99.24 ± 0.02%), whereas lower ratios were observed for IL8SP (37.32 ± 0.34%). Concerning biological activity, purified IL8SP showed a 1.6 and threefold-increase ($P < 0.0001$) of *IL-8* expression, compared with the control cells, using 9 and 90 μg, respectively. Protein MMP-9 obtained with this protocol was also fully active when tested by zymography. In summary, these results show that it is possible to obtain soluble, pure and fully-active proteins from *L. lactis* protein-rich nanoclusters through a novel, cost-effective, and easy protocol.

Key Words: nanoclusters, protocol, recombinant protein

0160 The negative effects of electromagnetic field exposure in male New Zealand White rabbits.

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The objective of the current study was to understand the possible effects of EMF on liver enzymes and organs of male New Zealand White rabbits under ecological conditions. Rabbits were assigned randomly to 2 treatment groups of 8 each; treatment group (T) was housed directly beneath high voltage power lines (21 μT, 380 kV), whereas controls (C) kept 500 m away from the power lines (0.21 μT) for 7 wk. At the end of 7 wk, blood samples were taken from each rabbit and 4 rabbits per treatment were euthanized. Remaining rabbits were kept in normal laboratory condition for another 7 wk for recovery. The liver enzymes and organ weights were analyzed by Proc T-Test procedure. The exposure to EMF significantly increased the serum γ glutamyltransferase (C = 12.1 ± 1.7 vs. T = 17.2 ± 2.9 IU/l, $P < 0.05$), alkaline phosphatase (C = 71.7 ± 4.9 vs. T = 84.3 ± 6.2 IU/l, $P < 0.05$), aspartate aminotransferase (C = 23.5 ± 2.6 vs. T = 31.4 I ± 3.1 IU/l, $P < 0.05$) and alanine transaminase (C = 35.3 ± 3.8 vs. T = 45.5 ± 5.2 IU/l, $P < 0.05$) levels. Although liver, kidney, heart, testis and brain weights between groups did not differ, significant histopathological alterations were apparent in the treated animals. Histopathological examination of the liver showed dilated sinusoids, degenerative changes in hepatocytes, moderate fatty vacuolation and infiltration of a small amount of inflammatory cells in the portal area. Hyalinated cylinders in tubule lumens, vacuolated renal tubules and infiltration of leukocytes were seen in the kidney. The decrease in seminiferous tubule diameters in testis, and vacuolation of neurons and focal gliosis in the brain was noted in treated rabbits. However, serum liver enzymes and histopathological lesions were transient and returned to normal by wk 7 of recovery. Therefore, EMF exposure may have an adverse effect on the male rabbits, but this effect was not permanent.

Key Words: liver enzymes, histopathology, EMF

0161 Embracing innovation in the animal drug approval process.

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The mission of the Center for Veterinary Medicine (CVM) in the U.S. Food and Drug Administration (FDA) is to protect human and animal health. CVM's Office of New Animal Drug Evaluation encourages the development of new innovative technologies and non-traditional therapeutic indications as one means of facilitating this mission and to meet the growing needs in the animal care and food and fiber production sectors. CVM is committed to maximizing use of all forms of available information to meet this challenge. Current tools being implemented and/or investigated include use of scientific focus groups/technology teams, evaluation of "Early Information," pre-development meetings with drug sponsors, and CVM Outreach to academic bench scientists through, webinars and industry meeting presentations. These tools allow CVM to gather information, identify data gaps, and implement benefit-risk analysis decisions early in the drug approval process. Drug application review also affords the opportunity for continued communication between CVM, research scientists, and sponsors, as well as providing a channel for end-user feedback to CVM. Additional tools include expanded use of literature to support data requirements, use of electronic data capture, systematic reviews and meta-analyses, and collaborative data sharing within CVM and across international regulatory groups. Many of these new tools and approaches rely heavily on the academic research community

through consultations, published peer-reviewed information, and as study investigators. Scientists should consider and identify the applicability of their research and, just as importantly, foster productive partnerships with drug sponsors. An understanding of the regulatory processes underlying animal drug development and the tools used by CVM to evaluate data to support drug development is critical to the growth of the animal drug industry and the animal sciences industries. The benefit of innovative approaches to drug sponsors includes but is not limited to early and continual feedback from CVM, increased predictability of drug development requirements, and consistent application of requirements leading to global approval and use of an animal drug. The benefit to the researcher is continued partnerships with the animal drug industry and increased communication on how their scientific program could support drug development. The benefit to the public is increased availability of safe and effective drugs for use in production animals.

Key Words: animal health, drug, FDA, food, innovation, livestock

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0162 Regulation of animal drugs and foods in the 21st century: Enhancing communication among industry, academics, regulators, and the public.

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The mission of the Center for Veterinary Medicine (CVM) in the Food and Drug Administration (FDA) is to protect human and animal health. One aspect of CVM's role is to ensure that animal drugs and foods are safe, have proper manufacturing processes and labeling, and that any food products from treated animals are safe. Scientists at CVM rely on communication with researchers, veterinarians, and producers to stay informed of common industry practices and any scientific information that may influence the conduct of safety and the effectiveness of studies for approval. CVM also conducts outreach to educate a variety of stakeholders on the wide array of information publicly available on the CVM website and in partnership with professional scientific and industry societies. These resources are valuable to individuals involved with drug and food additive development, including basic research, clinical and laboratory studies, and post-market evaluations. By understanding and implementing the appropriate regulatory requirements and guidance for animal drug or food approvals, researchers are more likely to generate high-quality data and improve CVM's ability to use that information as part of the approval process. The CVM website contains information on important initiatives needing further research, such as antiparasitic resistance, antimicrobial resistance, and unapproved drugs, and provides information for the Center's internal research efforts. Special initiatives to increase the availability of approved drugs for minor uses and minor species include conditional approval, expanded exclusivity, available funding for some designated product studies, and assistance with outside programs intended to support minor species drug approval. The CVM website also serves as an authoritative resource for important information on the use of approved drugs, labeling, and descriptions of the safety and effectiveness of studies supporting those approvals. CVM portals also serve a critical role in allowing end-users of CVM-approved products to report adverse events and complaints for animal drugs and food for pets, and livestock, allowing CVM to monitor for possible safety, effectiveness, and/or manufacturing concerns and take appropriate regulatory action. Continued education and outreach to researchers, veterinarians, and producers allows CVM to continue to make scientifically sound decisions and achieve our mission of protecting human and animal health.

Key Words: animal health, communication, FDA0

0163 Exploring a new presentation form of recombinant proteins for animal production.

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Bacterial cell factories are widely used for the biofabrication of recombinant enzymes, vaccines, and hormones. However, the use of treatments based on recombinant proteins in animal science is limited, mainly because the production of soluble proteins has two important drawbacks: low stability and high costs. In this scenario, we have developed an alternative based on protein nanoparticles produced in lactic acid bacteria (LAB) that can potentially revolutionize livestock production. These nanoparticles are a low-cost source of releasable, highly stable, and functional protein that can be easily produced through a fully-scalable process. The objective of this study was to demonstrate the potential of this new protein format by exploring the composition and the biological effect of nanoparticles composed of bovine metalloproteinase 9 (MMP-9) and 2 (MMP-2), which have critical roles during the dry period of cows. Because understanding the architecture of these protein nanoparticles is pivotal to tune and exploit their activity, stability, and slow-release properties, in a first

experiment, the particle size of MMP-9 and MMP-2 produced by 2 different strains was determined from 474 micrographs obtained by high-resolution microscopy techniques. Next, in Experiment 2, metalloproteinase activity was measured in vitro by zymography. Lastly, in a third experiment involving 12 Holstein cows at dry-off, we assessed the potential use of MMP nanoparticles in vivo. Briefly, 12 quarters were infused with MMP-9 nanoparticles and 12 with saline solution (control) and samples of mammary secretion were obtained during 7 d post-dry off. Data were analyzed using ANOVA. In Experiment 1, particle size was affected ($P < 0.0001$) by the combination of the specific protein and the bacterial strain used for their production (353.2 and 431.6 ± 8.47 nm for MMP-9 and 391.8 and 387.6 ± 8.47 nm for MMP-2 produced in strain A and strain B, respectively). In Experiment 2, MMPs tested in vitro showed activity in a strain- and protein-dependent manner (1.38 and 2.33 ± 0.16 AU for MMP-9 and 1.97 and 1.52 ± 0.16 AU for MMP-2 produced in strain A and strain B, respectively; $P = 0.0028$). Mammary secretions from the in vivo study (Experiment 3) indicated a clear increase ($P < 0.001$) in metalloproteinase activity in comparison with the control at d 1 and 3. In summary, this study shows that it is possible to produce tunable and fully functional MMP nanoparticles in LAB, proving an important combined effect of the strain and the protein used to define its final characteristics.

Key Words: metalloproteinase, nanoparticles, proteins

0164 Reduced severity of histological lesions in mink selected for tolerance to Aleutian mink disease virus infection- A field survey. A. H. Farid[*1] and L. E. Ferns[2], [1]*Department of Animal Science, Dalhousie University Faculty of Agriculture, Truro, NS, Canada,* [2]*Pathology Laboratory, Veterinary Services, Nova Scotia Department of Agriculture, Truro, Canada.*

Aleutian mink disease virus (AMDV) causes Aleutian disease (AD), which is a major problem for the mink industry worldwide. Chronically infected adult mink exhibit persistent antiviral antibody production, hypergammaglobulinemia, generalized plasmocytosis and immune complex-mediated glomerulonephritis and arthritis. The disease has no vaccine or treatment, and many years of testing for anti-viral antibodies by the counter-immunoelectrophoresis (CIEP) and eliminating seropositive animals has not been effective for virus eradication, encouraging some ranchers to select their herds for tolerance to the disease. The objective of this study was to assess the effect of selection for tolerance on the severity of AD histological symptoms. Carcasses of 680 sero-positive (CIEP-P) black mink from 28 ranches in Nova Scotia, Canada, and 132 sero-negative (CIEP-N) mink from 15 of these ranches were collected at pelting time. Animals on three of the ranches have been selected for tolerance to AMDV based on health, with or without the iodine agglutination test which identifies animals with high serum globulins. The severity of the AD lesions was assessed by histological examination of kidneys, lungs, heart, brain and liver. Only six unselected CIEP-P mink showed clinical symptoms of AD at necropsy, whereas histology confirmed the presence of AD-related microscopic lesions in at least one of the five organs in 89.5%, 68.1% and 66.7% of unselected CIEP-P, tolerant CIEP-P and unselected CIEP-N mink, respectively. The maximum intensity of lesion scores on any of the five organs showed that severe and very severe lesions in the unselected CIEP-P group (44.7%) was 5.7 and 29.8 times greater than those in the tolerant CIEP-P (7.8%) and unselected CIEP-N group (1.5%). A greater percentage of tolerant CIEP-P mink did not show any AD lesions on any of the organs (31.9%) or showed trace or minor lesions (44.8%) compared with unselected CIEP-P mink (10.5% and 24.7%). The GENMOD procedure of SAS with the cumulative logit model showed significant differences among the three groups for the maximum lesion score. The results implied that selection for AMDV tolerance was manifested as milder disease symptoms in infected mink.

Key Words: Aleutian disease symptoms, counter-immunoelectrophoresis, mink

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0165 Type of blood tube affects haptoglobin concentration when analyzed with a colorimetric assay. M. A. Campbell[*1,2], J. W. Darrah[1], and H. M. Dann[1], [1]*William H. Miner Agricultural Research Institute, Chazy, NY,* [2]*University of Vermont, Burlington, VT.*

Haptoglobin, an acute phase protein, serves as a biomarker for stress and inflammation in dairy cows. Consequently, obtaining an accurate value for haptoglobin is vital for research and management decisions on-farm. Blood collection methods reported in peer-reviewed articles differ greatly when similar assays are performed. The objective of this study was to determine the effect of type of blood collection tube on haptoglobin concentration using a commonly used, commercially available colorimetric assay. Coccygeal blood was obtained from 21 early lactation, 9 sick, and 30 late lactation dairy cows from three farms to obtain a range in haptoglobin concentrations. For each cow, blood was collected into four separate 10-mL BD Vacutainer tubes: serum separator, lithium heparin, sodium heparin, and K_2–EDTA. Blood was then processed according to tube type. Plasma and serum were analyzed for haptoglobin concentration using a colorimetric assay (Tri-Delta Development Ltd; Maynooth, Ireland). Inter-assay and intra-assay CV were 3.2% and 4.3%, respectively. Data were separated into two categories; low haptoglobin (< 0.2 mg/mL; $n = 35$) or high haptoglobin (≥ 0.2 mg/mL; $n = 25$). Data were logarithmically transformed and analyzed using the MIXED procedure in SAS with cow as the experimental unit. Plasma samples from lithium heparin, sodium heparin, and K_2–EDTA tubes appeared cloudier than serum samples

following addition of assay reagents and interfered with the optical density reading. Haptoglobin concentrations were lower ($P < 0.01$) for serum separator tubes (0.09 mg/mL, 0.76 mg/mL; SEM = 0.02, SEM = 0.06) compared with lithium heparin (0.57 mg/mL, 1.60 mg/mL), sodium heparin (0.55 mg/mL, 1.57 mg/mL), or K_2–EDTA (0.62 mg/mL, 1.60 mg/mL) tubes for the low and high haptoglobin categories, respectively. To assess bias, data were analyzed for agreement between tubes using the Bland-Altman method with the serum separator tube serving as the gold-standard. A maximum allowable difference was determined to exceed the inter- and intra-assay variations set by the manufacturer at 0.15 mg/mL. Compared with serum, there was a significant lack of agreement ($P < 0.01$) with lithium heparin, sodium heparin, and K_2–EDTA (mean biases of 0.66, 0.64, and 0.69 mg/mL, respectively). In addition, lithium heparin, sodium heparin, and K_2–EDTA demonstrated slope biases of 0.42, 0.40, and 0.40, respectively, compared with serum. These results indicate greater disagreement among tubes at higher haptoglobin concentrations. The use of lithium heparin, sodium heparin, and K_2–EDTA tubes before haptoglobin analysis using the Tri-Delta colorimetric assay overestimates haptoglobin concentrations due to interference with assay reagents and is not recommended.

Key Words: haptoglobin, inflammation, vacutainer

0166 Health and production benefits of feeding cowpeas to goats. S. Adjei-Fremah*, A. Everett, R. Franco, K. Moultone, E. Asiamah, K. Ekwemalor, L. E. Jackai, N. Whitley, K. Schimmel, and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

The effect of grazing on cowpea forage on growth, parasite egg counts and markers of immunity was evaluated in goats. Spanish ($n = 24$) and Savannah goats ($n = 24$) were stratified by initial body weight (BW) (42.0 ± 7.0 kg) and fecal egg counts (FEC), and randomly assigned to 1 of 12 grazing plots (4 animals/plot) for 4 wks. Plots contained either of two varieties of cowpea commonly used in the Southern U.S., Mississippi silver (MS) and Iron and Clay (IC) or pearl millet (PM) grass as control. Body condition scores (BCS), BW, *FAMACHA* scores, and FEC were measured weekly. Initial and end of study blood samples were collected and analyzed for PCV, total and viable cells, and white blood cell differential counts. The concentration of total proteins, pro-inflammatory cytokines, prostaglandin E2 (PGE2) and total antioxidant capacity (TAC) were evaluated in serum. Body weight, BCS and *FAMACHA* score data were analyzed by repeated measures analysis using the PROC MIXED model procedure of SAS. The model included treatment, time (sampling day), breed, and the treatment x time x breed interaction. The FEC data were log-transformed before statistical analysis. Two-way ANOVA was performed on all other data. Goats fed cowpea forage, BW ($P = 0.01$), percent lymphocyte ($P = 0.008$), and percent neutrophils ($P = 0.013$) increased, and FEC decreased ($P = 0.03$) compared with goats fed control PM forage. A significant interaction ($P = 0.01$) was observed between goat breeds, cowpea varieties and measured parameters such as BW, percent lymphocyte, percent neutrophil and percent viable cells. The MS cowpea forage was associated with greater BW and neutrophil counts in the Savannah breed and with increased lymphocyte counts in Spanish goats. Although feed did not affect serum protein concentration ($P > 0.05$), a decrease in PGE2, TNF-α, IL-8, and IP10, and an increase in TAC, G-CSF, Rantes and IFNγ was observed over time ($P < 0.05$). Results from the study suggest potential benefits and impact of cowpea forage grazing, particularly MS variety on growth, internal parasites burden, and markers of immunity in goats. Feeding a cowpea diet to goats may stimulate and prime innate immune responses for defense against gastrointestinal parasites and warrants further study under different management conditions.

Key Words: cowpea forage, goats, gastrointestinal nematode, inflammation cytokines, immunity markers

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0167 Exposure of bovine blood to pathogen associated and non pathogen associated molecular patterns results in transcriptional activation. K. Ekwemalor*, S. Adjei-Fremah, E. Asiamah, H. Ismail, and M. Worku, *North Carolina Agricultural and Technical State University, Greensboro.*

The effect of exposure of cow blood to non pathogen associated (probiotics) molecular patterns on the subsequent response to pathogen associated molecular patterns (PAMPS) was evaluated using transcriptional profiling. Probiotic supplements are beneficial for animal health and rumen function and represent non pathogen associated molecular patterns. Lipopolysacharides form gram negative bacteria are associated with inflammatory diseases and represent PAMPS. A global gene expression profile in whole blood collected from probiotics-supplemented cow was investigated in response to stimulation with lipopolysaccharide (LPS) in vitro. The recommended dose of FASTtrak microbial pack (Conklin Company, Kansas City, MO, USA) was administered orally in 50 ml of sterile water to Holstein-Friesian cows ($n = 10$) in mid lactation, for 60 d. Whole blood was collectedly aseptically and treated with 100 ng/ml of LPS and untreated samples served as control. Total RNA was extracted, and samples (0.5ug, RIN > 7) pooled together, were used for the microarray experiment on a bovine (v2) 4 × 44 arrays with 44,000 gene transcripts. A Real-time quantitative PCR was performed to validate the expression of Wnt signaling pathway and innate and adaptive immune response genes using RT-PCR profilers arrays (Qiagen) with 84 test genes each. Global gene expression analysis identified 13,658 differentially expressed genes

(fold change cutoff $\geq$ 2, $P < 0.05$), 3816 upregulated genes and 9842 downregulated genes. Treatment with LPS resulted in increased expression of TLR4 (Fold change (FC) = 3.16), TLR2 (FC = 2.4), TLR7 (FC = 2.13), WNT5A (FC = 2.68), and transcription factor NF-Kb (FC = 5.4). Genes downregulated in expression included WNT 11 (FC = -2.60), TLR1 (FC = -2.54), TLR3 (FC = -2.43), TLR10 (FC = -3.88), NOD2 (FC = -2.4), NOD1 (FC = -2.45) and pro-inflammatory cytokine IL1B (FC = -3.27). Thus, probiotic supplementation had an effect on the response to LPS exposure with specific effects on Toll-like receptor transcription. Exposure of bovine blood to pathogen associated (LPS) and non pathogen associated (probiotics) patterns resulted in transcriptional activation. Thus, probiotic supplementation may modulate the response to gram negative bacteria.

Key Words: probiotic, microarray, lipopolysaccharides, dairy cows

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0168 Prevalence of *Brucella suis* in hunting dogs in Hawai`i.

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This study examined the prevalence of *Brucella suis* in hunting dogs that have had extensive contact with feral swine, and potential risks for domestic livestock. Increasing feral swine populations across the U.S. increase the risk of transmission of swine diseases, such as the *B. suis* bacterium, to other animals and humans. Blood serum was collected from hunting dogs on the islands of O`ahu and Hawai`i by cooperating veterinary clinics. Based on previously reported prevalence of *B. suis* in feral swine on O`ahu and Hawai`i islands of 20.6% and 10.5%, and an estimate by extension agents of 300 to 500 hunting dogs, sample size needed for detection was calculated as 47 dogs. Serum was tested for *B. suis* specific antibodies using the buffered acidified plate antigen test, and positives were confirmed with the rivanol test. Data on potential risk factors was collected in a pre-structured questionnaire. Areas sampled include Royal Summit, Aiea and Kaneohe Bay on O`ahu and Halaula, Hawi, and North Kohala on Hawai`i. On O`ahu 1/7 (14%) samples were positive for *B. suis* and on Hawai`i 2/49 (4%) of samples were positive for *B. suis*. All positive samples had significant antibody titers on the rivanol test (two at 1:200 and one at 1:100) with no presentation of symptoms in the dogs. The positive dogs hunted in the Halawa/Royal Summit area on O`ahu and in the Hawi and North Kohala areas on Hawai`i. Questionnaire results showed that 83% of dogs were not neutered, 74% had never seen a veterinarian, 25% had contact with domestic pigs, and 46% had contact with other livestock. This study concludes that hunting dogs may be a previously unidentified risk factor for transmission of *B. suis* to domestic swine and other livestock.

Key Words: *Brucella suis*, feral swine, hunting dogs

0169 Pulmonary arterial pressure in yearling Angus cattle managed at high altitude: Study of a non-synonymous SNP in the oxygen-dependent degradation domain of the endothelial PAS domain-containing protein 1 gene.

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Bovine pulmonary hypertension (bPH) has a complex pathophysiology and can progress to right heart failure. Mean pulmonary arterial pressure (mPAP) has been used for decades as an indicator of risk of developing hypoxia-related bPH at altitudes above 1800 m. Veterinarians typically describe yearling bulls and heifers as low, moderate, or high risk for developing bPH using mPAP data. The objective of this study was to evaluate the relationship of a non-synonymous SNP in the oxygen-dependent degradation domain (ODDD) of the endothelial PAS domain-containing protein 1 (EPAS1) gene with mPAP in yearling Angus cattle managed at high altitude. The EPAS1 gene, also known as hypoxia-induced factor (HIF2α), is located on chromosome 11 and several sequence variants have been identified in its ODDD including a downstream G/A SNP (rs208684340). The A allele of this polymorphism was previously associated with hypoxemia in Angus cattle. In the current study, records from Angus cattle (n = 5296 of 280 sires) were obtained from the Colorado State University Beef Improvement Center (CSU-BIC; elevation 2150 m). Risk categories were constructed by estimating the heritability of mPAP as a categorical outcome based on veterinary recommendations. The combination of these efforts yielded mPAP risk categories of low (< 41), moderate (41 to 49) and high (> 49 mmHg) with a categorical-trait heritability of 0.26 ± 0.04 in this population. The percentage of cattle in each of these categories was 50.7, 38.0, and 11.3%, respectively. Forty-seven bulls and heifers, progeny of 33 sires, from this population were genotyped for the G/A SNP using a TaqMan assay (ABI-Roche Molecular Systems, Inc.). The minor allele frequency (MAF; A allele) of this SNP was 32.3% and mPAP averaged 45.2 ± 1.5 with a range of 32 to 95 mmHg. The MAF for the low, moderate and high categories were 46.4, 26.1, and 25.0%, respectively. Genotype was not a predictor (P = 0.4) of mPAP using a generalized linear model analysis. Mean PAP has been a useful tool to predict risk of bPH in yearling cattle for decades and is a moderately heritable trait. However, the

genotype results of this particular variant in the ODDD of the EPAS1 gene does not appear in this preliminary study to be useful to designate Angus cattle from the CSU-BIC into mPA-P-bPH risk categories.

Key Words: Angus cattle, pulmonary hypertension, SNP

0170 Subclinical right heart failure may contribute to the development of liver disease in feedlot cattle during the finishing phase. A. K. Gulick*, K. M. Freeman, B. C. Bernhard, J. O. Sarturi, and J. M. Neary, *Texas Tech University, Lubbock.*

The objectives of this study were twofold: first, to evaluate the relationship between mean pulmonary arterial pressure and mean central venous pressure, and determine if they increase through the finishing period; and second, to determine if mean central venous pressure is associated with liver disease. A cohort of crossbred yearling steers (n = 22; initial BW = 364 ± 52 kg) was studied at an altitude of 975m. Steers were fed for 171 d. Vascular pressures were measured twice: 6 and 54 d before slaughter. Serum biochemistry and liver histology were performed on steers that had the greatest (n = 5) and lowest (n = 5) mean central venous pressure at 54 d before slaughter. Biochemistry included total bilirubin, AST, GGT, and albumin; blood samples obtained 6 and 54 d before slaughter were evaluated. Liver samples were collected from the caudate lobe and lesions scored semiquantitatively. Both central venous and pulmonary arterial pressures increased from 54 d to 6 d before slaughter: 24 ± 1 mmHg to 28 ± 1 mmHg (P = 0.03) and 47 ± 2 mmHg to 54 ± 2 (P < 0.01), respectively. There was a positive association between mean pulmonary arterial and central venous pressures at 6 d (P < 0.01) but not 54 d before slaughter (P = 0.41) indicating that increased pulmonary arterial pressure contributed to right heart failure in cattle closest to slaughter weight. Serum biochemistry was within normal limits even though all steers showed histological evidence of liver damage centered on the centrilobular region (zone 3). All steers showed hydropic degeneration and sinusoid dilation. Lesion severity was greatest in the high mean central venous pressure group: One liver had cirrhosis; another had multifocal necrosis. Congestion was moderate to severe and centered on zones 1 and 2. The findings of this study indicate that subclinical right heart failure secondary to pulmonary hypertension may contribute to hepatic congestion and disease in feedlot cattle during the finishing phase. Serum biochemistry analyses may not represent the insidious liver damage of cattle close to slaughter. Right heart failure secondary to pulmonary hypertension, or cor pulmonale, may contribute to the development of liver disease in feedlot cattle during the finishing phase.

Key Words: health, pulmonary hypertension, steer

0171 Evidence of cor pulmonale and liver disease in association with pneumonia in feedlot and dairy cattle at an altitude of 975 m. A. K. Gulick* and J. M. Neary, *Texas Tech University, Lubbock.*

The objective of this observational study was to determine if cor pulmonale is evident in cattle at the moderate altitude of 975 m. Cor pulmonale is defined as right ventricular enlargement and dysfunction due to diseases affecting the lung or pulmonary vasculature. Right ventricular dysfunction can manifest as congestive hepatopathy. A convenience sample of necropsies were performed on one feedlot (n = 16) and one dairy (n = 4) between May 16 and September 4, 2015. A case history was obtained, gross lesions were recorded, and the cardiac ventricles weighed to determine the ratio of right ventricular free wall to total ventricular myocardium (RV:T). Sections of the right diaphragmatic, middle, and cranial lung lobes and liver were collected for histology. Vascular and hepatic lesions were scored semiquantitatively. Of the 16 feedlot cattle necropsied, 2 died from cor pulmonale secondary to bronchointerstitial pneumonia, 8 died from pneumonia, and 6 died from miscellaneous causes. Dairy cattle died from interstitial pneumonia (n = 3) and miscellaneous causes (n = 1). The RV:T ratio varied according to cause of death (P < 0.001): 0.37 ± 0.02 in cattle that died of cor pulmonale, 0.28 ± 0.01 in cattle that died of pneumonia, and 0.25 ± 0.01 in cattle that died of miscellaneous diseases. All cattle showed histological evidence of pulmonary vascular remodeling regardless of the cause of death or degree of right ventricular hypertrophy. The predominant vascular lesions included pulmonary arterial adventitial hyperplasia and pulmonary venous distension. Anatomic reduction of the pulmonary vascular bed was evident in cattle with pneumonia. Liver disease, consisting of sinusoidal dilation, lipidosis, and necrosis, was most severe in cattle that died of cor pulmonale and pneumonia. These findings indicate that cor pulmonale may be more problematic in cattle at modest elevation than is currently appreciated and confirm our previous epidemiological findings that respiratory disease is a risk factor for cor pulmonale in cattle. Venous congestion secondary to cor pulmonale may have contributed to the development of liver disease in cattle with pneumonia. Systemic consequences of right heart failure result from a reduction in cardiac output and venous congestion; consequently, organs with high oxygen requirements, such as the liver, are most at risk of cellular dysfunction and death. Moreover, because respiratory disease is a risk factor for cor pulmonale and the clinical signs overlap, the true incidence of cor pulmonale may be greater than current estimates suggest.

Key Words: heart, hypertension, pulmonary

0172 Porcine intestinal explants as *ex vivo/in vitro* model to study gastrointestinal disease. N. Reisinger*, P. Fuhrmann, C. Emsenhuber, B. Grenier, E. Mayer, and G. Schatzmayr, *BIOMIN Research Center, Tulln, Austria.*

Intestinal diseases play an important role in livestock animals especially in pigs. To gain more knowledge about pathological processes during intestinal disease usually animal experiments are needed. However, alternatives to animal testing are highly recommended. Ex vivo cultivation of explants might provide an alternative tool to investigate intestinal diseases in pigs. We therefore evaluated the cultivation of porcine intestinal explants.

Intestinal tissue from pigs was obtained from a local abattoir. About 10 cm of the jejunum were transported in prewarmed PBS to the lab. Intestinal tissue was flushed with PBS and was cut open longitudinally. Thereafter, tissue was washed again with PBS and cut into small pieces. Explants were placed into 12-well plates (mucosa facing upward) prefilled with 1.5 mL cultivation medium (D-MEM containing antibiotics and 10% FBS) and were incubated for up to 72 h at 39°C and 5% CO_2. Viability was measured with the water soluble tetrazolium (WST) −1 assay after 2, 4, 24, and 72 h (n = 6). In addition, explants were frozen in liquid nitrogen after incubation for 0, 2, and 4 h and stored at −80°C (n = 9). Gene expression of three different pro-inflammatory cytokines (TNF-α, IL-6, and IL-8) was measured via RT-qPCR. Statistical evaluation was performed with IBM SPSS Statistics software. If data were normally distributed ANOVA was performed. If data were not normally distributed, the Kruskal Wallis Test was used as non-parametric test.

Viability was already significantly decreased after 4 h of incubation compared with fresh explants. Furthermore, there was a significant increase of TNF-α expression after 4 h (25-fold) and IL-6 expression after 2 and 4 h (50 and 320-fold) compared with fresh explants. No effect of incubation time was seen for IL-8 expression.

Our study highlights the importance of measuring viability when cultivating intestinal explants. In addition, dissection of the tissue and isolation of explants seem to stimulate expression of certain pro-inflammatory cytokines.

We can therefore conclude that ex vivo cultivation of intestinal explants might be an alternative screening tool. However, optimization of dissection and culture conditions is needed to prolong possible incubation time.

Key Words: pigs, explants, gastrointestinal diseases

0173 Comparison of strategies for combining dynamic linear models with artificial neural networks for detecting diarrhea in slaughter pigs. D. B. Jensen* and A. R. Kristensen, *University of Copenhagen, Department of Large Animal Sciences, Frederiksberg, Denmark.*

The drinking behavior of healthy pigs is known to follow predictable diurnal patterns, and these patterns are further known to change in relation to undesired events such as diarrhea. We therefore expect that automatic monitoring of slaughter pig drinking behavior, combined with machine learning, can provide early and automatic detection of diarrhea. To determine the best approach to achieve this goal, we compared 36 different strategies for combining a multivariate dynamic linear model (DLM) with an artificial neural network (ANN). We used data collected in 16 pens between November 2013 and December 2014 at a commercial Danish pig farm. The pen level water flow (liters/hour/pig) and drinking bouts frequency (bouts/hour/pig) were monitored. Staff registrations of diarrhea were the events of interest. Mean water flow and drinking bouts frequency were each modeled using three harmonic waves in a multivariate DLM. The DLM was optimized using the pen-groups for which no events were observed (n = 26). The forecast errors produced by the DLM were normalized by the forecast variance and used as inputs for the ANN. In addition, the forecast errors were categorized based on the direction (positive or negative) and simga-1, sigma-2, or sigma-3 cutoff thresholds. Furthermore, observations from between 0 and 48 h before the day of the observation, with steps of 6 h, were included in the ANN training window. Thus between 87 and 277 diarrhea-associated observations were included. The diarrhea-associated observations were paired with an equal number of observations from healthy groups, based on the observation date and the age of the pigs. The complete set of diarrhea positive and negative observations was divided into a training set (80%) and a test set (20%). The ANN's consisted of three layers: an input layer corresponding to the number of forecast error categories, a hidden layer with 50 nodes, and an output layer with one node. The various ANN's were applied to all observations in the test set. The observation-level performance of the ANN predictions was evaluated by the error rate, the specificity (SP), and the sensitivity (SE). The best performance was seen when using a training window of 42 h for the numerical forecast errors, which produced an error rate = 0.16, a specificity = 0.88, and a sensitivity = 0.80. For the other tested strategies, the ranges of error rates and the corresponding specificities and sensitivities were 0.55–0.28, 0.43–0.71, and 0.50–0.74, respectively.

Key Words: artificial neural network, diarrhea, dynamic linear model

0174 Heat stress increases gut permeability in pigs–application of a non-invasive assay. N. Reisinger[*1], S. Schaumberger[2], I. Dohnal[1], B. Doupovec[1], E. Mayer[1], and G. Schatzmayr[1], *[1]BIOMIN Research Center, Tulln, Austria, [2]BIOMIN Holding GmbH, Getzersdorf, Austria.*

Heat stress plays an important role in livestock animals. Several studies already described increased gut permeability in pigs during heat stress using invasive technologies e.g., Ussing Chamber. In human studies non-invasive sugar tests are quite often used to measure gut barrier function. We therefore evaluated the influence of heat stress on gut permeability of pigs with the dual sugar assay. Eight pigs were placed into metabolic cages (two pigs per cage) at D35 after weaning. Pigs were allowed to adapt to the cages for 4 d. At d 0 of the trial period pigs were kept at thermoneutral conditions (32°C, 24 h) and on d 1,2 and 3 pigs were exposed to heat stress conditions (6 h 35°C, 18 h 32°C). At d 0 and 2 the dual sugar permeability assay was performed. Therefore, agar containing lactulose (500 mg/kg body weight) and rhamnose (100 mg/kg body weight) was fed to the pigs. Urine was sampled 2, 4, and 6 h after sugar intake. Urine samples were frozen at- 20°C and lactulose and rhamnose concentrations were determined via HPLC-MS/MS. All data obtained in the experiment were analyzed with a nonparametric test. There was no significant difference between the cumulative rhamnose and lactulose excretion between d 0 (2.1%; 0.52%) and d 2 (1.2%; 0.84%). However, the lactulose rhamnose excretion ratio was significantly increased ($p = 0.0286$) of pigs under heat stress conditions (0.66) compared with thermoneutral conditions (0.24). Our study showed that the dual sugar assay can be used to evaluate gut permeability with a non-invasive method. We furthermore could once more highlight the negative impact heat stress can have on the welfare and health of pigs.

Key Words: gut permeability, heat stress, pigs

0175 The effect of various parameters measured at farrowing on subsequent pig performance. A. L. Robinson[*1], J. Colpoys[2], G. Robinson[1], E. A. Hines[1], E. Edwards[1], J. Bundy[1], A. K. Johnson[1], H. D. Tyler[1], *[1]Iowa State University, Ames, [2]Truman State University, Kirksville, MO.*

The objective of this study was to evaluate birth weight, gender, stall conditions at birth, umbilical diameter, ratio of umbilical diameter to birth weight (as a potential indicator of placental efficiency), and umbilical antiseptic treatment as predictors of pre-weaning mortality, incidence of umbilical hernias, and 150 d weight of pigs in a commercial facility. A total of 466 mixed gender commercial piglets from a breed-to-wean sow farm were enrolled. Piglets were alternately assigned by birth order within a litter to four umbilical treatment groups; iodine (2%), Zurex umbilical dip, a dry dip created using an antibacterial peptide (nisin) mixed with talc (formulation concentration = 3.105 g nisin/100 g talc on a wt/wt basis), and no treatment. At birth, stall conditions (wet/dry and clean/dirty) were evaluated on a 3 point scale (3 = most dirty or most wet and 1 = dry or clean). Before treatment, diameter of the umbilical cords were determined using digital calipers. All data were analyzed using mixed model methods. Models included the fixed effects of birth weight, umbilical diameter at birth, gender, stall conditions and treatment. Pre-weaning mortality was significantly affected by umbilical treatment ($p < 0.05$) and by ratio of umbilical diameter to birth weight ($p < 0.001$). Piglets treated with 2% iodine had a higher mortality rate than piglets treated with other antiseptics or those that were untreated. Piglets with the lowest umbilical cord diameter to birth weight ratio had the highest survival rate. Stall conditions at birth ($p < 0.005$) and the ratio of umbilical diameter to birth weight ($p < 0.05$) affected the incidence of umbilical hernias. Piglets born in wet stall conditions or those with a high umbilical cord to birth weight ratio had a higher incidence of umbilical hernias in the growing phase. Final 150 d weight of pigs was affected by the ratio of umbilical diameter to birth weight ($p < 0.0001$) and gender ($p < 0.0001$), and tended to be affected by stall conditions at birth ($p = 0.06$). Male pigs weighed 93.5 kg, while female pigs weighed 86.5 kg. Piglets with the highest ratio of umbilical cord diameter to birth weight and those born in wet stall conditions weighed less. In conclusion, measuring the umbilical cord to birth weight ratio was a much better predictor of pre-weaning mortality, incidence of umbilical hernias, and 150 d weight than birth weight alone.

Key Words: birth weight, piglet, pre-weaning mortality

0176 Environmental persistence of porcine epidemic diarrhea virus, porcine delta corona virus, and transmissible gastroenteritis in feed ingredients. M. P. Trudeau[*1], H. Verma[2], F. Sampedro[2], P. E. Urriola[1], G. C. Shurson[1], and S. M. Goyal[2], *[1]Department of Animal Science, University of Minnesota, St. Paul, [2]Veterinary Population Medicine, University of Minnesota, St. Paul.*

Porcine epidemic diarrhea virus (PEDV), porcine delta corona virus (PDCoV), and transmissible gastroenteritis (TGEV) are major threats to swine production. Investigations of recent outbreaks confirmed that contaminated feed plays a role in virus transmission. This risk makes it necessary to evaluate the survival of such viruses in various feed ingredients. The objective of our experiment was to characterize the inactivation of PEDV, PDCoV, and TGEV in various feed and ingredient matrices. To determine differences in virus survival, 5-g samples of complete feed, spray-dried porcine plasma, meat meal, meat and bone meal, blood meal, corn, soybean meal, and low, medium, and high oil dried distillers grains with solubles were weighed into separate scintillation vials. These samples were inoculated with 1 mL of PEDV, PDCoV,

or TGEV and incubated at room temperature for up to 56 d. At each time point, surviving virus was eluted and the supernatant was inoculated into vero-81 cells for PEDV, or swine testicular cells for PDCoV and TGEV. Cells were observed daily for 10 d for cytopathic effects, and this information was used to calculate a median tissue culture infectious dose ($TCID_{50}$) using the Karber method. Inactivation kinetics were determined using the Weibull model. A delta value was estimated from the model, indicating the time necessary to reduce virus concentration by 1 log. This delta value was then compared across ingredients using the mixed procedure of SAS, and correlations between ingredient proximate analysis data and delta values were determined. Results showed that soybean meal had the greatest delta value (7.50 d) for PEDV compared with other ingredients ($P < 0.06$). Likewise, PDCoV (42.04 d) and TGEV (42.00 d) delta values were highest in soybean meal ($P < 0.001$). There was a moderate positive correlation between moisture and the delta value for PDCoV ($r = 0.49$, $P = 0.01$) and TGEV ($r = 0.41$, $P = 0.02$). There was also a moderate negative correlation between lipid content and the delta value for TGEV ($r = -0.51$, $P = 0.01$), suggesting that TGEV is less stable in ingredients with greater lipid content compared with ingredients with less lipid content. In conclusion, these results indicate that the first log reduction of PDCoV and TGEV takes the greatest amount of time in soybean meal and it appears to be the result of greater moisture content.

Key Words: feed, inactivation kinetics, virus transmission

0177 Bovine macrophage phenotype influences inflammatory response to lipopolysaccharide.

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Severe inflammation during gram negative bacterial disease is common in periparturient dairy cows and increases the severity of diseases such as *Escherichia coli* mastitis. Tissue inflammation is partly orchestrated by macrophage responses to bacterial infection. Studies in monogastric species showed classical phenotype macrophages have proinflammatory responses and alternative phenotype macrophages have protective and restorative responses during disease. However, responses of diverse bovine macrophage phenotypes to lipopolysaccharide are unclear. The objective of this research was to compare the lipopolysaccharide-induced inflammatory response in several phenotypes of bovine primary monocyte-derived macrophages. Peripheral blood mononuclear cells were isolated from whole blood using Ficoll ($n = 8$ cows). Monocytes were identified using mouse anti-bovine CD172α monoclonal antibody and separated from lymphocytes using magnetic assisted cell sorting. Monocytes were cultured with interferon-γ or interleukins (IL) 4 and 13 to induce a classical or alternative macrophage phenotype, respectively, then stimulated with lipopolysaccharide. Macrophage mRNA was quantified in adipose using qPCR. Fold changes in mRNA concentration were calculated by $2^{-\Delta\Delta Ct}$, using the untreated cells as calibrator and three endogenous control mRNA. Treatment differences in mRNA expression were identified using Fisher pairwise comparisons and ANOVA ($P \leq 0.05$). Flow cytometry showed magnetic assisted cell sorting increased CD172α^+ cells from 22.3 ± 1.9 to 81.6 ± 2.8%. After 48 h *in vitro, CD68* expression increased and CD172α^+ was 95.2 ± 0.4%. Lipopolysaccharide increased *IL6*, *IL10*, *TNF,* and *CCL2* expression. Lipopolysaccharide stimulated *IL6* and *IL10* expression was decreased in alternative macrophages, whereas lipopolysaccharide stimulated *TNF* expression was increased in classical macrophages. Lipopolysaccharide stimulated *CCL2* expression was not different between macrophage types. Together these results show an exacerbated proinflammatory cytokine profile in a model of classical bovine macrophages during gram negative bacterial disease. Results suggest that macrophage phenotype could be involved with severe inflammatory responses seen during dairy cow periparturient periods characterized by prolonged and exacerbated lipolysis and increased disease susceptibility. Ongoing research will describe macrophage phenotype during bovine disease and identify factors contributing to phenotype change. Such factors could ultimately be manipulated to control the bovine macrophage inflammatory response.

Key Words: inflammation, macrophage, periparturient

0178 High immune response technology for use in commercial swine herds: A broad based approach to disease resistance.

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Societal concern regarding food safety and animal health are increasing, encompassing issues including the presence of antibiotic residues in meat, antimicrobial resistant organisms and the risk of zoonotic disease. Therefore, effective economic alternatives, with the potential to improve productivity in addition to animal health and robustness, are essential to the industry's continued success. Previous research in pigs has clearly demonstrated favorable responses to breeding pigs for high immune response (HIR). However, this method has not been tested in commercial swine herds. Since the HIR technology identifies animals with increased capacity for immune response (IR) and subsequently increased disease resistance, its implementation and integration into commercial pig breeding programs is expected to bring health and production benefits. The HIR test measures IR to benign and carefully selected test antigens (Ag), one that elicits antibody-mediated IR (AMIR) and another that elicits cell-mediated IR (CMIR). The study objective was to re-establish and refine the HIR test for pigs in a pilot study and then to utilize this test within a commercial

facility. Two groups of weaned piglets, 24 piglets/group were HIR phenotyped. Antibody-mediated IR, as measured by antigen-specific ELISA, was greater in the older versus younger test piglets ($p < 0.0001$, un-paired t test). Cell-mediated IR, was observed by delayed-type hypersensitivity, measured by change in double-skin-fold thickness (DSFT) both 24 and 48 h after intradermal injection of CMIR-associated antigen, and did not differ between test groups. Results indicate it is possible to phenotype and rank pigs for IR using a standardized HIR protocol. Applying this protocol to approximately 3600 weaned F1-barrows from seven different swine genetics companies is now underway as part of a large collaborative Genome Canada project examining associations between IR with swine health, production and genomic information.

Key Words: broad-based disease resistance, immune response phenotype, swine

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0179 Immunomodulatory activities of polyphenol extract from cowpea (*Vigna unguiculata*) on bovine polymorphonuclear neutrophils.

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The response of the bovine neutrophils to bacterial endotoxin and its significance in the inflammatory response has been studied widely. Studies have also shown that a cowpea diet is protein-rich and contains phenolic compounds with antioxidant properties beneficial for animal health and wellbeing. In this study, the effect of a polyphenol extract (CPE) from cowpea *(Vigna unguiculata)* on modulation of the response to endotoxin from gram negative bacteria was evaluated. Secretion of mediators of inflammation, such as cytokines, and prostaglandin E2 (PGE2), and expression of innate immune response genes by LPS stimulated bovine polymorphonuclear neutrophils (PMNs) were measured. Neutrophils were isolated from whole blood collected from Holstein-Friesian cows (n = 10) in mid-lactation. Lipopolysaccharide-stimulated PMNs were treated with 10 μg/ml of CPE. The secretion of cytokines (TNF-α, IFNγ, GM-CSF, G-CSF, IL-1A, IL-8, IP10, and RANTES), and prostaglandin E2 (PGE2) were measured using commercial ELISAs. Real-time qRT-PCR was performed using an innate and adaptive immune response array with 84 test genes. Cowpea polyphenolic extracts decreased PGE2 levels (8.2 ± 2.5 pg/ml) in LPS-stimulated PMNs, relative to control LPS-only treated PMNs (48.7 ± 4.1 pg/ml). Treatment with CPE resulted in decreased concentrations of six of the tested cytokines, except GM-CSF and IP10. Real-time qRT-PCR analysis of LPS-exposed PMNs revealed downregulation of proinflammatory cytokines (TNF-α, IL-1A, IL-1B, IL-8) and transcription factor NF-kB, and up-regulation of anti-inflammatory cytokine IL13(8.4-folds) by the cowpea phenolic extract. Thus cowpea polyphenolic extract may exert their anti-inflammatory activities and modulate innate immune response through modulation of the neutrophil under pathogen- induced conditions in cows. Therefore, integrating and utilizing cowpea into animal production system may enhance nutrition and improved health and needs further study.

Key Words: bovine, cowpea, cytokines, phenolic compounds, polymorphonuclear neutrophils, prostaglandin e2

0180 Prevalence of digital dermatitis in Canadian Holsteins classified as high, average, or low antibody and cell-mediated immune responders.

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Lameness is one of the major issues affecting production and animal welfare in the Canadian dairy industry, with digital dermatitis being the most common lesion. Studies have shown dairy cattle classified as high immune responders have lower incidence of disease, therefore it may be possible the immune response (IR) plays a role in preventing hoof lesions. The objective of this study was to compare the prevalence of digital dermatitis in Canadian dairy cattle that were classified for antibody (AMIR) and cell-mediated immune response (CMIR). Cattle (n = 341) from five commercial dairy farms in Ontario were evaluated for IR using a protocol that captures both AMIR and CMIR. They were classified as high, average and low responders based on standardized residuals for AMIR and CMIR. Residuals were calculated using a SAS general linear model that included the effects of herd, parity, stage of lactation and stage of pregnancy. Hoof health data was collected in 2012 by the farm's hoof trimmer using Hoof Supervisor software. Only the first trim date for each animal was included and multiple lesions per cow were considered. Trimmers scored each lesion for severity with 1 = least, 2 = moderate, 3 = most. Hoof health data was analyzed using a SAS general linear model which included the effects of herd, stage of lactation (at trim date), parity (at trim date) and IR category (high, average and low). Data is presented as prevalence within IR category. Preliminary results showed that high (17% of highs) AMIR cattle had a trend (P = 0.098) toward lower prevalence of digital dermatitis then average (28% of averages) AMIR cattle. It was observed that high (17% of highs) CMIR cattle had a trend (P = 0.081) toward lower prevalence of digital dermatitis compared with average (27% of averages) CMIR cattle and significantly (P = 0.04) lower digital dermatitis compared with low (30% of lows). Similarly high CMIR

cows also had significantly lower ($P = 0.03$) prevalence of the most severe type of digital dermatitis lesion compared with low CMIR cows. Since digital dermatitis is primarily caused by extracellular bacteria which is typically associated with AMIR these results still indicate that having a more robust or high IR is associated with lower prevalence of infectious hoof lesions. Therefore by breeding animals for high IR it is likely that improvements in hoof health can be made.

Key Words: digital dermatitis, immune response, dairy cattle

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181 MiRNaseq of neutrophils during the transition period in cows with divergent metabolic phenotypes. M. A. Crookenden*[1], C. G. Walker[1], A. Heiser[2], J. J. Loor[3], K. M. Moyes[4], J. K. Kay[1], S. Meier[1], A. Murray[5], V. S. R. Dukkipati[5], M. D. Mitchell[6], and J. R. Roche[1], *[1]DairyNZ, Hamilton, New Zealand, [2]AgResearch, Palmerston North, New Zealand, [3]University of Illinois, Urbana, [4]Department of Animal and Avian Sciences, University of Maryland, College Park, [5]Massey University, Palmerston North, New Zealand, [6]University of Queensland, Australia.*

Several adaptations in leukocytes, i.e., neutrophils, are required for a successful transition to lactation in dairy cows. Micro RNA (miRNA) molecules are small non-coding RNAs that regulate gene expression; their importance in immune cell function has been well documented. We characterized the miRNA of neutrophils isolated from dairy cows divergent in their risk of infection or metabolic dysfunction, at three time points over the transition period: day of calving, 1 wk, and 4 wk post-calving. From a total of 150 cows, 10 cows were selected with high ($n = 5$; High Risk) and low ($n = 5$; Low Risk) concentrations of non-esterified fatty acids, β-hydroxybutyrate, and liver triacylglycerol during wk 1 and 2 post-calving. Neutrophils were isolated from whole blood using differential centrifugation. Flow cytometric analysis of these isolates revealed a median of 75% ± 2% neutrophils (± SEM). Total RNA was extracted from neutrophils using TRIzol®, size selected for miRNA, and sequenced on the Illumina HiSeq. The miRNA reads were mapped to the *Bos taurus* 6 genome (UMD 3.1) using Bowtie 2 and counted. Differential expression analysis was conducted using the limma/voom R-package and pairwise analyses were conducted to assess differential expression between risk categories and across time points, with a false discovery rate set at 0.05. There was no effect of risk category on miRNA expression on the day of calving or 4 wk post-calving. However, expression of mir-19b, mir-148a, and mir-21 in the Low Risk cows tended (adj $P = 0.1$) to be greater at 1 wk post-calving. When assessed for the effect of time relative to the day of calving, regardless of risk, expression of miR-150 and −486 increased ($P \leq 0.05$) at 1 wk post-calving and eight miRNA genes were differentially expressed at 4 wk post-calving ($P \leq 0.05$): miR-150 and −30c were greater, and miR-19b, −19a, −30d, −101–1, and −106b were lower. The results indicate that the divergent metabolic phenotype did not significantly alter miRNA in neutrophils during early lactation. However, the altered miRNA profile in neutrophils over time indicates an important role for miRNA in the regulation of immune cell function during the peripartum period.

Key Words: microRNA, dairy cows, transition

0182 Short chain nitrocompounds treatment of poultry excreta; in vitro survivability of *Salmonella*, *E. coli* and nitrogen metabolism. C. Arzola-Alvarez*[1], J. Corrales[1], O. Ruiz-Barrera[1], R. C. Anderson[2], M. E. Hume[2], Y. Castillo-Castillo[3], A. Corral-Luna[1], J. L. Guevara-Valdez[1], J. Salinas[4], and C. Rodriguez-Muela[1], *[1]Universidad Autonoma de Chihuahua, Mexico, [2]USDA-ARS, College Station, TX, [3]Universidad Autonoma de Ciudad Juarez, Chihuahua, Mexico, [4]Universidad Autonoma de Tamaulipas, Reynosa, Mexico.*

Poultry litter is a byproduct produced in large amounts by intensive poultry production systems. While it contains appreciable amounts of nitrogen as uric acid, which makes it an excellent crude protein feed supplement for ruminants, it is usually a carrier of enteropathogenic bacteria of importance to human health. The objectives of this study were to determine the bactericidal effectiveness of several nitrocompounds, assess their potential to produce a feedstuff that is environmentally safe and their potential as a sustainable technology to preserve the nitrogen contained in poultry litter. Twenty grams of 6-mo-old poultry litter (82.5 ± 1.1% dry matter) were distributed in 709-mL plastic containers, mixed with 7.5 mL of deionized water containing no added nitrocompound or 40 mM 2-nitroethanol, 2-nitro-1-propanol (2nitropropanol), nitroethane, 3-nitropropionic acid or ethylnitroacetate. Each container was then inoculated with approximately 2×10^4 CFU of a *Salmonella enterica* serovar Typhimurium (NVSL 951776), naturally resistant to 25 μg/mL novobiocin and made resistant to 20 μg/mL nalidixic acid, and incubated aerobically at 37°C for 24 h. Samples collected at 0, 6, and 24 h were enumerated for *Salmonella.* Generic *E. coli* were enumerated on 3M *E. coli*/coliform petrifilm in samples collected at 0 and 24 h. Samples were also analyzed spectrophotometrically for determination of uric acid. Data were analyzed for main effects of treatment, time of incubation and their potential interaction on temperature and pH as well as on microbiological concentrations by a repeated measures analysis of variance. Main effects of treatment ($P < 0.0001$; SEM = 0.159), time ($P < 0.0001$; SEM = 0.170) and their interaction ($P = 0.0001$; SEM = 0.417) were observed on *Salmonella* concentrations. *Salmonella* concentrations in samples treated with 44 mM 2nitroethanol, 2nitropropanol or ethylnitroacetate were decreased by 0.7 to 1.7 $\log_{10}$CFU/mL within the first 6 h of incubation. Main effects of treatment (P

= 0.0100; SEM = 0.108), time (P = 0.0020; SEM = 0.065) and their interaction (P = 0.0145; SEM = 0.160) were observed on generic *E. coli* concentrations. Main effects of treatment were observed on rates of ammonia accumulation and the residual uric acid concentrations. Urea concentrations were below the limit of detection which under conditions of use was 1 µmol/ml. Results indicate that these environmentally sustainable and safe nitrocompounds negatively impacted potential enteropathogens contained in poultry litter. Additionally, litter treated with these compounds maintained appreciable levels of nutritionally available nitrogen in the form of uric acid, enhancing the value of used poultry litter as a ruminant feed supplement.

Key Words: *E. coli*, poultry excreta, *Salmonella*, uric acid

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0183 Effect of protected sodium butyrate on *Salmonella* spp. excretion in a pig fattening unit.

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This study was conducted to evaluate if the addition of protected sodium butyrate (SB) to a pig diet affected the level of *Salmonella* shedding in feces. The study was performed in a commercial *Salmonella*-infected fattening unit (8 pens, 110 pigs). Feed with 70% SB protected with vegetable fat (3 kg/t) was administrated to animals from 4 randomly selected pens during the fattening period (4 mo) (BUT). Pigs from the remaining 4 pens were fed the same diet without additive (CON). Individual serum and fecal samples were collected at 30, 60, and 90 d of fattening and at slaughter, where mesenteric lymph nodes (MLN) were also collected. Bacteriology on fecal and MLN samples were performed following the ISO 6579:2002 protocol. Serum samples were analyzed by means of an indirect ELISA using 3 cut-off values (OD% $\geq$ 10, $\geq$ 20 and $\geq$ 40). Chi-squared analyses were performed to compare microbiological and serological results between groups at different time periods, and a repeated measures analysis was used to estimate differences in mean OD% after taking into account sampling times and the interaction treatment × time. Although a lower proportion of positive animals in BUT was observed for samplings at 60d (4 vs. 0%), 90d (8 vs. 4%), and at slaughter (9.3 vs. 6.2%), no significant differences were detected, which was likely associated to the overall low prevalence of infection/shedding in both groups. In addition, the proportion of dead/withdrawn pigs in CON was significantly higher than in BUT (13.7 vs. 1.9%; P = 0.03). A higher (P < 0.05) seroprevalence was observed in CON compared with BUT for the sampling just before slaughter and for all cut-off values used (82.2 vs. 64.7%; 53.3 *vs*. 33.3% and 31.1 vs. 13.7%, at OD% $\geq$ 10, $\geq$ 20 and $\geq$ 40, respectively). Also, an overall significant positive relationship was observed between serology before slaughter (cut-off OD% $\geq$ 40) and shedding at slaughter (P < 0.01). The withdrawn of sick pigs in CON may have contributed to its low prevalence of infection/shedding, despite of which a higher seroprevalence was detected in this group at slaughter which, in general, appeared to be positively related to shedding. Thus, overall results suggested that the addition of protected SB at 3 kg/t may reduce the shedding of *Salmonella* spp. under farm conditions. The lowest number of pigs removed from pens in BUT also indicated an overall positive effect on health status of pigs in this group.

Key Words: *Salmonella*, protected butyrate, fattening pigs

0184 Study of genetic basis of immune response in gilts vaccinated with a modified live PRRS virus in a swine farm from southern Sonora Mexico.

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Porcine respiratory and reproductive syndrome (PRRS) is a disease of high negative impact on Mexican porcine production; one of the main reasons is the highly-variable response to vaccination. The objective of this study was to validate the favorable relationship among genotypes and immune response after PRRS vaccination for SNP previously associated with serum antibody response (SAR) and rectal temperature (RT). This study included 6-mo-old 3/4-Landrace × 1/4-Yorkshire replacement gilts (n = 100). After a 7-d acclimation period, all gilts were vaccinated with a modified live PRRS virus (d 0). The antibody response was measured from blood serum samples collected the d 7, 21, and 35 after vaccination using a commercial antibody ELISA kit (IDEXX Laboratories, Inc.). Rectal temperature data were collected the d 7, 14, 21, 28, and 35 using a digital GLA M750 thermometer (GLA Agricultural Electronics). A blood sample was also collected from each gilt approximately 40 d after vaccination and spotted onto FTA cards. All cards were processed for genomic analyses using a low-density chip to obtain genotypes from 8826 SNP (Infinium BeadChip, Illumina, San Diego, CA). In a previous analysis of these data, multi-locus mixed models performed in SNP Variation Suite 7 identified nineteen SNP associated with immune response (P < 0.001). The associative relationship between these SNP and the phenotypes SAR and RT was validated using a mixed effects model; this model included SNP genotype and age of

dam as fixed effects, and sire as a random. Allele substitution effect was also calculated using a regression model that included genotype term as a covariate. Mean S/P values for SAR were 2.26 ± 0.08 and mean values for RT were 39.0 ± 0.05°C. From the SNP previously identified, ASGA0019937, ALGA0025501 and H3GA0020133 were associated with SAR after PRRS vaccination ($P < 0.01$), and the favorable alleles increased S/P levels in 0.21 ± 0.06, 0.19 ± 0.07 and 0.46 ± 0.10, respectively. However, only ALGA0017541 was associated to RT ($P < 0.01$), and the favorable allele reduced 0.21 ± 0.01°C the rectal temperature. In conclusion, four specific genetic markers that underlie genetic variation in response of gilts to PRRS vaccination were validated using a SNP genotype to phenotype association analysis. We propose such SNP as candidates for use in a marker assisted selection program that further evaluates the immune response to PRRS vaccination in gilts of southern Sonora production systems.

Key Words: gilts, immune response, PRRS vaccination.

UNDERSTANDING INFLAMMATION AND INFLAMMATORY BIOMARKERS TO IMPROVE ANIMAL PERFORMANCE

0185 Overview of the inflammatory response and its nutritional costs.

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Innate immune cells respond quickly to a potential pathogen due to the presence of a common set of receptors on all phagocytic cells that recognize broad categories of pathogens. Thus, a very large number of cells can recognize invading microbes and respond to them quickly. A consequence of this is pathogen clearance, usually by phagocytosis, followed by the release of inflammatory cytokines and chemokines that amplify the local infiltration of additional inflammatory cells and activate them. If the challenge is large or if it is accompanied by damage to host tissue, cytokines are released in sufficient amounts that they have endocrine-like effects throughout the body. This cytokine storm induces metabolic changes, including increased protein degradation and insulin resistance in skeletal muscle, which diverts nutrients from muscle and other tissues so that they become available for the increased demands of leukocytes and for the production of protective proteins. Importantly the liver transitions from maintaining homeostasis and supporting the nutritional demands of growth or reproduction to the production of protective proteins such as complement, mannan binding protein, and C-reactive protein that aid in the detection and neutralization of pathogens. This transition is accompanied by hepatic hypertrophy. A study of the costs of a systemic inflammatory response in chickens to *Salmonella* that examined the amount of nutrients in 6 different leukocyte types in 5 different tissues (blood, spleen, bursa, thymus, bone marrow) and 12 protective proteins (acute phase proteins and immunoglobulins) found that the amount of essential amino acids in the protective proteins greatly exceed that in the cellular component of the immune system during both a normal and an inflammatory state. The ideal balance of amino acids for the acute phase of an inflammatory response differs greatly from that needed for growth and there is a critical need for additional cysteine and threonine. Ongoing research indicates that higher metabolic rate, decreased intake of food, a mismatch between the nutrient balance needed for the inflammatory response relative to that in body tissues and less efficient digestion that accompany a robust inflammatory response are, together, even more costly than the direct use of nutrients by inflammatory cells and the liver. Together, these costs result in decreased productivity that cannot be completely reversed by supplying additional nutrients.

Key Words: inflammation, cytokines, nutrients

0186 Ruminal microbes, microbial products, and systemic inflammation.

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The ruminal ecosystem is inhabited by complex communities of microbes that include bacteria, archaea, protozoa, fungi and viruses. The immune system of the animal has evolved to maintain tolerance to innocuous gut commensals and induce protective responses to pathogens. Besides fermentative role, ruminal microbes do have the potential to influence the overall health of the host because of their ability to induce systemic inflammation. The ruminal epithelium-vascular interphase allows absorption of fermentation products and also serves as a selective barrier to prevent translocation and systemic dissemination of bacteria, bacterial toxins, and immunogenic factors. Ruminal dysbiosis that increases ruminal acidity and osmolarity may increase permeability and even induce a breach in the integrity of the epithelial and vascular endothelial barriers, thus facilitating entry of bacteria or bacterial antigens into the portal vein. A classic example is the delivery of ruminal bacterium, *Fusobacterium necrophorum,* into the liver to cause abscesses, which is facilitated by ruminal damage induced by excessive accumulation of lactic acid or VFA. Bacteria that manage to exit or bypass the liver can cause systemic inflammation in other organs, such as lungs, heart, joints, hoof, etc. Shifts in microbial populations associated with dysbiosis result in increased concentrations of potentially toxic and inflammatory substances, which include endotoxic lipopolysaccharide (LPS), biogenic amines, ethanol, etc. A bacterial product that has received a lot of interest is LPS, a component of all Gram negative bacteria. The entry of LPS into the systemic circulation, either from the rumen or the lower gut, could trigger release of proinflammatory cytokines, reactive oxygen and nitrogen intermediates, and bioactive lipids. The inflammatory response to the presence of ruminal LPS in the blood is evidenced by increase in acute phase proteins, such as haptoglobin and LPS binding protein.

Biogenic amines generated in the rumen that could lead to inflammation include histamine, tyramine, and ethanolamine. Histamine that is absorbed from the rumen or produced endogenously in tissues during inflammation plays a key role in the development of laminitis. Ethanolamine derived from bacterial phospholipids has the potential to enhance growth and virulence of certain gut pathogens. In conclusion, ruminal microbes and their products generate many complex interactions with the host immune system, and dysbiosis has the potential to induce systemic inflammation. Although inflammation is a protective reaction, the persistence of inflammatory mediators could have negative consequences for the host.

Key Words: ruminal microbes, dysbiosis, inflammation

0187 Usefulness (or not) of inflammatory biomarkers: The good, the bad, and ugly. C. Chase*, *South Dakota State University, Brookings.*

The innate immune system has the job of sensing the host's environment–looking for infections and tissue damage. It then does its second job, which is to recruit in the "right" cells to handle the problem. There is ample evidence that both physical and psychological distress can induce innate immune system pro- and anti-inflammatory cytokines that can cause immune dysfunction in animals, leading to an increased incidence of infectious disease. In livestock, there are several factors that will compromise immune function. There is the stress of transportation, dehydration, feed change (with the resulting negative energy balance), acidosis, and associated microbial changes in the gut. Overstimulation of the innate immune system can result in a pro-inflammatory cytokine storm, which will increase tissue damage. Both pro-inflammatory cytokines [such as tumor necrosis factor-α (TNF-α), interleukin-1, and interleukin-6] and anti-inflammatory cytokines (such as interleukin 10, transforming growth factor β and interleukin 1 receptor antagonist) can be elevated in the serum of animals experiencing a cytokine storm. These in addition to acute phase proteins are often monitored to "measure inflammation". An overview of "inflammation" and an experimental approach in cattle to study these local interactions will be discussed along with the proof of concept immunological measurements.

Key Words: innate immunity, inflammation, pro-inflammatory, anti-inflammatory

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0188 Nutritional and management considerations in beef cattle experiencing stress-induced inflammation. R. F. Cooke*, *Oregon State University-EOARC, Burns.*

When transported to feedlots, beef cattle are exposed to several stressors within a short period of time that directly impact their performance and welfare. The main stressors associated with this "feedlot transfer phase" (FTP)—weaning, road transport, and feedlot entry—increased ($P < 0.05$) plasma concentrations of cortisol, pro-inflammatory cytokines, and acute-phase proteins (APP), while the magnitude of this response was negatively correlated ($r = -0.50$, $P < 0.01$) with feedlot receiving ADG and DMI. Further, feed and water deprivation elicited ($P < 0.01$) an APP response and reduced ($P < 0.03$) receiving performance similarly as in cattle transported for long distances. Hence, strategies to alleviate the APP response elicited during the FTP were evaluated: (1) Steers were assigned to continuous road transport for 1300 km (TRANS), or road transport for 1300 km with rest stops every 430 km (STOP). During feedlot receiving, ADG and G:F were similar ($P > 0.68$) between TRANS and STOP. Plasma concentrations of APP were greater ($P \leq 0.04$) in TRANS compared with STOP on d 1 of receiving. (2) Steers transported for 1300 km received (SUP) or not (CON) Ca soaps of soybean oil during a 28-d preconditioning. Upon transport, plasma TNF-α increased for CON but decreased for SUP steers ($P < 0.01$). Steers assigned to SUP had greater ($P = 0.02$) ADG compared with CON steers during the receiving phase. Upon slaughter, carcass yield grade and marbling were greater ($P < 0.05$) for SUP compared with CON. A subsequent trial evaluated the inclusion of camelina meal in similar research design. During feedlot receiving, SUP steers had reduced ($P < 0.01$) plasma APP concentrations and tended ($P = 0.10$) to have greater G:F compared with CON. 3) Steers were transported for 1300 km and administered flunixin meglumine (1.1 mg/kg BW) at truck loading and unloading, or meloxicam (1 mg/kg of BW) at loading and during the initial 7 d of feedlot receiving. Both anti-inflammatory drugs reduced ($P < 0.05$) the APP response elicited during the FTP compared with non-treated cohorts, but only meloxicam increased ($P < 0.04$) receiving ADG and G:F. In summary, inclusion of rest-stops during transport, preconditioning PUFA supplementation, and use of anti-inflammatory drugs are alternatives to alleviate the APP response elicited during the FTP, whereas PUFA and meloxicam administration enhanced feedlot performance of feeder cattle.

Key Words: beef cattle, inflammation, management, nutrition

CELL BIOLOGY SYMPOSIUM: MEMBRANE TRAFFICKING AND SIGNAL TRANSDUCTION

0189 Introduction: What is the relevance of this topic? J. L. Klotz*, *USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY.*

Knowledge of membrane dynamics and receptor-ligand related responses are critical to a complete understanding of many of the tissue-level and whole animal level observations made in physiologic, pharmaceutical and toxicological research. The outcome of this basic research can have significant implications in animal agriculture in terms of impact

of disease states, toxin exposure, and use of pharmaceutical and natural products on various aspects of animal production. Can studies that further the understanding of the membrane trafficking and cell signaling relationship be applied to solve problems relevant to livestock production? How do disease states alter the trafficking-signaling interconnection? To answer these questions, the objective of this symposium is to address protein and lipid aspects of transport within a membrane, how functions may change as a result of a pathological state, and how this basic science can be used to further the needs of livestock at the production level.

Key Words: cell signaling, livestock production, membrane trafficking

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0190 SNAREs in exocytosis and membrane trafficking.
S. W. Whiteheart*, *University of Kentucky, Lexington.*

In 1993, Rothman and colleagues sought to explain the specificity of membrane trafficking between cellular compartments by proposing the SNARE hypothesis. Since that time, we have gained significant insights into the conserved mechanisms that control membrane fusion in all eukaryotes. Integral membrane proteins called SNAREs (Soluble NSF Attachment protein Receptors) mediate the membrane fusion that is required to move cargo from one cellular compartment to another. In general, SNAREs on cargo-carrying vesicles are known as v-SNAREs (also called R-SNAREs due to conserved arginines) and those on the destination or target membranes are called t-SNAREs (also called Q-SNAREs due to conserved glutamines). There are large families of both v- and t-SNAREs, all of which contain at least one amphipathic, helical domain that forms a four helical bundle with other SNAREs. This heteromeric complex spans the two membranes to promote lipid mixing for membrane fusion and cargo transfer. Though the significance of their diversity is unclear, certain SNARE combinations (v and t) are optimal for the fusion steps required for specific membrane trafficking steps. For extracellular secretion (exocytosis), t-SNAREs are a heterodimer of syntaxins and SNAP-23/35s. Despite being the minimal components required for fusion, in order for SNAREs to mediate physiologically significant processes, they must be controlled by regulators and post-translational modifications. The regulators affect, where, when, and how fast membrane fusion occurs. Most of the regulators affect the t-SNAREs. Syntaxins are controlled by chaperones of the Sec1/Munc18 (SM) family, which not only stabilize the syntaxins but also guide their binding to other SNAREs. SNARE-23/25s are dynamically anchored in the membranes via thioester-linked acyl groups. SNAP-23 also appears to be acutely controlled by phosphorylation. Regulation of the v-SNAREs appears less wide-spread. Several SNARE accessory proteins have C2 domains that enable calcium-dependent, membrane binding to acidic lipids. Syntaptotagmins are membrane proteins on vesicles thought to be key, calcium sensors that, together with complexins, control the final steps of membrane fusion. Other C2 domain-containing proteins, *e.g.,* Munc13 family members, are docking factors that bring the two membranes together to engage the SNAREs for subsequent vesicle-target membrane fusion. The Munc13 proteins work with small GTP-binding proteins, called Rabs, to promote docking. Together the SNAREs and SNARE regulators mediate the highly controlled membrane fusion events that underlie many diverse processes such as neurotransmission, hormonal regulation, and hemostasis.

Key Words: Munc, secretion, SNAREs

0191 Signaling endosomes and epithelial morphogenesis.
C. D'Souza-Schorey*, *University of Notre Dame, Notre Dame, IN.*

Tumor development in glandular tissues is associated with structural alterations in the hollow ducts and spherical structures that comprise such tissues. We have described a signaling axis that provokes dramatic changes in the organization of epithelial cysts, reminiscent of tumorigenic glandular phenotypes. In reconstituted basement membrane cultures of renal epithelial cysts, enhanced activation ARF6 (ADP-ribosylation factor 6) downstream of receptor tyrosine kinases induces the formation of cell-filled glandular structures with aberrant phenotypes. All of these alterations are accompanied by growth factor receptor internalization into signaling endosomes and reversed by blocking ARF6 activation or receptor endocytosis. Receptor localization in signaling endosomes results in hyperactive extracellular signal-regulated kinase signaling leading to abnormal cellular alterations. These findings identify a link between ARF6-regulated receptor internalization and events that drive dramatic alterations in epithelial glandular morphogenesis providing new mechanistic insight into the molecular processes that can promote epithelial glandular disruption.

Key Words: ARF6, epithelial morphogenesis, signaling endosomes

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0192 Structural and signaling functions of sphingomyelinases during inflammation.
M. N. Nikolova-Karakashian*, *University of Kentucky, Lexington.*

Sphingolipids are lipid molecules with structural, signaling, and metabolic functions. Sphingomyelinases (SMases) convert sphingomyelin, a mostly structural lipid, to ceramide, a bioactive metabolite. Two of the five known SMases play distinct roles in inflammation. Neutral sphingomyelinase-2 (nSMase-2) is a plasma membrane-localized enzyme and mediates the hepatocyte response to IL-1b. Our experiments have identified PP2A, IRAK1, JNK, FoxO1, and the insulin-like growth factor binding protein 1 (IGFBP1) as components of a novel pathway in the IL-1b signaling network that are dependent on nSMase-2. Surprisingly, we also found that

conditions associated with chronic, subclinical inflammation (like oxidative stress, hepatic steatosis, and aging), affect the basal activity of nSMase2, causing up-regulation of that specific pathway and IL-1b hyperresponse. Experiments in mice and rats also show that silencing of nSMase-2 in hepatocytes can be achieved in vivo and can help alleviate an exacerbated IL-1b response.

Acid sphingomyelinase (ASMase) is localized in the endo-lysosomal compartment of the cells and impacts the dynamics of lipid raft domains and endosomes. These effects are especially important for the functions of macrophages during the innate immune response. In activated macrophages, ASMase activity modulates the magnitude of LPS-induced secretion of TNFa. The mechanism is complex and involves the regulation of: (1) the activity of TACE, an enzyme that cleaves the inactive TNFa precursor (pro-TNFa) to its active form and (2) the rate of recycling of pro-TNFa between lysosomes and the plasma membrane. Together, these experiments delineate a novel understanding of the bioactive functions of SMases in chronic and acute inflammation.

Key Words: inflammation, liver, macrophage

0193 Practical application of the basic aspects of membrane trafficking and receptor-mediated signaling on issues related to animal agriculture.
S. B. Smith*, *Texas A&M University, College Station.*

Because of the relatively short life spans of beef cattle, membrane trafficking in relation to inflammation is not considered important unless it overtly affects productivity. However, glucose uptake and utilization is important for adipose tissue development in beef cattle, and increasing glucose utilization in intramuscular adipose tissue can increase carcass quality. Research from the 1980s demonstrated a lack of insulin sensitivity in isolated bovine adipocytes and adipose tissue explants incubated in vitro. Insulin did not stimulate glucose or acetate incorporation into fatty acids, nor did it increase concentrations of glycolytic intermediates in bovine adipose tissue incubated with exogenous glucose. Specific binding of [I125] iodoinsulin and insulin degradation in bovine isolated adipocytes was low to non-detectable. These early studies indicated that insulin-dependent receptor-mediated signaling was less important in bovine adipose tissue than in adipose tissues of humans or laboratory species. Recent research demonstrated that GLUT4 expression in muscle and adipose tissue declined markedly after birth in calves, indicating the development of insulin resistance as cattle transitioned from suckling to functional ruminants. Insulin resistance is important in dairy cattle, and causes ketosis and fatty liver. In dairy cattle, s.c. adipose tissue GLUT4 expression decreased 50% following parturition, although insulin responsiveness in s.c. adipose tissue was restored as early as 3 wk postpartum. Expression of genes associated with insulin responsiveness (*IRS1*, *INSIG2*, *SREBF1*, and *ZFP423*) was upregulated in similar fashion. Understanding the underlying mechanisms of insulin resistance and inflammation would increase animal health and thereby improve productivity.

Key Words: adipose tissue, bovine, insulin

ASAS GRADUATE STUDENT SYMPOSIUM

0194 Marketing 101: Learning how to market yourself for a successful career.
R. M. Yamka*, *Blue Buffalo Company Ltd., Wilton, CT.*

The animal science industry can be a competitive marketplace as new graduates begin to look for a new job. Having good grades, the right skill set (laboratory experience, publication experience, good grades, etc.) and work experience (collecting samples, computer experience, working with animals, etc.) is not always enough to secure employment. Especially in a competitive job market. As a result, identifying ways to stand out from the crowd becomes important. Unfortunately, most job candidates do not realize that it is important to learn how to market and sell yourself to your target audience to meet their current and future business goals. How you market and sell yourself will be career and industry dependent (academia vs. consumer goods vs. pharma). Marketing and selling yourself does not end once you get your foot in the door. Marketing and selling yourself continues as you advance in your career. Although it is not as formal as the interview, marketing yourself requires you to network, communicate and engage management inside & outside your department. In addition, looking for new opportunities to build your credentials (board certification, become the "go to" person) and identifying ways to be unique will help set you apart and differentiate you from your peers. In this session, some of these key strategies will be discussed and how they can be applied for a successful career.

Key Words: marketing yourself, target audience, successful career, professional development

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0195 Personal branding.
M. Calvo-Lorenzo*, *Elanco Animal Health, Greenfield, IN.*

Who you are and how you carry yourself are very important to becoming successful. As a student and professional, your personal brand keeps you current in your own field, opens doors of opportunities for you, and creates a lasting impression. While making an unforgettable first impression in person is important, it is no longer the only way to establish your brand. Personal branding should help individuals define themselves in their workspace, while also incorporating the personal elements that make you who you are. In this session, several strategies will be discussed on creating a successful personal brand, while providing an overview on how to articulate one's

skills, experience, knowledge, and overall aspirations. The world wants to hear what professionals and experts have to say, and given the real-time connectivity of online social media today, learning how to create a powerful personal brand couldn't be more important.

Key Words: personal brand, success, professional development

0196 Bridging the gaps. J. D. Crosswhite*, *North Dakota State University, Fargo.*

The animal science community is constantly changing to meet the needs of the consumer. The same is true for animal science departments striving to meet the three pronged goals of land grant universities. The landscape of research in animal science is always evolving as our knowledge of basic science expands. The competitiveness of research funding is higher than ever, and this puts increased pressure on the researchers vying for these funds. In addition to this, the generation gap between the average consumer and production agriculture is increasing, making extension education as important as ever. These challenges are making split appointment positions within academia harder to accomplish, as the education of students taking animal science classes is still a major focus. This environment has opened up the opportunity for individuals with a completed master's degree to become instructors. Having a 100% teaching appointment allows these lecturers the unique opportunity to focus all of their attention on bridging the gap between a research mindset and production animal science within the classroom. Thus, opening up time and opportunity for research and extension faculty.

Key Words: lecturer, classroom, teaching

0197 Doctoral programs in animal science: Strategies for targeting academic careers. J. S. Caton*, *Department of Animal Sciences, North Dakota State University, Fargo.*

Objectives of this review are to discuss successful doctoral student professional development strategies for targeting academic positions in the animal sciences and related fields. Entry level positions for academic careers are most often 2-way split appointments containing proportions of research, teaching, and extension responsibilities. Occasionally, institutions will offer 1- or 3-way split appointments. Positions will usually range from 9 to 12 mo appointments on a tenure-track, though variations exist. Successfully targeting these types of career positions requires deliberate planning and action by the doctoral student and mentoring team. Carefully selecting an advisor, institution, doctoral training committee, and other mentoring and training structures are essential early components in the process. Research experiences need to contain both discovery and application based aspects, present opportunities for leadership and collaborative team efforts, be solid in experimental design and methodologies, demonstrate focus in targeted areas, and breadth across species, mechanisms, methods, and systems. Data should be published in multiple venues, including refereed manuscripts. Mentoring and training in teaching at the university level needs to be real and relevant. Experience in formal and informal aspects of teaching are needed and should be supported with both student and peer teaching evaluations when possible. Mentoring in extension needs to include significant clientele contact, evidence of proficiency with a breadth of communication techniques, and clear goals and assessments. Effective training in perusing and securing grant funds to support research, teaching, and extension activities should be evident. Leadership, collaborative skills, and professionalism should be developed and effectively demonstrated. Evidence of effectively managing research teams, mentoring undergraduate students, and overseeing undergraduate research projects helps demonstrate preparedness for the transition from doctoral student to assistant professor. Strategically targeting and successfully accomplishing specific professional development activities within research, teaching, and extension will foster excellence and help secure effective and successful academic careers in animal sciences and related fields.

Key Words: academic careers, doctoral programs, professional development strategies

ASAS UNDERGRADUATE STUDENT POSTER COMPETITION

0198 Antimicrobial activity of tropical spice extracts against *Escherichia coli* O157:H7. E. Olasoji[*1], I. M. Ogunade[2], D. Kim[2], and A. T. Adesogan[2], *[1]Department of Food Science, University of Florida, Gainesville, [2]Department of Animal Sciences, IFAS, University of Florida, Gainesville.*

This study examined the antibacterial effects of spices (Alligator Pepper, Yellow Nutmeg, Tumeric, Green Pepper, Nutmeg, Ginger, African Guinea Pepper, Bayleaf, and Rosemary) on *Escherichia coli* O157:H7 (EC). Stock solutions containing 0.2 g of each spice per mL of ethanolic extract were prepared. The antimicrobial activity of each extract was examined using the agar disc diffusion method. Approximately 100 μL of EC culture was surface-plated on MacConkey agar supplemented with cefixime and tellurite. An aliquot (10 μl) of each spice extract was pipetted onto a 6.2-mm sterile paper disc on the agar surface and incubated for 24 h at 35°C. The inhibition zones around the discs were measured in millimeters. The Minimum Inhibition Concentration (MIC) of each of the spice extracts was determined by macrobroth dilution method. The experiment was repeated twice. Results were analyzed using the GLIMMIX procedure of SAS. The inhibition zones

observed for Green Pepper (19.33mm), Alligator Pepper (18.67mm), Rosemary (18.83mm), Tumeric (15.33mm), Nutmeg (16.50mm), African Guinea Pepper (16.67mm), Bayleaf (15.50) and Ginger (15.67mm) were greater ($P = 0.0001$) than that of the Control (11.67mm). African Guinea Pepper had the lowest MIC (2 mg/mL) while others inhibited EC at MIC less than 16 mg/mL. In conclusion, extracts of these tropical spices showed antimicrobial activity against EC.

Key Words: *Escherichia coli* O157:H7, inhibition zone, spices

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0199 Effect of low- and high-fat dry distillers grains supplementation on forage intake and digestibility in beef heifers. E. L. Stephenson*[1], A. L. Jones[2], J. S. Luther[1], and A. E. Radunz[1], *[1]University of Wisconsin, River Falls, [2]University of Wisconsin, Madison.*

The objective of this study was to evaluate low-medium quality intake and apparent total tract digestibility supplemented with of low-fat vs. high-fat corn dried distillers grains with solubles (DG) in yearling Angus, Hereford, and Angus-cross beef heifers ($n = 30$; 399 ± 16 kg). Heifers were stratified by BW and breed composition and then assigned to 1 of 3 treatments: (1) no supplementation (CON); (2) supplementation of low-fat DG (LDG; 5.04% EE); (3) supplementation of high-fat DG (HDG; 9.09% EE). Heifers were provided ad libitum intake of low to medium quality chopped grass hay (7.82% CP; 1.14 Mcal NE_m/kg). Both LDG and HDG were supplemented at 0.8% body weight (BW) to provide a similar CP intake of 0.22% of BW. Hay was fed twice a d at 0800 and 1600 and supplement was fed once a d before hay feeding at 0700. Individual feed intake was recorded for 37 d. Two-day BW were collected at the beginning and end of the trial. To determine apparent total tract digestibility feed-offered, feed refusals, and fecal grab samples were collected on d 27 from a subset of 3 heifers per treatment and then DM, OM, CP, ADF, NDF, and EE analysis was performed and ADIN was used an indigestible marker. Heifers supplemented with DG (LDG or HDG) had greater BW gain and ADG ($P < 0.0001$) and lower ($P = 0.002$) total DMI in g/kg of BW compared with CON, however no differences were detected ($P \geq 0.14$) in BW gain, ADG, or total DMI in g/kg of BW between HDG and LDG. Furthermore, a change in BCS was not detected ($P = 0.46$) among treatments. Heifers that were supplemented LDG had lower DM, N, and NDF apparent digestibility than heifers supplemented HDG and heifers with no supplementation ($P \leq 0.004$). Apparent digestibility of OM and ADF did not differ among treatments ($P \geq 0.05$) while heifers supplemented LDG had lower apparent digestibility of EE ($P = 0.001$) and HDG supplementation was intermediate as compared with CON. Supplementation of DG regardless of fat content reduced total DMI and improved BW gain for yearling beef heifers, but supplementing the LDG vs. HDG resulted in lower DM, N, and NDF digestibility fed with low to medium quality grass hay.

Key Words: corn distillers grains, protein supplementation, forage digestibility

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0200 Nutritive and digestibility parameters of invasive grasses in northwest Missouri. F. C. Huneke*, M. H. Richardson, A. M. Snyder, and J. D. Allen, *Northwest Missouri State University, Maryville.*

The purpose of this study was to determine nutritive and digestibility parameters of invasive grasses located in improved pastures in northwest Missouri. Samples from 18 grass species were gathered at reproductive maturity in 3 of 6 grazing pastures located at the R. T. Wright farm of Northwest Missouri State University (3 samples/species). Grasses were dried, ground, and subsequently subjected to the following laboratory analyses: NDF, ADF, and ash. Samples were also analyzed for 12-, 24-, and 48-h in situ digestibility using 2 cannulated Holstein dairy cows fed a consistent corn silage based diet. Dry matter was relatively similar (range 23.2 to 33.8 ± 4.78%DM) across species except for Stinkgrass (*Eragrostis cilianensis*; 41.7% DM) and Prairie cordgrass (*Spartina spectinata*; 45.3% DM; $p < 0.01$). Prairie cordgrass also had the greatest ($p < 0.01$) NDF and ADF (64.3 and 30.8%, respectively) when compared with the other species (range 49.1 to 60.7 ± 2.17% NDF and 22.6 to 30.8 ± 1.51% ADF). Ash content also varied (range 7 to 13.1 ± 1.48%; $p < 0.05$). Twelve hour in situ digestion was similar across species ($p > 0.10$), however, species diverged in 24- and 48-h digestion (range 42.2 to 65.4 ± 3.41% and 52.9 to 73.7 ± 3.70%, respectively, $p < 0.01$). In situ digestion developed 3 distinct digestion groups among the species, with Little barley (*Hordueum pusillum*), Foxtail barley (*Hordeum jubatum*), and Prairie cordgrass being the least ($p < 0.01$) digestible over a 48-h period (58.9, 56.4, and 52.9%, respectively). Results indicate that nutritive quality of invasive grasses varies by species, which may disrupt overall forage quality.

Key Words: cattle, digestibilty, invasive species, nutrient composition

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0201 Poor maternal nutrition during gestation alters mesenchymal stem cell (MSC) metabolism in offspring. N. H. Sereda*[1], S. M. Pillai[1], M. L. Hoffman[1], S. A. Zinn[1], Y. K. Park[2], J. Y. Lee[2], and K. E. Govoni[1], *[1]Department of Animal Science, University of Connecticut, Storrs, [2]Department of Nutritional Sciences, University of Connecticut, Storrs.*

Poor maternal nutrition due to excess or reduced nutrient intake during gestation has negative effects on fetal growth and metabolism including reduced bone and muscle, and increased adipose tissue. There is evidence that poor maternal

diet during gestation impairs the function of MSC, stem cells that contribute to bone, muscle, and adipose development, in the offspring. It was hypothesized that poor maternal nutrition during gestation would negatively alter MSC metabolism in offspring. Eighteen pregnant ewes were individually housed and randomly assigned to one of three diets (100%, 60%, or 140% of NRC requirements for TDN) at d 31 ± 1.3 of gestation. One lamb per ewe was euthanized within 24 h of birth (100% = CON, 60% = RES, 140% = OVER; n = 6/treatment) and MSC were isolated from the bone marrow of left tibia and femur. For analysis of glycolytic and mitochondrial functions, cells were plated at 30,000 cells/well and incubated at 37°C for 48 h. Assays were performed using Glycolysis Stress and Cell Mito Stress Test Kits and analyzed using the Seahorse XF^{e}24 Extracellular Flux Analyzer. Data were normalized for total cellular DNA and analyzed using PROC MIXED in SAS. Basal respiration was reduced in RES and OVER, compared with CON (127.4 ± 7.48, 90.17 ± 9.75, 87.51 ± 8.48 ρmol O_2^{-1}·min^{-1}·μg; CON, RES, OVER, respectively; $P \leq 0.008$). Compared with CON, RES and OVER had reduced ATP production (121.09 ± 6.08, 84.86 ± 11.05, 77.7 ± 6.44 ρmol O_2^{-1}·min^{-1}·μg; CON, RES, OVER, respectively; $P \leq 0.006$) and reduced maximal respiration (149.29 ± 17.05, 90.64 ± 23.81, 67.93 ± 10.15 ρmol O_2^{-1}·min^{-1}·μg; CON, RES, OVER, respectively; $P \leq 0.03$). Spare respiratory capacity was reduced in OVER compared with CON (P = 0.02) while RES were intermediate (21.9 ± 10.8, 0.47 ± 12.3, and −19.56 ± 9.24 ρmol O_2^{-1}·min^{-1}·μg; CON, RES, OVER, respectively; $P \leq$ 0.25). There were no significant differences between groups for proton leak, non-mito-derived OCR, coupling efficiency, MSC glycolysis, glycolytic reserve, non-glucose-derived extracellular acidification rate, and glycolytic reserve capacity ($P \geq 0.18$). In conclusion, maternal over- and under-nutrition during gestation reduced the basal metabolic state of offspring MSC, and the ability of these cells to up-regulate ATP production during energetic deficits. The altered MSC metabolism may contribute to impaired muscle, bone, and adipose growth and maintenance in offspring.

Key Words: mesenchymal stem cells, metabolism, nutrition

0202 The abundance of myosin heavy chain Ilb mRNA in porcine Longissimus dorsi muscle was not affected by dietary lysine level.

M. B. Lewis*[1], S. F. Liao[2], T. Wang[2], and J. M. Feugang[1], *[1]Mississippi State University, Starkville, [2]Mississippi State University, Starkville.*

Successful swine production is about raising leaner pigs, because the lean meat (i.e., the skeletal muscle) is the most desired component of pork. Myosin, the most abundant contractile protein, constitutes approximately 45% of the total myofibrillar proteins, among which myosin heavy chain IIb (MyHC-IIb) isoform appears to be the determining protein contributing to pig muscle growth. This study was conducted to determine how dietary lysine level affects the expression of MyHC-IIb mRNA in pig skeletal muscle, as lysine is the first limiting amino acid in typical swine diets. Nine crossbred barrows (94.4 ± 6.7 kg) were randomly assigned to one of three groups fed either Diet 1 (lysine-deficient), 2 (lysine-adequate), or 3 (lysine-excess), which contained 0.43, 0.71, or 0.98% total lysine, respectively. After 5 wk on the trial, pigs were slaughtered, and approximately 2 g muscle sample was collected from the middle portion of *Longissimus dorsi* of each pig. Real-time RT-PCR technology was employed to determine the abundance of MyHC-IIb mRNA in each sample using the ΔΔCT quantitative method. Results showed that there was no difference ($0.42 < P < 0.90$) in the MyHC-IIb mRNA abundance between the pigs fed Diet 1 and Diet 2, as well as between the pigs fed Diet 3 and Diet 2. These results suggest that changing dietary lysine level to either below or above the adequate requirement level did not affect the abundance of MyHC-IIb mRNA in Longissimus dorsi of finishing pigs. Since our previous study using these pigs showed that the loin eye areas of the pigs fed Diets 2 and 3 were increased by 18 and 9% when compared with Diet 1, respectively, we further hypothesized that the level of dietary lysine has a significant effect on the abundance of MyHC-IIb protein in the Longissimus dorsi of finishing pigs. Therefore, our next study will be conducted to quantify the MyHC-IIb protein in these Longissimus dorsi samples.

Key Words: myosin heavy chain Ilb, lysine, pig

0203 Identification of loci on chromosome 3 associated with susceptibility to bovine paratuberculosis using genotypes imputed to whole genome sequence in Holstein cows.

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Bovine paratuberculosis or Johne's disease (JD) is an infectious disease of ruminants caused by Mycobacterium avium paratuberculosis (Map) infection. JD continues to increase in prevalence in dairy cattle resulting in loss of profitability and increased animal suffering and death. Several studies have been conducted to identify loci associated with susceptibility to JD with the goal of using selection to reduce the prevalence of the disease. One study with 219 Holstein cows identified a locus on chromosome 3 (BTA3) associated with risk of JD. The objective of this study was to test the association with this locus, identify new quantitative trait loci (QTL), and better characterize the QTL regions in a new population of dairy cows using genotypes imputed to whole genome sequence.

Ileo-cecal lymph nodes were removed from 205 Holstein dairy cows from an Idaho abattoir at harvest, were PCR tested for the presence of Map and DNA was extracted and genotyped with the Illumina BovineSNP50 BeadChip. Cows with genotype call rates < 90% were removed, leaving 190 cows of which 70 were positive for Map (cases) and 120 were negative for Map (controls). Whole genome sequence-level genotypes were imputed from run 4 data from the 1000 bull genomes project. Indels and SNPs with MAF < 0.01 were removed leaving 708,788 biallelic SNPs for analysis on BTA3 with Efficient Mixed Model Association expedited (EMMAX) additive and allelic models. Little evidence for population stratification was evident as l = 1.01. The additive model identified 10 QTL that were moderately associated ($p < 5.5x10^{-5}$) with JD on BTA3, and the allelic model identified 21 QTL (20 that were moderately associated with JD, and one QTL strongly associated ($p = 5.13 \times 10^{-7}$), but did not include the previously identified locus on BTA3. The use of imputed genotypes aided in identifying new QTL, more narrowly defining the QTL regions and testing if QTL were replicated in new cattle populations.

Key Words: bovine paratuberculosis, genetics, chromosome 3

0204 Effect of the total Western diet via direct or ancestral exposure on estrous cycling in third-generation offspring in mice. K. Contreras*[1], J. Cuthbert[1], S. Phatak[1], D. Larson[2], and A. Benninghoff[1], *[1]Utah State University, Logan, [2]USTAR Applied Nutrition Research, Logan, UT.*

Obesity is a contributing factor to many diseases, such as cancer and diabetes. Moreover, mounting evidence points to a role for obesity as a risk factor for infertility and other reproductive dysfunctions. In a previous study, mice fed a diet containing 60% of energy from fat experienced abnormal estrous cycles, with significant extended time in the diestrus phase (Brothers et al., 2010 *Cell Metab*. 12(3): 295–305). Animal model studies investigating the contribution of obesity to other adverse health outcomes usually do not account for typical Western dietary patterns with respect to macro- and micronutrient content. Previously, our group developed the Total Western Diet (TWD) for rodents, which models the typical American diet with respect to macro- and micronutrient content on an energy density basis, as opposed to other simple high fat diets traditionally used in pre-clinical studies. The primary objective of this study was to determine the impact the TWD on estrous cycling in mice. Based on prior observations with a very high fat diet, we expected mice fed TWD would have abnormal estrous cycles. C57BL/6J mice were bred for three generations, during which they were fed an optimized diet (AIN93G), TWD or a simple high fat diet (45% fat DIO) in the F_0 only, F_0 through F_3 or the F_3 generation only ($n = 14$ to 17 mice all but one group, which had $n = 6$). Vaginal cell smears were obtained over 10 d from individual F_3 offspring at 23 wk of age. Samples were stained, fixed and then examined via light microscopy to assess estrous stage. The percent time in proestrus, estrus, metestrus and diestrus were calculated for each individual, and data were analyzed using a mixed model analysis of variance with cage as a random nested factor. No significant differences were observed among any of the diet treatment groups for any of the estrous cycle stages ($p > 0.18$). These data disagree with prior observations that a high fat diet prolonged time in diestrus, although the current study used diets with fewer calories from fat (35% for TWD and 45% for DIO) compared with the study by Brothers et al. (2010), which employed a 60% fat diet. As part of the present study, other ongoing work will assess impacts of these test diets on other reproductive parameters, including birth rate, cannibalism rate, weaning weight and biomarkers of oocyte quality.

Key Words: Western diet, estrous cycle, obesity

0205 Maternal over-feeding during gestation alters islet size and number in the pancreas of 135-d-old fetuses. M. C. Wynn*, M. L. Hoffman, S. M. Pillai, A. K. Jones, K. K. McFadden, S. A. Reed, S. A. Zinn, and K. E. Govoni, *Department of Animal Science, University of Connecticut, Storrs.*

Maternal over-feeding during gestation can lead to increased circulating insulin concentrations, increased carcass adiposity and reduced insulin sensitivity in the offspring. However, the mechanisms behind these changes are not well known. We hypothesized that maternal over-feeding during gestation would affect structures of the endocrine and exocrine pancreas of fetuses at d 135 of gestation. For this study, ewes were fed either 100% (control-fed; $n = 6$) or 140% (over-fed; $n = 7$) of NRC requirements for TDN starting at d 30 ± 0.02 of gestation. Ewes were euthanized at d 135 of gestation and the pancreas from each fetus ($n = 11$ fetuses per treatment group) were collected. Fetal body weight as well as pancreas weights were recorded and pancreas tissue was embedded in optimal cutting temperature medium for histological analysis. A total of 8 fetuses from control-fed ewes (CON) and 9 fetuses from over-fed ewes (OVER) were used for histological analysis. Three 5 µm thick sections per fetus were stained with Harris Hematoxylin and Eosin Y. Sections were imaged using a Zeiss Axiovert 200M microscope with 3 to 4 images taken per section. Islet and duct size and number were quantified using ImageJ across 5 and 10 images per fetus, respectively. Data were analyzed using a student's *t* test. An effect of maternal diet was not observed for fetal BW or pancreas weight expressed as a percent of BW at d 135 of gestation ($P \geq 0.71$). In OVER lambs, islet size was 63% greater compared with CON (5404 ± 477 µm and 8836 ± 300 µm for CON and OVER, respectively; $P < 0.01$). There was an 18% decrease in islet number in OVER lambs compared with CON (8.8 ± 0.5 and 7.2 ± 0.4 islets for CON and OVER lambs, respectively; $P =$

0.03). No effects of maternal over-feeding were observed for offspring duct size or number ($P > 0.13$). The observed effect of maternal over-feeding on islet size and number could be due to changes in cell function and differentiation as a result of being exposed to excessive nutrients during gestation. In conclusion, maternal over-feeding during gestation alters the fundamental structural aspects of the endocrine pancreas of the fetus, which may contribute to altered pancreas function during gestation and later in life. Further studies are needed to determine the link between changes in pancreas structure and function later in life.

Key Words: maternal nutrition, pancreas, sheep

0206 Comparison of high definition Zenmuse X3 and X5 video cameras onboard unmanned aerial vehicles for future use in precision ranching.

C. F. Solecki* and J. S. Church, *Thompson Rivers University, Kamloops, BC, Canada.*

The use of unmanned aerial vehicles (UAVs) in agriculture to increase the efficiency of management is a new and rapidly advancing field. Being able to locate and identify cattle with UAVs would enable producers to better utilize spatiotemporal data from range livestock to better manage both livestock herds and range. UAVs provide a method of capturing aerial video observation data of cattle on extensive range that is more flexible, affordable, and safer for the pilot than traditional aircraft. In this study we used common industry cattle ear tags of two sizes (large tags = 7.5 × 5 cm, small tags = 5.5 × 3 cm) of varying colors as well as back tags (23 × 14 cm, used in behavioral studies) to assess the visual acuity of two commercially available aerial high definition cameras. The aim of this project was to assess the capabilities and limitations of these aerial cameras specifically designed for UAV use, with the goal of determining their practical use in the field as tools for observing and identifying cattle. A set of images from each camera was obtained using the DJI Inspire 1 Pro flight platform (Da-Jiang Innovations Science and Technology Co. Ltd., Shenzhen, China). Images were captured at an initial height of 5 m and progressing upward at 5 m intervals to 80 m above ground level (ABL). An onboard GPS module on the UAV was used to monitor and record the height of the aircraft at each interval. Recorded images were then assessed on a computer monitor to determine whether identification of numbering and lettering on the tags was possible. Through qualitative visual assessment of these aerial photographs, it was determined that the capabilities of the Zenmuse X5 were significantly superior than that of the Zenmuse X3 and will therefore be of greater use in future identification of animals using UAVs. We concluded that identification by cattle ear tags using a UAV is likely not a practical application due to the maximum ABL that is required to identify numbering and lettering on tags (15 m using the Zenmuse X5); however, identification of numbering on back tags to identify individual animals was possible up to an ABL of 70 m using the Zenmuse X5 camera.

Key Words: cattle, drone, ear tags

0207 Leucine supplementation increases mouse mammary cell proliferation in vitro.

M. M. McGuckin*, R. Manjarin, and D. G. Peterson, *California Polytechnic State University, San Luis Obispo.*

The objective of this study was to determine if leucine supplementation increases mammary epithelial cell proliferation in vitro, and whether this effect is associated with the upregulation of leucine transporters, cell cycle protein regulators, and leucyl-tRNA synthetase, which mediates leucine-induced activation of the mammalian target of rapamycin complex 1. Growth of HC11 mouse mammary epithelial cells in either control (CON; 0.38 mmol/L leucine) or leucine-supplemented HMEM media (LEU; 1.52 mmol/L leucine) was assessed by the MTT proliferation assay over 6-d, followed by RNA extraction and quantification of gene expression. Transcript abundance of leucine transporter LAT1 (*SLC7A5*), cyclin D (*CCND1*), leucyl-tRNA synthetase (*LARS2*), and reference genes hypoxanthine guanine phosphoribosyl transferase (*HPRT*), RNA polymerase 3 (*POL3*) and ribosomal protein L3 (*RPL3*) was determined using reverse transcription quantitative PCR. Data were analyzed using a linear mixed model procedure of SAS that included the fixed effect of treatment and the random effect of replicate. Compared with CON, proliferation of leucine-treated cells tended to increase at d 5 ($P < 0.1$), and was significantly higher at d 6 ($P < 0.01$). Similarly, expression of genes encoding LAT1 and leucyl-tRNA synthetase was increased ($P < 0.05$) in cells exposed to LEU. Messenger RNA abundance of cyclin D did not differ between treatments. Taken together, these results suggest that leucine supplementation increases the proliferation of mouse mammary epithelial cells in vitro, which may be mediated by the upregulation of LAT1 and leucyl-tRNA synthetase at the gene expression level. These results represent a novel contribution to our understanding of how amino acid nutrition regulates mammary gland growth, and to the critically needed tools for development of mechanistic models of nutrient utilization for improving efficiency of milk production.

Key Words: mammary gland, proliferation, leucine, growth

0208 Effects of maternal nutrition during gestation on placental steroid metabolizing enzyme activity in sheep. K. J. McCarty*[1], M. P. T. Coleson[1], S. M. Pillai[2], M. L. Hoffman[2], A. K. Jones[2], K. E. Govoni[2], S. A. Reed[2], S. A. Zinn[2], and C. O. Lemley[1], [1]*Mississippi State University, Starkville,* [2]*Department of Animal Science, University of Connecticut, Storrs.*

Normal pregnancy in sheep relies heavily on placental secretion of steroids during the last half of gestation. Maternal nutrient restriction or over-nutrition has been shown to increase or decrease peripheral concentrations of steroids, respectively. The objective was to determine the effects of maternal nutrition on placental steroid metabolizing enzyme activity in sheep. Pregnant ewes ($n = 60$) were allocated to receive either 100% [control-fed (CON; $n = 20$)], 60% [restricted-fed (RES; $n = 20$)], or 140% [over-fed (OVER; $n = 20$)] of NRC requirements for TDN beginning at d 30.2 ± 0.2 of gestation. Ewes from each nutritional treatment were slaughtered at d 45 ($n = 20$), 90 ($n = 20$), or 135 ($n = 20$) of gestation. At slaughter the maternal (caruncle) portion of the placenta was collected for enzymatic activity analysis. Activity of cytochrome P450 1A (CYP1A), cytochrome P450 3A (CYP3A), and UDP-glucuronosyltransferase (UGT) were determined using specific luminogenic substrates. Activities were expressed relative to mg of tissue protein. Data were analyzed using MIXED procedure of SAS and the model statement included nutritional treatment, day of gestation, and their respective interaction. Main effects are discussed in the absence of nutritional treatment by gestational day interactions. Activity of CYP1A in the caruncle was not different across gestational d ($P = 0.15$) or nutritional treatment ($P = 0.94$). Similarly, activity of CYP3A in the caruncle was not different across gestational d ($P = 0.29$) or nutritional treatment ($P = 0.98$). Activity of UGT was not different across gestational d ($P = 0.26$). Activity of UGT in the caruncle tended ($P = 0.07$) to be different across nutritional treatment, whereby activity was increased ($P = 0.02$) by 170% in OVER compared with CON ewes. In addition, activity of UGT in the caruncle tended ($P = 0.10$) to be increased by 86% in OVER compared with RES ewes, while activity was not different ($P = 0.50$) between RES and CON ewes. In conclusion, over-fed ewes had an increase in activity of UGT in the caruncle compared with control-fed and restricted-fed ewes. Therefore, the increase in caruncle UGT could be involved in stimulating additional steroid metabolism during gestation, thereby contributing to the decrease in peripheral concentrations observed in over-fed animals.

Key Words: cytochrome P450, maternal nutrition, steroid

0209 Relationship between antioxidants and residual feed intake in grazing heifers. J. N. Kidrick*, E. Felton, K. S. Shaffer, and K. M. Barnes, *West Virginia University, Morgantown.*

Residual feed intake (RFI) has been established to be a more accurate measure of feed efficiency; however, questions remain about the specific factors that contribute to individual variation. It has been determined that heat production from metabolic processes, body composition, and physical activity explain a large proportion of the variation but not 100%. Additionally, because RFI is an expensive trait to measure, identification of an easily measured biomarker of RFI would be beneficial in animal selection. Our current objective was to determine if antioxidant status contributes to variation in RFI. Serum was collected from a group of genetically similar heifers that were maintained on the same diet. During the feeding period, feed intake and body weight were recorded and used in the calculation of ADG and RFI. Serum nitric oxide ($n = 48$), glutathione peroxidase ($n = 34$), and total antioxidant capacity ($n = 34$) were measured using colorimetric assay kits. Nitric oxide levels were estimated using a nitrate/nitrite kit. Serum nitric oxide tended ($P = 0.08$) to be positively ($r = 0.26$) correlated with RFI. Glutathione peroxidase and total antioxidant capacity were not correlated with RFI, but total antioxidant capacity did tend ($P = 0.06$) to be negatively ($r = -0.33$) correlated with ADFI. Our data indicate that total antioxidant status may not be an adequate indicator of RFI. Increased intake may require a greater utilization of antioxidants, thus the reduced levels we observed in high intake heifers. The positive correlation we observed between RFI and nitric oxide could indicate less tissue turnover in the more efficient animals (low RFI). Therefore nitric oxide does show some potential as a biomarker of RFI.

Key Words: antioxidants, residual feed intake, nitric oxide

0210 Effects of spices on in vitro enteric methane production. S. Taylor*, I. M. Ogunade, D. Kim, K. G. Arriola, and A. T. Adesogan, *Department of Animal Sciences, IFAS, University of Florida, Gainesville.*

This experiment was conducted to study the effects of spices (*Rosmarinus officinalis*, RO and *Allium cepa*, OP) on in vitro rumen fermentation, methane production and digestibility of corn silage-based ration. A corn silage-based total mixed ration (TMR; 0.5 g/sample) for dairy cows was treated with each of the spices at doses of 0 (Control), 5 (Low), 10 (Med) and 15% (High) of the TMR or with monensin (1.2 mg/g of TMR). Each mixture was incubated in triplicate in 50 mL of a rumen fluid-buffer inoculum (ratio 1:2) in a 120-mL gas-tight culture bottle at 39°C for 24 h in each of two runs. In vitro DM digestibility (DMD), fermentation parameters, gas

and methane production were measured. Data were analyzed using the GLIMMIX procedure of SAS. The high dose of RO decreased DMD and acetate-propionate ratio relative to the Control, whereas, all doses of OP increased DMD and decreased acetate-propionate ratio relative to Control and monensin treatments. Gas volume (mL/g DM) and methane (mL/g DMD) were reduced ($P < 0.05$) by the High dose of RO and monensin, but not by Low and Med doses, relative to the control. Compared with monensin, adding OP at Low, Med and High doses reduced ($P < 0.05$; mL/g DMD) the gas volume (158 vs. 140, 136 vs. 110) and methane production (13.48 vs. 9.98, 9.46, and 10.38), respectively. Ruminal pH was increased by monensin and reduced by the High dose of OP. In conclusion, the High rate of *Rosmarinus officinalis* reduced methane production but decreased TMR digestibility whereas, all doses of of *Allium cepa* reduced methane production and increased TMR digestibility compared with the control and monensin treatments.

Key Words: methane, monensin, spices

0211 An exploratory observational study to quantify ante- and post-mortem complete blood count variables in fed beef cattle. C. L. Rogers*[1], T. J. McEvers[1], J. T. Richeson[1], S. L. Roberts[2], and T. E. Lawrence[1], [1]*West Texas A&M University, Canyon,* [2]*Department of Agricultural Sciences, West Texas A&M University, Canyon.*

Our objective was to quantify changes in complete blood count (CBC) variables before and after terminal marketing of fed beef cattle. Steers ($n = 39$; BW = 622 ± 6.6 kg) were used to obtain individual blood samples the morning before harvest (0600 h; BASAL), the morning of harvest (0600 h; ANTE), and on exsanguination at a nearby commercial abattoir (1500 h; POST). Blood was collected via jugular venipuncture (BASAL and ANTE) or proprietary method (POST) and analyzed within 4 h using an automated hemocytometer. Repeated measures analysis was used to determine changes in the concentration (K/μL) of total white blood cells (WBC), neutrophils (NEUT), lymphocytes (LYMPH), monocytes (MONO), eosinophils (EOS), basophils (BASO), platelets (PLT), and red blood cells (RBC, M/uL), hemoglobin (HGB, g/dL), and mean corpuscular HGB concentration (MCHC, g/dL). The percentage of NEUT (NP), LYMPH (LP), MONO (MP), EOS (EP), and BASO (BP) relative to WBC was also calculated. Moreover, hematocrit (HCT, %), mean corpuscular volume (MCV, fL), mean corpuscular HGB (MCH, pg), and NEUT to LYMPH ratio (N:L) were determined. No differences were detected ($P \geq 0.10$) among CBC variables between BASAL and ANTE except for MONO, MP, MCV, and MCHC ($P \leq 0.01$). However, marked and frequent alterations in CBC variables were observed between BASAL and POST; increased ($P \leq 0.05$) NEUT (1.94 K/uL), BASO (0.003 K/uL), MCV (2.13 fL), NP (24.21%), and N:L (1.04) were coupled with decreased ($P \leq 0.05$) PLT (175.87 K/uL), LYMPH (2.53 K/uL), WBC (1.12 K/uL), MONO (0.37 K/uL), EOS (0.16 K/uL), MCHC (1.67 g/dL), HGB (0.37 g/dL), MCH (0.15 pg), LP (20.07%), MP (2.94%), and EP (1.24%). Likewise, ANTE to POST resulted in increased ($P \leq 0.04$) values for NEUT (1.72 K/uL), BASO (0.004 K/uL), MCV (1.47 fL), NP (22.78%), BP (0.03%), and N:L (0.98) concomitant with decreased PLT (172.66 k/uL), LYMPH (2.38 K/uL), WBC (1.31 K/uL), MONO (0.49 K/uL), EOS (0.16 K/uL), MCHC (1.10 g/dL), HGB (0.32 g/dL), MCH (0.09 pg), LP (17.63%), MP (4.05%), and EP (1.14%). Few variables differed from BASAL to ANTE, yet NEUT and N:L increased and EOS decreased between ante- and post-mortem collection times. This indicates that terminal marketing is stressful, but further research is needed to delineate the specific stressors such as handling, transportation, lairage time or immobilization, that may be most impactful during terminal marketing.

Key Words: cattle, complete blood count, slaughter

0212 Body fat distribution is a determinant of pulmonary arterial and central venous pressures in feedlot cattle. K. M. Freeman*, A. K. Gulick, B. C. Bernhard, R. J. Rathmann, J. O. Sarturi, and J. M. Neary, *Texas Tech University, Lubbock.*

The objective of this study was to determine if adiposity is associated with mean pulmonary arterial and central venous pressures in feedlot cattle during the finishing phase. These pressures are measures of the severity of pulmonary hypertension and venous congestion due to right heart failure, respectively. Pressures were measured in a cohort of crossbred yearling steers ($n = 23$, initial BW = 364 ± 52 kg) at an altitude of 975m, 6 d before slaughter. Steers were fed for 171 d. Measures of body fat evaluated included 12th rib fat thickness, USDA quality grade, KPH fat percentage, and empty body fat percentage (EBFP). These served as proxies for subcutaneous fat, intramuscular fat, visceral fat, and total body fat, respectively. The EBFP was calculated from hot carcass weight, 12th rib fat thickness, USDA quality grade, and longissimus muscle area. KPH fat was evaluated subjectively by a USDA grader. Mean (± SD) pulmonary arterial and central venous pressure were 54 ± 6 mmHg and 28 ± 5 mmHg, respectively, and were positively associated ($P < 0.01$, $r^2 = 0.26$). Cattle with a KPH fat of 2% ($n = 18$) had mean central venous and pulmonary arterial pressure that were 8 ± 2 mmHg ($P < 0.01$, $r^2 = 0.41$) and 8 ± 3 mmHg ($P < 0.01$, $r^2 = 0.26$) greater than cattle with a KPH fat of 1.5% ($n = 5$), respectively. When controlling for mean pulmonary arterial pressure as a covariate ($P = 0.20$), cattle with KPH fat of 2% had a mean central venous pressure that was 7 ± 2 mmHg greater than a KPH fat of 1.5% ($P = 0.01$, $R^2 = 0.43$). This indicates that KPH fat is deleterious to cardiac function independent of its effect on mean pulmonary arterial pressure. None of the other body fat measures evaluated were associated with either central venous or

pulmonary arterial pressures ($P > 0.40$). These findings are in agreement with the many peer-reviewed studies that have reported visceral adiposity to be a strong risk factor for cardiovascular disease in humans. Increasing visceral adiposity may, in part, explain why mean pulmonary arterial and central venous pressures increase in cattle through the feeding period.

Key Words: heart failure, adiposity, visceral, steer

0213 The effects of lavender oil on stalled horses subjected to a stressor. S. R. Adkins*, A. I. Apel, K. D. Vogel, and D. N. Smarsh, *University of Wisconsin, River Falls.*

The use of alternative medicine, such as aromatherapy, has increased in recent years within the equine industry. Lavender oil is commonly thought to have a calming effect, however, there is limited data in horses to confirm these claims. In addition, there are questions regarding the efficacy of such products. Therefore, the two objectives of this research were to conduct a basic chemical analysis of lavender essential oil products, and to assess the potential anti-anxiety effects of lavender essential oil on stalled horses subjected to a stressor. In the first part of this study, gas chromatography analysis was performed on lavender oil products from two companies looking at linalool concentrations. Both oils were of the *Lavendual augstifolia* species, and results were then compared with standards set by the International Standards Organization and published third-party tests. In the second part of this study, 18 horses (12 Quarter Horse geldings and 6 Thoroughbred geldings, aged 10 ± 5 yr) were organized into a Latin Square design with each horse acting as its own control. Horses were individually stalled for a total of 2 h, during which heart rate (HR) and salivary samples were collected at 10, 30, 50, 60, 80, 90, 100, and 110 min. The treatment group was administered lavender oil by aromatic application for 15 min at 40 min and 95 min. The control group did not have an application of lavender oil. The stressor used was a sound recording of sirens played for 10 min. Salivary cortisol and HRs were later analyzed. Gas chromatography results confirmed that both lavender oil products tested did contain linalool. There was an overall effect of time ($p < 0.0001$) on HR, with HR lower at 10, 30, and 50 min as compared with 60 min ($p < 0.0001$), and higher at 80, 90, 100, and 110 min as compared with 60 min ($p < 0.0017$). There was an overall effect of treatment on salivary cortisol ($p = 0.04$), and a trend for an overall effect of treatment on HR ($p = 0.0518$). While the stressor did increase HR, the application of lavender oil did not have a direct effect on HR or cortisol at any specific time point. Further research is needed to identify an effective dose of lavender oil via aromatic application as a means of reducing stress in horses.

Key Words: horse, lavender, anti-anxiety

0214 FSH dependent and IGF-1 independent phosphorylation of β-catenin is similar in bovine and human granulosa cells. C. R. Smith*[1], B. H. Aloqaily[2], C. A. Gifford[3], B. I. Gomez[2], and J. A. Hernandez Gifford[2], *[1]Oklahoma State University, Stillwater, [2]Oklahoma State University, Stillwater, [3]Department of Animal Science, Oklahoma State University, Stillwater.*

Estradiol is a steroid hormone and is required for female fertility. Ovarian granulosa cells (GC) are the major source of estradiol, and synthesis of estradiol relies on the pituitary gonadotropin FSH and local ovarian signaling molecule, insulin-like growth factor 1 (IGF-1). In GC, FSH signals primarily through protein kinase A (PKA), which contributes to β-catenin phosphorylation at Ser^{675} and Ser^{552}. Beta-catenin is a co-transcriptional protein required for the maximal aromatase gene expression and subsequent estradiol production. Ovarian derived IGF-1 signals primarily through protein kinase B (AKT) to regulate steroidogenesis. The objective of the current study was to identify which one of these kinases is responsible for β-catenin activation, and if the phosphorylation has a species specific pattern. Bovine GC and human GC line (KGN) were cultured and treated with IGF-1 (50 ng/mL), FSH (100 ng/mL), or the FSH agonist Forskolin (FSK) (10 μM) for 24 h. At the termination of the treatment period, cells were collected for protein quantification of total and phosphorylated β-catenin abundance via Western blot analysis and protein abundancies were analyzed using densitometry software and the values were analyzed using GLM procedure of SAS. In bovine GC total β-catenin protein increased with FSH, IGF-1, and FSH+IGF-1 ($n = 3$; $P < 0.1$) treatments compared with control. Similarly, in KGN cells FSK increased total β-catenin abundance. However, IGF-1 did not stimulate β-catenin abundance when compared with control. These species differences may be due to a downregulated IGF-1 receptor in the KGN cell line. Phosphorylation of β-catenin Ser^{675} did not differ among treatment groups regardless of cell types. In contrast, phosphorylated Ser^{552} on β-catenin was dramatically increased by FSH or co-treatment of FSH+IGF-1 ($n = 3$; $P < 0.1$), and by FSK and FSK+IGF-1 ($n = 3$; $P < 0.001$) in bovine and KGN cells, respectively. These results suggest that activation β-catenin via phosphorylation at Ser^{552} affected by FSH but not IGF-1 signaling. Follicle stimulating hormone signaling induces β-catenin phosphorylation in cattle and human, indicating that phosphorylated β-catenin is essential in estradiol production regardless of species.

Key Words: β-catenin, FSH, IGF-1

0215 Receptor (chemosensory) transporter protein-4 expression and regulation in bovine granulosa cells. C. N. Horsley[*1], B. H. Aloqaily[1], J. A. Hernandez Gifford[1], and C. A. Gifford[2], *[1]Oklahoma State University, Stillwater, [2]Department of Animal Science, Oklahoma State University, Stillwater.*

In the ovary, the female egg is developed within a follicle, and a follicle is composed of thecal and granulosa cells (GC). These two cell types coordinate development of the oocyte and well as synthesize the steroid hormones progesterone and estrogen. Both FSH and insulin-like growth factor-1 (IGF-1) are known to regulate follicle development and drive steroid hormone production. Receptor (chemosensory) transporter protein-4 (RTP4) belongs to a gene family whose function is to transport G protein coupled receptors. Work in our laboratory suggests that the message for *RTP4* is found in GCs, but the function(s) and regulation of RTP4 is unclear. The objective of current study was to evaluate the effect of FSH and IGF-1 on expression of RTP4 in bovine GC and determine RTP4 localization in bovine ovaries. A rabbit was immunized using 18 AA in an antigenic region of the amino terminus of RTP4. Rabbit serum was collected pre-immunization and at sacrifice (immune serum). Cross-sections from 3 bovine ovaries were incubated with pre-immunized serum and immune serum (1:600) and were developed using biotinylated anti-rabbit IgG for visualization. Primary bovine granulosa cells (n = 3/treatment) were treated with vehicle control, FSH (100 ng/mL; 24 h), IGF-1 (50 ng/mL; 24 h), Forskolin (10 μ M; 24 h) and a combination of the treatments for 24 h and protein lysates collected. Fifty μg of protein was separated by SDS-PAGE. Pre-immunized and immune serum was incubated on separate blots and detected using biotinylated anti-rabbit IgG and horseradish peroxidase development, protein abundancies were analyzed using densitometry software and the values were analyzed using GLM procedure of SAS. Pre-immunized serum displayed no signal in ovarian cross-sections while immunized serum exhibited a robust signal that was ubiquitously expressed in the ovary. Western blot analysis revealed a unique band in immunized serum that showed greater expression ($P < 0.05$) in IGF-1-treated samples compared with controls or FSH-treated samples. However, the unique band was observed at unexpected size; thus, further experiments are necessary to elucidate the size of RTP4 in ovarian tissue. These data suggest that RTP4 is present in the ovary and is regulated by IGF-1 indicating that RTP4 may play a role in steroidogenesis or follicular development.

Key Words: ovary, RTP4, steroidogenesis

0216 Protein expression and localization of receptor (chemosensory) transporter protein 4 in the endometrium during early pregnancy in sheep and cattle. K. S. Wilson[*1], J. A. Hernandez Gifford[1], T. L. Ott[2], and C. A. Gifford[3], *[1]Oklahoma State University, Stillwater, [2]Department of Animal Science, Pennsylvania State University, University Park, [3]Department of Animal Science, Oklahoma State University, Stillwater.*

Reproduction in domestic ruminants continues to challenge efficiency in livestock operations. During early pregnancy, the conceptus produces a unique type I interferon, interferon-tau (IFNT), which acts both locally and systemically to regulate IFN-stimulated genes (ISG) in the maternal uterus and circulating immune cells. Previous work demonstrated that mRNA levels for receptor (chemosensory) transporter protein-4 (*RTP4*) was regulated by pregnancy in peripheral immune cells, the endometrium, and corpus luteum. Receptor transporter protein-4 belongs to a class of G protein coupled receptor transporters, but the function(s) of RTP4 in reproduction remains unclear. Though, mRNA levels for RTP4 are spatially and temporally regulated during early pregnancy in ruminants, there is no information regarding RTP4 protein expression. The objective of the current experiment was to evaluate RTP4 protein expression and localization in the endometrium during early pregnancy in cattle and sheep. A rabbit was immunized using 18 AA in an antigenic region of the amino terminus of RTP4. Rabbit serum was collected pre-immunization and at sacrifice (immune serum). Cross-sections of a D15 pregnant ewe were incubated with pre-immune serum and immune serum (1:600 primary antibody concentration), and protein presence was detected after incubation with biotinylated anti-rabbit IgG and horseradish peroxidase development. No signal was detected for pre-immunized serum, while immune serum exhibited a robust signal in the luminal and glandular epithelium and in the stromal compartments. In the second experiment, cross-sections from D17 pregnant and cyclic Holstein heifers were utilized for immunofluorescence detection of RTP4 protein. Pre-immune serum showed no fluorescence, but immune serum exhibited strong fluorescence in the luminal epithelium, glandular epithelium, and stroma during pregnancy. Interestingly, previous work using in situ hybridization did not detect a presence of *RTP4* mRNA in the luminal epithelium, but the RTP4 protein was clearly expressed in the luminal epithelium in the current experiment. These results demonstrate that RTP4 protein is expressed in the uterus and is regulated by pregnancy. Because RTP4 protein is both expressed in maternal tissues and regulated by pregnancy, it seems likely that RTP4 plays a role in establishment of pregnancy in domestic ruminants.

Key Words: uterus, interferon-tau, RTP4

0217 Follicle-stimulating hormone regulation of proenkephalin in granulosa cells. A. D. Gullic*[1], B. I. Gomez[1], B. Couger[1], C. A. Gifford[2], and J. A. Hernandez Gifford[1], [1]*Oklahoma State University, Stillwater,* [2]*Department of Animal Science, Oklahoma State University, Stillwater.*

Estradiol biosynthesis by ovarian granulosa cells (GC) is crucial for normal female reproductive function and is mediated primarily by FSH. Binding of FSH elicits a multitude of signaling cascades to enhance or inhibit the expression of target genes to regulate estradiol production. The objective of the current experiment was to utilize global expression analysis to identify genes significantly regulated by FSH. Primary rat GC were cultured in the presence or absence of FSH (100 ng/mL) for 24 h and gene expression was analyzed via microarray. Of the 1104 FSH-regulated genes, the opioid precursor proenkephalin *(Penk)* was downregulated ($P < 0.001$) with FSH treatment. Endogenous opioid peptides originate from three protein precursors Penk, proopiomelanocortin (Pomc), and prodynorphin (Pdyn). Stimulation of the μ, δ, and κ opioid receptors in GC downregulate basal estradiol concentrations in cultured GC. Therefore, we hypothesized that Penk blocks FSH-induced estradiol production. Real-time PCR was used to confirm *Penk* regulation in response to FSH treatment. Rat GC were treated with and without FSH for 24 h ($n = 3$) for quantification of *Penk*. Relative fold change values were evaluated using the GLM procedure of SAS and means were separated using the PDIFF function when the model was significant. In agreement with microarray data, FSH downregulated *Penk* 12.81-fold ($P < 0.01$) when compared with control. To determine if the opioid pathway disrupts FSH target genes, KGNGC, a human granulosa tumor cell line, were pre-treated with vehicle or β-endorphin (100 nM), a ligand for the μ opioid receptor, for 5 h followed by treatment with or without 5 μM forskolin (FSK) for 24 h ($n = 3$). Steady state mRNA levels for aromatase (*Cyp19a1)* were quantified via real-time PCR. As expected, FSK increased ($P < 0.01$) *Cyp19a1* 33.5-fold compared with vehicle control whereas treatment with β-endorphin was similar to controls ($P = 0.97$). Co-stimulation of KGN GC with β-endorphin and FSK did not decrease *Cyp19a1* ($P < 0.01$). Results from these experiments indicate that FSH regulates opioid peptides in granulosa cells and work in the literature suggests that opioids regulate steroidogenesis. In the current experiment, stimulation of the μ receptor and subsequent opioid signaling pathway did not inhibit the ability of FSK to increase *Cyp19a1* indicating that opioid regulation of steroidogenesis could be through mechanisms other than disruption of the cAMP signaling pathway or through other opioid receptors.

Key Words: FSH, opioid, aromatase

0218 Optimization of probes and PCR conditions for the correlation between 4 genes and production of high citrate in milk. V. A. Smith*[1], R. Manjarin[1], and R. Jimenez-Flores[2], [1]*California Polytechnic State University, San Luis Obispo,* [2]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

We have previously demonstrated the existence of 4 gene products associated to key metabolic pathways that are necessary for the production of citrate in milk, namely isocitrate dehydrogenase 1 (*IDH1*), pyruvate dehydrogenase β (*PDHB*), pyruvate kinase (*PKM2*), and solute carrier family 25 member 1 (*SLC25A1*). Following sequencing of genome of a small sample of cows in the Cal Poly herd, it was shown several single nucleotides (SNP) within these genes that were significantly associated with increased milk citrate content, and therefore that could be potentially selected on to influence the outcome of citrate in milk. We now aimed to design primers for identifying the SNPs in the various genes involved in citrate production, and to optimize the conditions for PCR amplification. Primers for *IDH1*, *PDHB*, *PKM2* and *SLC25A1* were designed based on publicly available bovine cDNA and on expressed sequence tag (EST) sequences deposited in the National Center for Biotechnology database using Primer Express software with default settings. Primer pairs were optimized for concentration using a primer optimization matrix and a relative standard curve was used to determine the efficiency. The standard curve was constructed using cDNA synthesized from a RNA pool made of all samples using the following amounts of cDNA (in duplicate): 40 ng, 4 ng, 0.4 ng, 0.04 ng and 0.004 ng. Specific hybridization of the primers was validated by agarose gel electrophoresis of the PCR products. Non-template controls were included to validate that primers were not amplifying contaminating DNA. Our work demonstrates that each set of primers has singular characteristics that deeply influence the efficiency of PCR conditions. We have also developed accurate PCR conditions for the 4 genes of interest. These results are fundamental for our future studies where SNPs identification will be correlated with citrate levels in milk.

Key Words: milk, citrate, SNPs

ASAS/ASN JOINT SYMPOSIUM: GUT MICROBIOTA, DIET AND HEALTH

0219 Modulation of the gut microbiota: An ecological perspective. J. Walter*, *University of Alberta, Edmonton, Canada.*

Diverse strategies have been used for several decades to improve human and animal health through the modulation of

the gut microbiota, spanning from the administration of defined probiotic strains (or Live Biotherapeutics), whole microbial consortia (e.g., fecal bacteriotherapy), to the provision of bacterial growth substrates (prebiotics and dietary fiber). However, we still lack a conceptual understanding on how the gut microbiota can be modulated. In this presentation I will summarize how ecological theory can provide a framework by which to understand characteristics of the human gut microbiota and the impact of microbiome-modulating strategies. I will present some of our own studies that investigated basic ecological questions regarding how the temporal, spatial, and global patterns of the human microbiome, the factors that shape these patterns, and the ecological constraints within the human microbiome can be manipulated by diet and probiotics. The methodological toolset that is now available (e.g., through next-generation sequencing) provides an unprecedented opportunity to obtain phylogenetic, compositional, and functional information of microbial communities. When analyzed in the light of ecological theory, this has the potential to elucidate the factors and ecological processes that determine and potentially predict the response of the gut microbiota to therapeutic modulations.

Key Words: gut microbiota, probiotic, ecological theory

0220 Effects of early antibiotic exposure on host metabolism. L. M. Cox*, *Harvard Medical School and Brigham and Women's Hospital, Boston, MA; New York University Langone Medical Center, New York.*

The intestinal microbiota, consisting of trillions of bacterial, viral, and fungal cells, can influence growth and development. From infancy through early childhood, the microbial community develops with a succession of key organisms that likely have important roles in shaping metabolic health. Disrupting these ancient patterns of microbe-host maturation may have lasting metabolic consequences. Low-dose antibiotics, especially administered during infancy, can increase weight gain and feed efficiency in a wide variety of host species. To identify key members of the microbiota that may participate, we administered low-dose penicillin (LDP) to mice, measured changes in body composition, and characterized changes in the microbiota by high-throughput sequencing. We found that LDP administered only during the first 4 wk of life increased fat mass later in adulthood, despite the fact that the microbiota recovered, indicating microbiota interactions in infancy may be critical determinants of long-term host metabolic effects. In addition, LDP enhanced the effect of high-fat diet induced obesity. The growth promotion phenotype was transferrable to germ-free hosts by LDP-selected microbiota, showing that the altered microbiota, not antibiotics per se, play a causal role. Four different bacteria were consistently suppressed during infancy in multiple independent experiments, suggesting that they may have beneficial roles in metabolic development. These studies characterize important variables in early-life microbe-host metabolic interaction and identify several bacteria consistently linked with metabolic alterations.

Key Words: antibiotics, microbiome, weight gain

0221 Impact of gut microbiota on brain and behavior. J. F. Cryan*, *University College Cork, Ireland.*

The concept of the gut influencing brain and behavior has existed for almost two centuries. However, a new player has emerged in the past decade: the gut microbiota, which is now seen as a key regulator of the gut-brain axis. The gut is home to a diverse array of trillions of microbes which significantly to outnumber human cells. Advances in sequencing technologies show that the microbiota influences almost all aspects of human biology. Bacterial colonization of the gut plays a major role in postnatal development and maturation of key systems that have the capacity to influence central nervous system (CNS) programming and signaling, including the immune and endocrine systems. Individually, these systems have been implicated in the neuropathology of many CNS disorders and collectively they form an important bidirectional pathway of communication between the microbiota and the brain in health and disease. Evidence of a crucial role for the microbiota in regulating stress-related changes in physiology, behavior, and brain function has emerged mostly from animal studies. Mice that grow up devoid of a microbiome (in a germ-free environment) have an exaggerated hypothalamic-pituitary axis response to stress and altered anxiety-related behaviors. Converse findings have shown that stress (either early in life or in adulthood) changes microbiota composition. Moreover, the concept that bacteria were required for normal brain development has emerged and that the microbiota is regulates many key processes in the adult brain, such as neurogenesis, blood brain barrier function and microglia activation. Thus, the ability to target the brain via the microbiome is viewed as a paradigm shift in neuroscience and psychiatry and has led to the concept of psychobiotics (bacteria with positive effects on mental health) being put forward. Moreover, microbiota is essential for both social cognition and visceral pain. Finally, there are critical time-windows early in life when the effects of microbiota on brain and behavior appear to be more potent. Our data also demonstrates that these effects may be mediated via the vagus nerve, spinal cord, or neuroendocrine systems. Such data offer the enticing proposition that specific modulation of the enteric microbiota by dietary means may be a useful "psychobiotic"-based strategy for brain disorders.

Key Words: stress, neurodevelopment, probiotic

0222 The human milk microbiome and oligosaccharides: What's normal and so what? M. K. McGuire*[1] and M. A. McGuire[2], [1]*Washington State University, Pullman,* [2]*University of Idaho, Moscow.*

Human milk is inarguably the only food "designed" to be consumed exclusively by humans, providing all the essential nutrients (and other bioactive compounds and constituents) needed for growth and development of the human infant. As such, understanding human milk composition and variation therein is critical to optimizing human health during this vulnerable time, particularly in the most at-risk infants. More complete characterization of human milk composition may also lend important insight as to what constitutes optimal nutrition in other phases of the lifecycle, not only for the human host but also for the myriad commensal, mutualistic, and sometimes pathologic microbes with which we coexist. However, our understanding of human milk composition and its impact on host and microbial health is far from complete. For instance, until recent advances in instrumentation allowing the detection and identification of difficult-to-culture bacteria, common dogma was that human milk was sterile unless produced by an infected mammary gland or contaminated after expression. As such, focus on the roles played by complex (an indigestible) human milk oligosaccharides (HMO) has been directed exclusively toward those related to the recipient infant and his/her gastrointestinal microbiota- roles that are without a doubt important for infant health. We now know that human milk contains a diverse population of bacteria. As such, we and others postulate that HMO may impact the microbial communities present in milk and the mammary gland producing it. Here we will briefly describe what is currently known about variation in the human milk microbiome and HMO as well as relationships among maternal diet, milk composition (including microbes and HMO), and the infant gastrointestinal microbiome. In addition, we will introduce an ongoing cross-cutting study funded by the Integrated National Science Foundation Support Promoting Interdisciplinary Research and Education (INSPIRE) mechanism designed to help us better understand what is normal in terms of milk microbes, HMO, and infant fecal microbiome in various locations worldwide. The importance of cooperation and interdisciplinary discussion around methods and vocabulary will be discussed, as will some of the challenges faced in terms of sample collection, storage, transport, and data analysis. Finally, selected preliminary data from the INSPIRE study and a framework for considerations for future studies designed to use big (and interdisciplinary) data to understand variation in global milk composition and how this is related to infant health will be presented.

Key Words: human milk, microbiome, oligosaccharides, HMO, health, development

0223 Dietary fiber and starch, digestive physiology, and metabolic health. R. T. Zijlstra*, J. M. Fouhse, T. Vasanthan, and M. G. Gänzle, *Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

In monogastric nutrition, analyses of fiber and starch have focused on assessing quantity. However, both have a wide range of functional properties. Fibers ranging from low to high viscous affect digesta flow and from slowly to rapidly fermentable alter production of volatile fatty acid (VFA) serving as energy for the gut or the whole body. Likewise, starches ranging from low to high amylose change from rapidly digestible in the upper gut to poorly digestible but fermentable in the lower gut, thereby changing from glucose source into VFA source. Poorly digestible or resistant starch thus basically acts as dietary fiber. Functionality of these carbohydrates for nutrition or health was studied in lab and pig models. Our hypothesis is that total extent, kinetics, and site of digestion or fermentation of starch and fiber are important for whole body energy utilization and gut health. To elucidate their effects, we developed in vitro, lab-based methodologies to describe kinetics of digestion and fermentation and linked these with in vivo models including: (1) ileal cannulation to collect digesta, (2) portal-vein catheterization to sequentially sample blood, (3) slaughter method to collect site-specific intestine tissue and digesta, and (4) indirect calorimetry. Using these models, kinetics of absorption of glucose was associated with insulin and incretin release into the portal vein, intestinal microbiota, and gene expression in intestinal tissue and microbiota. These studies confirmed that slowly digestible starch is partially degraded in the large intestine and fermented into VFA including butyrate (10-fold increase in net portal appearance), reducing insulin responses by 60% and reducing whole body energy utilization. Starch entering the distal intestine altered mRNA abundance of nutrient transporters, increased portal release of the incretin glucagon-like peptide-1 (GLP-1), and was bifidogenic in the large intestine. Extreme viscous purified fiber dampened glycemic responses and reduced digesta passage rate by 50%, thereby increasing small intestine digestion of dietary nutrients, whereas increased fiber in feed grains reduced nutrient digestibility. Fermentable fiber increased butyrate and insulin production. In whole grains with ranging content of amylose and fermentable fiber, effects of similar direction but less extreme were observed. In summary, fiber and starch characteristics influence digestive physiology and thereby gut health, metabolic health, and whole body nutrient utilization. Functional characteristics of fiber and starch should also be considered is diet formulation.

Key Words: digestive physiology, fiber, starch

0224 Methane matters: From blue tinged moos, to boozy roos, and for the health of humans too.

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Methane production is a typical occurrence within the digestive tracts of warm blooded animals, including humans. Methanogens and methane emissions however, means something different to each host. Methane emissions from ruminant livestock has been a major focus of research over the last decade because of the attribution of ~10–20% of the annual anthropogenic methane output to these animals. This has led in part to methane emission measurements for a broad range of animal species and breeds, including Australia's native herbivores, to identify "low emitters"; and resulted in comparative studies to define how the gut microbiota in these animals might account for the differences. The presence of methanogens within the human gut has long been recognized via a combination of breath methane measurements and microbiota surveys, and linked to a range of functional gastrointestinal disorders and non-communicable diseases. Historically much of the focus has been directed to the numerically most predominant species, principally assigned to the genus *Methanobrevibacter,* which are canonically involved with the conversion of gaseous substrates (CO_2 and H_2) arising from bacterial fermentation. However, recent studies by our group and others have revealed that, perhaps, the heterotrophic methanogens (i.e., those capable of using small organic molecules such as alcohols and methylated amines) warrant closer attention if "methane matters" in animals and man are to better managed. Here, we provide a brief overview of recent research on these heterotrophic archaea, with a specific focus on the genus *Methanosphaera,* which so far has been found only in the gastrointestinal tracts of animals, by using specific examples of our own and others recently published research with livestock, Australian macropodids (kangaroos and wallabies) and human clinical and nutritional studies. We propose this specific guild of methanogenic archaea not only warrants further attention, but provides new opportunities for the better management of the "animal-methane" axis.

Key Words: methane and methanogens, gut function, human health and animal productivity

0225 Sub-acute ruminal acidosis (SARA): A tale of two microbiomes.

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Most mechanistic studies of sub-acute ruminal acidosis (SARA) in cattle involve the experimental induction of SARA by dietary starch or legume. Our aim was to determine how these observations relate to on-farm conditions in northeastern Scotland. In six beef farms, management practices, feed composition/particle size and animal activity using motion sensor collars were monitored using 20 animals per farm. At slaughter, rumen wall condition was assessed under four categories: color, papillae integrity, papillae shape, and post-washing blackness. Ruminal fluid and cecum contents were collected for VFA and soluble lipopolysaccharide (LPS) analysis, and also for microbial community analysis. Eighty-six ss rRNA amplicon libraries were generated by PCR, which were subsequently sequenced in equimolar concentrations using Illumina MiSeq.

Close examination of the feed indicated that the process of mixing grain with forage was critical. Rumen wall damage did not appear to be correlated with the particle size of the total mixed ration, but rather with the dustiness of the barley component of the feed. Motion sensor data showed that the rate of change of movement appeared to be correlated with the condition of the rumen wall across farms. Ruminal LPS concentrations were significantly different ($P < 0.001$) between farms, and caecal LPS concentrations were significantly higher (up to 27-fold) than corresponding ruminal LPS concentrations, and exhibited a stronger relationship with the rumen damage scores. We therefore postulate that the hindgut has a greater effect on ruminal health than previously thought.

Microbial community and subsequent PCA analysis revealed significant ($P < 0.001$) clustering of ruminal fluid and caecal content communities. Within each sample type, there was also significant clustering by farm; however, the clustering was weaker when grouped by damage score. Bacteroidetes, Firmicutes and Proteobacteria were the predominant phyla in the ruminal digesta. In the caecal content, Proteobacteria were barely detected and comprised mainly the Moraxellaceae family (known pathogens, "pink eye" in cattle). This was surprising as LPS from Enterobacteriaceae has been implicated with SARA. It is possible that growth of Proteobacteria is not supported in the cecum and the bacteria therefore lyse, causing the high LPS concentrations. In conclusion, the particle size of the barley component of the feed appears to have a relationship with SARA related pathology. Further-

more, this study has highlighted the role of the hindgut in the pathology of SARA, which warrants further investigation.

Key Words: cecum, rumen, sub-acute ruminal acidosis (SARA)

0226 Dietary manipulation of canine and feline gut microbiome. K. S. Swanson*, *Department of Animal Sciences, University of Illinois, Urbana.*

Dogs and cats evolved as Carnivora and have traditionally relied on high-protein, high-fat diets containing relatively low fiber concentrations. Despite having a simple gastrointestinal tract designed to digest such diets, a rich microbial community exists. Today's pet dogs and cats live in close proximity to humans and have similar environmental exposures, serving as potential vectors for pathogen exposure. Dogs and cats are also afflicted by many of the complex diseases present in humans, including obesity, diabetes, inflammatory bowel diseases, and cancers, all of which may be influenced by diet and the gut microbiota. Given their proximity to humans, similar disease incidence and etiology, and unique metabolism, microbiome research in dogs and cats may not only lead to improved pet nutrition and veterinary care, but may increase our understanding of host-microbe interactions, with relevance to human metabolism and diseases and public health at large. Molecular techniques, including high-throughput sequencing, have dramatically changed the research landscape in regards to gastrointestinal microbiology. These techniques have been used to characterize the phylogeny and functional capacity of the canine and feline gastrointestinal microbiota and identify the effects of diet, age, and disease on these communities. Several hundred bacterial phylotypes, predominated by members of Firmicutes, Fusobacteria, Proteobacteria, Bacteroidetes, and Actinobacteria, are now known to inhabit the dog and cat gastrointestinal tract. Recent studies have revealed that the functional capacity of the gastrointestinal microbiota in dogs and cats is quite broad and similar to that of humans and rodent models. Although these populations are quite stable over time, our laboratory has demonstrated that macronutrient profile (e.g., dietary protein:carbohydrate ratio), dietary fiber amount and type, and the form of food consumed (e.g., raw vs. extruded diets) may have dramatic effects on the gastrointestinal microbiome of these host species. These dietary changes have not only been reported to impact microbial diversity and richness, gene content, and metabolic activity, but to alter host physiology and metabolism as well. Unfortunately, the majority of research has been performed in healthy animals housed in research colonies rather than free-living pets. Continued research on the composition and activity of the canine and feline gastrointestinal microbiomes, and how they are impacted by dietary intervention and other environmental exposures, is needed to increase our understanding of the host-microbe interactions that occur in the gastrointestinal health and their relevance to health and disease.

Key Words: canine nutrition, feline nutrition, gut microbiota

BEEF SPECIES I

0227 Relationship between forage quality parameters and mineral intake in grazing beef cattle. J. D. Rivera*, M. L. Gipson, and R. G. Gipson, *Mississippi State Univ. South Branch Exp. Sta., Poplarville.*

One hundred ninety-two forage samples were collected over a 2-yr winter grazing season from cool-season pastures grazed by beef cattle (avg. BW = 294 kg) to determine the effects of periodicity and forage quality on mineral intake. Beef cattle minerals were offered to each pasture (n = 24 pastures) every 28 d from December through June. Refusals were weighed at the end of each interval, and forage samples were collected at the same time. Mineral refusals were used in conjunction with offered mineral to calculate mineral DMI. Forage samples were weighed and dried for 72 h at 50°C to determine DM; dried samples were analyzed using NIR technology to determine ADF and CP content. Data were analyzed to determine correlation (PROC CORR) of periodicity, CP, ADF, DM and mineral intake. As expected, as the season progressed, sampling period was highly correlated to forage quality ($P <$ 0.01) with decreasing CP ($r^2 = -0.92$), increasing ADF ($r^2 =$ 0.96) and DM ($r^2 = 0.80$) associated with periods later in the grazing season. No effect ($P = 0.25$) of sampling period was observed for DMI of mineral. Average mineral intake through the grazing season was 81.6 g ± 1.7 g. Crude protein averaged 18.7% ± 8.4%; ADF averaged 31.3% ± 11.7%. Crude protein had no effect on mineral intake ($P = 0.34$). Acid detergent fiber tended to negatively correlate ($P < 0.06$; $r^2 = -0.14$) with mineral DMI; greater mineral DMI was associated with lower ADF. Forage DM had a negative impact on mineral DMI ($P = 0.001$; $r^2 = -0.38$); with greater forage DM associated with lower mineral DMI. Results suggest that mineral intake of beef cattle grazing cool-season forages is not affected by forage quality (ADF, CP), nor sampling period, but rather more likely affected by forage DM content.

Key Words: beef cattle grazing mineral intake

0228 Feeding antibodies against interleukin-10 improved gain efficiency in beef steers. M. R. Schaefer*, M. E. Cook, D. M. Schaefer, *University of Wisconsin, Madison.*

Recent studies showed that oral anti-interleukin-10 antibody (aIL-10) is protective against gastrointestinal pathogens. The current objective was to evaluate oral aIL-10

Table 0229.

Table 1. Intakes (mean ± SD) for steers based on various marker predictions.

		LIPE®[2]			Cr_2O_3				
	LRNS[1]	iDM	iNDF	iADF	iDM	iNDF	iADF	C31:C32	C33:C32
Pasture DMI (kg/d)	7.10 ± 1.57	3.96 ± 1.33	5.42 ± 1.08	9.19 ± 1.48	5.36 ± 1.90	7.09 ± 2.05	11.81 ± 3.04	11.62 ± 5.30	14.93 ± 7.17
Total DMI (kg/d)	8.69 ± 0.75	5.55 ± 0.56	7.01 ± 0.75	10.79 ± 1.20	6.95 ± 1.45	8.69 ± 1.87	13.40 ± 2.88	12.86 ± 6.06	15.59 ± 7.96

[1]LRNS=Large Ruminant Nutrition System

[2]LIPE®= purified lignin product, iDM=indigestible dry matter, iNDF=indigestible neutral detergent fiber, iADF=indigestible acid detergent fiber

administration on top of best management practices in newly arrived weaned steers. Laying hens immunized with peptide VMPQAENG-conjugate with Freund's adjuvant (aIL-10 hens) or only Freund's adjuvant (control hens) were used to produce eggs containing aIL-10 and Control antibodies. One hundred thirteen black hided steers (initial BW 297 ± 7 kg) were purchased from a local auction barn (160 km) via 14 lot purchases, and allowed to rest for 4 d before starting the trial. Steers were blocked by initial BW and allotted to 18 pens (6 or 7 steers/pen). Pens (9/treatment) were randomly assigned to either Control antibody (42 g · hd^{-1} · d^{-1} whole liquid egg from control hens) or aIL-10 antibody (42 g · hd^{-1} · d^{-1} whole liquid egg providing 500 µg aIL-10 antibody) mixed in a common diet (70.0% corn silage, 15.9% cracked corn, 5.8% DDGS, 5% wheat midds, and 3.3% supplement, DM basis) for the initial 14 d of the trial. No additional eggs were fed for the remainder of the 64 d trial. Antibiotics were administered to treat bovine respiratory disease based on visual observations and whether rectal temperatures exceeded 39.7°C. Data were analyzed as a randomized complete block design using the PROC MIXED procedure of SAS, with pen as the experimental unit. Average DMI was similar between treatments (8.1 kg, $P = 0.84$), however G:F was greater for steers fed aIL-10 vs. Control (0.193 vs. 0.182, $P = 0.04$) over the 64 d trial. Average daily gain over 64 d was 1.58 and 1.48 kg/d for aIL-10 and Control groups, respectively ($P = 0.13$). Frequency of steers requiring a single antibiotic treatment was similar between treatments (16%, $P = 0.97$), but a greater percentage of steers fed the Control eggs required a second antibiotic treatment relative to steers fed the aIL-10 (7 vs. 0%, $P = 0.09$). Total antibiotic treatments per animal were statistically similar between treatments ($P = 0.15$), but was numerically lower for the aIL-10 vs. Control group (0.16 vs. 0.35, SEM = 0.08, respectively). Feeding aIL-10 increased G:F in newly received feedlot steers possibly by improving cattle health immediately after commingling.

Key Words: interleukin-10, respiratory disease, feedlot cattle

0229 Animal and digestibility marker variation influence predictions of dry matter intake and dry matter digestibility. K. A. Weld*[1], J. R. R. Dorea[1], F. A. P. Santos[2], and D. E. Oliveira[3], *[1]University of Wisconsin, Madison, [2]University of São Paulo, Piracicaba, Brazil, [3]Santa Catarina State University, Lages, Brazil.*

The current literature shows that there is animal and marker variability in digestibility marker recovery, but does not address the effect of this variability on individual animal DMI predictions. The objective of this study was to test the use of various markers and administration methodologies to predict DMI in grazing systems and determine the main contributors to variability. Eight rumen cannulated Nellore steers were randomly assigned to two 4 × 4 Latin squares. Steers had ad libitum access to pasture of *Brachiaria brizantha*. Steers were either not supplemented or individually supplemented with a mixture of fine ground corn and sodium monensin at 0.3, 0.6 or 0.9% of body weight. Steers were each administered 3 external markers via rumen cannula: a C32 controlled release capsule (CRC) on d 3; LIPE® (purified lignin), once daily on d 7 to 15; and Cr_2O_3 once daily on d 1 to 15 of each period. Fecal grab samples were collected twice daily for the last 5 d of the 15-d periods. Intake predictions were calculated using the Large Ruminant Nutrition System (LRNS), C31:C32 ratio, C33:C32 ratio, LIPE®, and Cr_2O_3. Indigestible DM (iDM), indigestible NDF (iNDF) and indigestible ADF (iADF) were used as internal markers. LIPE® was determined by infrared spectroscopy, Cr_2O_3 by inductively coupled plasma optical emission spectroscopy and alkanes by gas chromatography. A 240-h rumen incubation was used for the internal markers. A mixed model with the fixed effect of supplementation level and random effects of Latin square, animal(Latin square), period, and animal x period was used to determine treatment effects. LIPE® and Cr_2O_3 detected a treatment effect on pasture intake ($P < 0.10$) except for the Cr_2O_3/iADF combination ($P = 0.43$). Only LIPE® detected a treatment effect on total intake ($P < 0.03$). The alkanes provided greater and variable intake predictions. The final 4 d in each period demonstrated decreased CRC release rate compared with the previous 8 (mm/d = -0.012*d^2 + 0.091*d + 3.93, R^2

= 0.79). A completely random model containing internal and external markers, and their interactions with animal, period, and supplementation level determined which variables contributed to intake prediction variability. Variability was mainly due to internal and external markers (11–66% of variation), residual error (11–24% of variation), and external marker x animal interactions (5–16% of variation). Digestibility markers should be used cautiously to predict individual intakes in a grazing system due to animal by marker interactions, though markers can detect treatment differences.

Key Words: digestibility marker, intake prediction, steer

0230 Using hair cortisol concentrations to assess the adrenocortical stress response in beef cattle administered corticotrophin-release hormone.

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Our objective was to determine if hair cortisol concentrations can be used to assess the adrenocortical stress response in beef cattle receiving corticotrophin-release hormone (CRH) injections. Eight halter-trained Angus heifers (BW 189 ± 4 kg; age 225 ± 4 d) were ranked by BW and allocated to 2 groups (4 heifers/group), which were randomly assigned to a crossover design containing 2 periods of 35 d (d −7 to 28) and the following treatments: (1) 0.5 μg of CRH/kg of BW twice daily (i.v. at 0600 and 1800h) from d 0 to 13 (CORT), or (2) 5 mL of 0.9% saline (i.v.) concurrently with each treatment administration to CORT heifers (CON). Heifers were maintained in individual pens from d −7 to 13, or as a single group from d 14 to 28 of each period. Between periods, heifers were maintained as a single group and were not exposed to any experimental procedures for 24 d. Blood samples were collected via jugular venipuncture before and 90 min after each treatment administration. On d 0, 13, and 28, hair samples were collected from the tail switch before the first treatment administration of the day. Hair was collected using scissors as close to the skin as possible, and the hair material closest to the skin was stored (2.5 cm of length, 300 mg of weight). Plasma samples were analyzed for cortisol using a chemiluminescent enzyme immunoassay. Hair samples were cleaned with water and isopropanol, and then ground in a ball mill once dry. Cortisol was extracted with methanol before being measured using ELISA. Data were analyzed using the MIXED procedure of SAS, whereas hair cortisol concentration was analyzed using results obtained on d 0 of each period as covariate. A treatment × time interaction was detected for plasma cortisol concentrations ($P < 0.01$), which were less for CORT vs. CON heifers before treatment administration, but greater for CORT vs. CON heifers 90 min after treatment administration (2.1 vs. 4.8 ng/mL and 20.5 vs. 3.9 ng/mL, respectively; SEM = 0.8). Mean hair cortisol concentration was greater ($P = 0.04$) for CORT vs. with CON heifers (20.2 vs. 11.9 pg/mg of hair, respectively; SEM = 3.3). These results indicate that cortisol concentrations in hair samples collected from the tail switch can be used as an indicator of adrenocortical stress response in beef cattle.

Key Words: beef cattle, cortisol, hair, plasma, tail switch

0231 Effects of static or oscillating dietary crude protein levels on fermentation dynamics of beef cattle diets using a dual-flow continuous culture system.

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In nature several animal, microorganism, and plant species experience seasonal periods of undernourishment followed by periods of nutrient abundance. This nutrient oscillation promotes a period of accelerated growth defined as compensatory growth. The objective of this study was to evaluate the effects of increasing dietary crude protein (CP) levels and also comparing the effects of static versus oscillating dietary CP on ruminal nutrient digestibility, ruminal fermentation, nitrogen (N) metabolism, and microbial efficiency in beef cattle diets using a dual-flow continuous culture system. Eight fermenters (1223 ± 21 mL) were used in a replicated 4x4 Latin square design with periods lasting 12 d each (8 d for adaptation and 4 d for sampling). Dietary treatments were: (1) 10% CP, (2) 12% CP, (3) 14% CP, and (4) 10 and 14% CP diets oscillating at 48-h intervals. Experimental diets consisted of 50% orchard hay and 50% concentrate. Fermenters were fed 72 g/d and solid and liquid dilution rates were adjusted to 5.5 and 11%/h, respectively. Data were analyzed using the MIXED procedure in SAS. Partial data are presented in Table 1. Digestibilities of dry matter and organic matter were not affected ($P > 0.05$) by increasing dietary CP, nor by oscillating dietary CP. Total volatile fatty acids concentration and molar proportions of acetate, propionate, butyrate, valerate, iso-butyrate and iso-valerate were not affected ($P > 0.05$) by increasing or oscillating dietary CP. Ruminal NH_3–N concentration increased linearly ($P < 0.01$) in response to increasing dietary CP. Total N, non-ammonia N, and rumen undegraded protein flows did not differ among treatments or between oscillating dietary CP and static 12% CP. Microbial N and NH_3–N flows and microbial efficiency did not differ when comparing oscillating versus static CP ($P > 0.05$). However, there was a quadratic effect ($P < 0.05$) for these variables when dietary CP was increased.

Table 0231.

Table 1. Effects of static or oscillating dietary crude protein levels on fermentation dynamics.

Item	Treatment, CP%				SEM	*P*-value		
	10%	12%	14%	OSC		OSC vs. 12%	Linear	Quadratic
Total N flow, g/d	1.8	2.0	2.1	1.8	0.15	0.27	0.30	0.81
NAN flow, g/d	1.8	1.9	1.8	1.9	0.09	0.70	0.72	0.24
Microbial N flow, g/d	0.9	1.1	1.0	1.1	0.04	0.78	0.06	0.01
Microbial efficiency	31.3	40.5	37.4	36.5	2.20	0.19	0.05	0.02
RDP supply, g of N/d	0.8	1.1	1.2	1.1	0.07	0.84	<0.01	0.34
RUP flow, g of N/d	0.9	0.9	1.0	0.9	0.07	0.95	0.27	0.34
NH_3-N, mg/100 mL	2.9	3.1	8.9	4.8	1.10	0.12	<0.01	<0.01
Total VFA, m*M*	60.5	64.7	64.7	63.0	3.37	0.58	0.17	0.41
Acetate, % total VFA	35.6	34.5	30.9	38.8	2.99	0.29	0.25	0.72
Propionate, % total VFA	28.9	31.2	33.2	28.9	2.38	0.41	0.14	0.95
Butyrate, % total VFA	29.1	29.1	30.5	26.1	3.37	0.51	0.76	0.85
CP digestibility, %	77.5	70.0	67.0	68.4	7.43	0.86	0.30	0.79
DM digestibility, %	41.8	39.0	39.1	43.6	2.21	0.15	0.39	0.61

These results indicate that either ruminal microorganisms do not respond to oscillating CP levels or are capable of coping with 48-h periods of undernourishment. It is possible that other levels of CP, other CP sources, or other oscillating regimes could help elucidating these issues. The diet with 12% CP provided positive effects on microbial N flow and microbial efficiency in the rumen; therefore, it was the best strategy to improve N utilization in the rumen. Beyond that level, there were no further benefits of feeding greater dietary CP.

Key Words: microbial protein, nitrogen metabolism, in vitro fermentation

0232 Reproductive development of rotationally grazed beef heifers when supplemented chelated trace minerals. H. A. Tucker*, S. Bettis, T. Hampton, and M. Vázquez-Añón, *Novus International Inc., St. Charles, MO.*

Supplementation of trace minerals, Zn, Cu, and Mn, impact the health and productivity of ruminants resulting in increased growth and greater reproductive performance. Furthermore, increasing the availability of key trace minerals to the animal through technologies, such as chelation, not only reduces the amount released back into the environment, but may allow for a reduction in the amount of minerals being provided to the animal for optimum performance. Therefore, the objective of this study was to evaluate reproductive development of beef heifers supplemented with chelated trace minerals provided at a reduced inclusion rate. Sixty beef heifers (BW = 264 ± 6 kg; mean ± SEM) were utilized in a randomized complete block design with 2 treatments. Heifers were rotationally grazed and offered pelleted supplements for 91 d. The control (CON) supplement supplied 8.8 ppm Cu, 28.4 ppm Zn, and 31.6 ppm Mn from inorganic sources (133% of NRC requirement). The treatment (MAAC®) supplement contained reduced concentrations of Cu, Zn, and Mn (100% of NRC requirement) achieved through a partial replacement (50%) of inorganic trace minerals with MAAC® chelated trace minerals (Novus International Inc., St Charles, MO). To determine cyclicity of heifers, reproductive tract score (RTS) and plasma progesterone concentrations, along with BW and BCS, were assessed on d −1, 21, 35, 49, 63, 77, and 91 of study. Body weight (P = 0.81), BCS (P = 0.72), and ADG (d 0 to 91; P = 0.34) were not altered by treatment. Heifers supplemented with MAAC® (2.8 ± 0.1) had significantly (P < 0.01) greater RTS than CON (2.5 ± 0.1) throughout the trial. Furthermore, RTS was significantly (P < 0.01) greater on d 91 for MAAC® (3.9 ± 0.2) compared with CON (3.2 ± 0.2). Progesterone levels were significantly (P = 0.02) greater on d 21 (0.56 vs. 0.39 ± 0.06 ng/mL; MAAC® vs. CON) and tended (P = 0.06) to be greater on d 77 for MAAC® (1.05 vs. 0.54 ± 0.19 ng/mL; MAAC® vs. CON). Heifers supplemented MAAC® had 1.66 greater odds of cycling by d 91 of study compared with those supplemented CON. These data suggest that supplementation of MAAC® chelated trace minerals improve reproductive performance of beef heifers. Additionally, current data suggests that a reduction in trace mineral supplementation may benefit reproductive performance while maintaining growth and ADG.

Key Words: chelated trace mineral, reproduction, beef

0233 Comparison of treatment protocols for bovine respiratory disease in high-risk, newly received beef calves. J. J. Ball*[1], E. B. Kegley[1], J. A. Hornsby[1], J. L. Reynolds[1], J. Sarchet[2], and J. G. Powell[1], [1]*Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville,* [2]*Zoetis, Kalamazoo, MI.*

The objective of this study was to evaluate different treatment protocols for bovine respiratory disease (BRD) on performance, morbidity, antibiotic usage, and cost in newly received beef calves. Crossbred male calves (n = 176; BW = 232 ± 1.6 kg) were stratified by bodyweight and assigned randomly to 1 of 2 treatments in a randomized complete block design. Upon

arrival, calves were tagged with an individual identification tag, vaccinated for respiratory and clostridial pathogens, dewormed, castrated (if applicable), branded, tested for persistent infection with BVDV, and administered either 1.1 mL/45 kg BW of tulathromycin with a 7-d post-metaphylactic interval (PMI) or 1.5 mL/45 kg BW of tilmicosin with no PMI. A blinded pen rider observed cattle daily for signs of morbidity and a Clinical Attitude Score (0 [normal] to 5 [morbid]) was recorded. Calves that scored a 1 or greater and were PMI eligible were pulled and rectal temperatures were recorded; if temperature exceeded 40°C, calves on the tulathromycin treatment were given ceftiofur with a 7-d post-treatment interval (PTI) as the initial treatment antibiotic and tilmicosin calves were given enrofloxacin with a 3-d PTI. If the calf was pulled a second time and met the treatment criteria, a final antibiotic was administered, tulathromycin cattle received danofloxacin and tilmicosin cattle received florfenicol + flunixin meglamine. Calves were assigned to 1 of 16 replicated 0.4 ha grass lots with automatic waterers. Calves had ad libitum access to bermudagrass hay and were fed a grain supplement to exceed nutritional requirements. Calves were weighed on d −1, 0, 15, 41, and 42. Performance was similar across treatments throughout the duration of the study ($P \geq 0.10$). Percentage morbidity was greater for first treatment, second treatment, and relapse in the tilmicosin calves compared with the tulathromycin calves ($P < 0.01$). Initial antibiotic cost was greater in tulathromycin calves compared with tilmicosin calves ($P < 0.01$). Both first and second treatment antibiotic cost for cattle were greater in tilmicosin calves compared with tulathromycin calves ($P < 0.01$). However, there were no differences across treatments in terms of overall medical cost ($P = 0.51$), exclusive of labor or chute charges. Metaphylaxis treatment protocols did not affect performance, but differences were found in the percentage of calves treated with antibiotics for BRD and in the number of antibiotics used.

Key Words: bovine respiratory disease, tulathromycin, tilmicosin

0234 Glycerin as alternative energy source for ruminants: In vitro fermentation, total gas and methane production. P. Del Bianco Benedeti[1,2], T. Shenkoru[2], M. Fonseca[3], R. Bittner[2], K. Murphy[2], D. Ivey[2], B. Ribas[2,4], E. Marostegan de Paula[2], L. Galoro da Silva[2], H. Monteiro[2,5], I. Nicolis[2], L. Mariz[1,2], H. Costa[2,6], P. Amaral[1,2], M. I. Marcondes[1], and A. Faciola[*2], *[1]Federal University of Vicosa, Brazil, [2]University of Nevada, Reno, [3]Texas A&M University, College Station, [4]São Paulo State University, Botucatu, Brazil, [5]Maringa State University, Brazil, [6]Federal University of Minas Gerais, Belo Horizonte, Brazil.*

Glycerin has the potential to increase glycogenic potential of beef cattle diets; however, its effects on total gas and CH_4 production have been inconsistent. The objective of this study was to evaluate the effects of glycerin compared with corn and starch on ruminal fermentation, total gas, and CH_4 production using an in vitro system. Twenty-four bottles (620 mL each) equipped with wireless pressure sensors (Ankom[RF] Gas Production System) were used in 4 consecutive 48-h runs. Three ingredients were tested (corn, glycerin, and starch) at 0.5 g per bottle. The experimental design was: 4 incubation runs × 3 ingredients × 7 bottles per treatment, plus 12 blank bottles (3 per run), totaling 96 observations. Rumen fluid was collected from two rumen-cannulated steers and mixed with a buffer solution (1:2 v/v) in water bath at 39°C under anaerobic conditions. Bottles were inoculated with 75 mL of rumen/buffer solution. The data acquisition software was set

Table 0234.

Table 1. Least-square means of *in vitro* fermentation of dietary corn, starch, and glycerin

Item	Corn	Starch	Glycerin	SEM	*P*-value
24h total gas production, mL/g DM	324[a]	324[a]	287[b]	19.1	< 0.01
48h total gas production, mL/g DM	384[a]	344[b]	354[b]	24.1	< 0.01
Final pH	5.89[a]	5.67[b]	5.93[a]	0.13	< 0.01
N-NH_3, mg/100mL	18.9[a]	10.5[b]	16.6[a]	2.11	< 0.01
Total volatile fatty acids, mM/g DM	15.3[ab]	14.4[b]	17.4[a]	3.67	0.01
Acetate, mol/100mol	35.8[a]	35.2[a]	24.8[b]	0.42	< 0.01
Propionate, mol/100mol	24.8[b]	29.5[a]	30.0[a]	1.43	< 0.01
Butyrate, mol/100mol	23.0[b]	21.4[b]	28.9[a]	1.27	< 0.01
Valerate, mol/100mol	6.26[b]	5.67[c]	8.34[a]	0.41	< 0.01
Iso-butyrate, mol/100mol	3.13[a]	2.62[b]	2.40[c]	0.09	< 0.01
CH_4, %	5.22[b]	5.16[b]	8.92[a]	0.42	< 0.01
CH_4, mL/g DM	9.71[b]	8.49[b]	13.6[a]	1.67	< 0.01
CO_2, %	30.9[a]	30.1[a]	26.5[b]	1.29	< 0.01
CO_2, mL/g DM	57.1[a]	48.5[b]	40.8[c]	6.85	< 0.01

[a,b,c] Within a row, different subscripts differ at $P < 0.05$.

to record cumulative pressure every 5 min for 48 h. At the end of the incubation, 10-mL samples were filtered through two layers of cheesecloth, preserved with sulfuric acid and centrifuged for ruminal NH_3 and VFA analyses. The production of CO_2 and CH_4 were determined by chromatography. Data were analyzed using the MIXED procedure of SAS, with ingredients as fixed factors and replicate within ingredient as random. Least-square means are presented in Table 1. Glycerin decreased 24-h total gas production, and acetate concentration ($P < 0.01$). The 48-h total gas production was highest for corn ($P < 0.01$), and similar between glycerin and starch. Compared with glycerin, pH and NH_3–N decreased with feeding starch ($P < 0.01$) but not for corn. Starch had the lowest total VFA concentration ($P = 0.01$), while corn had the lowest propionate concentration ($P < 0.01$). Compared with corn and starch, glycerin had the highest butyrate and valerate concentrations ($P < 0.01$). Glycerin increased CH_4 (% and mL/g) production ($P < 0.01$). CO_2 (mL/g) was higher ($P < 0.01$) for corn, but similar for glycerin and starch. CO_2 (% and mL/g) production was lowest for glycerin ($P < 0.01$). These results suggest that glycerin may change ruminal fermentation relative to corn, increasing propionate, butyrate, and valerate concentrations. Glycerin had higher CH_4 concentration than both corn and starch; therefore, results indicate that glycerin would contribute more to the enhancement of methanogenesis than these carbohydrates.

Key Words: beef cattle, finishing diet, greenhouse gases

0235 The effects of supplementing ruminal bypass unsaturated fatty acids during late gestation on cow and calf serum fatty acids in beef cows.

R. E. Ricks, E. K. Cook, S. K. Duckett, and N. M. Long*, *Clemson University, Clemson, SC.*

The objective of this study was to determine if supplementation with ruminal protected unsaturated fatty acids (FA) increased unsaturated FA in both maternal serum and colostrum during late gestation and in serum from their newborn beef calves. Commercial Angus and Angus crossbred heifers and young cows all bred to a single Angus sire were blocked by breed and parity and randomly assigned to either control (1.5 kg of corn gluten feed, CON $n = 29$) or an isocaloric isonitrogenous supplement containing 200 mg of ESSENTIOM (EFA, $n = 29$) for the last 90 d of gestation. All supplements were individually fed 5 d/wk. All cows had ad libitum access to the same pastures throughout the study. Maternal blood samples were collected at 90 and 45 d before expected parturition. At parturition, blood and colostrum samples were obtained from each cow. Blood samples was collected from calves at parturition and then at 5 d of age. Serum and colostrum FA content were determined. All data were analyzed using PROC MIXED procedure of SAS either as repeated measures or ANOVA depending on parameters. Maternal serum concentrations of C16:0, C18:0 C18:1c9, C18:2, C20:4, and total FA were similar in all cows at start of supplementation but increased (treatment × day interaction $P < 0.01$) in the EFA cows at 45 d before and at parturition compared with CON cows. Colostrum DM was increased ($P = 0.01$) in EFA cows compared with CON cows (30.4 vs. 25.4%, 1.30 SEM). Colostrum concentrations on a DM basis of C18:2, total FA, and total unsaturated FA were increased ($P < 0.05$) in EFA cows compared with CON cows. Serum from calves at birth whose dams were supplemented with EFA had increased ($P \leq 0.01$) concentrations of C16:0, C18:0, C18:1 t9, C18:2, C20:4 and total FA compared with calves whose dams were supplemented CON. At 5 d of age calves from EFA supplemented dams had increased ($P \leq 0.05$) serum concentrations of C18:0, C18:2, C20:4 and total FA compared with serum from calves whose dams were supplemented CON. The results of this study indicate that supplementation of rumen protected unsaturated FA in late gestation beef cows increased circulating and colostrum unsaturated FA, and this resulted in increased unsaturated and total FA at parturition and at 5 d of age in their calves.

Key Words: colostrum fatty acids, ruminal bypass fat, serum fatty acids

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0236 The effects of supplementing ruminal bypass unsaturated fatty acids during late gestation on transfer of passive immunity and growth in calves.

R. E. Ricks, E. K. Cook, L. K. Lewis, and N. M. Long*, *Clemson University, Clemson, SC.*

The objective of this study was to determine if supplementation with ruminal protected unsaturated fatty acids (FA) increased colostrum and serum concentrations of IgG of calves and subsequent calf growth. Commercial Angus and Angus crossbred heifers and young cows all bred to a single Angus sire were blocked by breed and parity and randomly assigned to either control (1.5 kg of corn gluten feed, CON $n = 29$) or an isocaloric isonitrogenous supplement containing 200 mg of ESSENTIOM (Arm & Hammer Animal Nutrition, Princeton, NJ; EFA, $n = 29$) for the last 90 d of gestation. All supplements were individually fed 5 d/wk. All cows had ad libitum access to the same pastures throughout the study. At parturition a colostrum sample was collected from the dam and a blood sample was collected from calves at 24 h of age. Calf BW was collected every month and adjusted back to every 30 d of age. Serum and colostrum IgG content were determined by ELISA. All data were analyzed using PROC MIXED procedure of SAS either as repeated measures or ANOVA depending on parameters. Dam BW and BCS during late gestation were similar ($P > 0.14$) between treatments. Colostrum concentrations of IgG were increased ($P < 0.01$) in EFA cows compared with CON cows (166 ± 13 vs. 102 ± 18 mg/ml, respectively). Calves from EFA dams had a tendency for a reduced ($P = 0.08$) birth weight compared with calves from CON dams (30.9 ± 0.6 vs. 32.5.6 ± 0.6 kg, respectively). Serum from calves at 24 h of age whose dams were

supplemented with EFA had increased ($P \leq 0.01$) concentrations of IgG compared with calves whose dams were supplemented CON (11.4 ± 0.7 vs. 7.6 ± 0.7 mg/ml, respectively). Calf growth had a treatment X parity X day interaction ($P < 0.01$). Calves from EFA dams that had their second or third calves had increased BW ($P < 0.05$) at 90 to 210 d of age and at 210 d of age respectively compared with calves from CON dams. The results of this study indicate that supplementation of rumen protected unsaturated FA in late gestation beef cows increased colostrum and calf serum IgG and increased calf BW in cows with their second and third calves.

Key Words: calf growth, colostrum IgG, ruminal bypass fat, serum IgG

0237 Effect of OmniGen-AF® dietary supplementation on ultrasound parameters in purebred Angus steers fed a finishing diet.

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Dietary supplementation to aid the immune system of finishing steers is recommended to maintain health and growth; however limited knowledge exists regarding the influence on performance. The objective of this study was to determine the effect of OmniGen-AF® supplementation on ultrasound parameters in steers through the finishing phase. Nine purebred Angus half-sibling steers were divided into one of two treatment groups; Control (CNTL $n = 4$) and OmniGen-AF® (OG; $n = 5$). Cattle were offered 0 g/hd/d (CNTL) or 56 g/hd/d of OG through backgrounding and transition (42d). At the beginning of the finishing phase, cattle were scanned by ultrasound using an Aloka SSD- 500V console with UST-5044–3.5 linear transducer and analyzed using BIA Pro software (Designer Genes Technologies, Harrison, AR). Cattle were subsequently scanned on d 69 and 104 of supplementation to examine the effects of OG supplementation on ultrasound carcass parameters during the finishing phase. Weights, average daily gain (ADG), and dry matter intake (DMI), were collected through the backgrounding and finishing phases. Rib eye area (REA), 12th rib fat thickness (FT), rump fat (RF), REA/cwt and percent intramuscular fat (%IMF) were collected. Predicted yield grade was completed using FT, REA, live weight × 62% dressing percent and 2.5% Kidney Pelvic Heart fat (KPH); predicted quality grade was calculated using %IMF data. Data were analyzed using multiple *t* tests procedure of GraphPad Prism 6.03 with significance declared at $P < 0.05$. No difference between groups was detected for REA, FT, RF, %IMF, predicted yield on d 42 or 69. Predicted quality grade, weight, ADG and DMI did not differ between CNTL or OG. On d104 OG finished cattle had a tendency to have lower FT (CNTL 0.38 ± 0.01, OG 0.32 ± 0.02; mean ± SEM; $P = 0.06$), and higher REA/cwt (CNTL 0.86 ± 0.04; OG 1.01 ± 0.06; $P = 0.07$), and scan with a lower %IMF (CNTL 3.54% ± 0.11 OG 3.03% ± 0.18; $P = 0.06$) compared with controls. Similarly, OG finished cattle scanned with lower RF (CNTL 0.34 ± 0.034 in, OG 0.24 ± 0.02 in; $P = 0.03$) and larger REA (CNTL 11.56 ± 0.44 sq in, OG 13.79 ± 0.67 sq in; $P = 0.04$). Upon evaluation, the OG supplemented cattle had lower predicted numerical yield grades (2.64 ± 0.24) than their control counter parts (3.42 ± 0.16; $P = 0.04$). In this study, supplementing OG during finishing decreased predicted numerical yield grades by increasing REA and decreasing fat deposition.

Key Words: OmniGen-AF, ultrasound, beef cattle

0238 Total gastrointestinal tract digestibility of dry matter, neutral detergent fiber and starch of Nellore and 1/2 Angus x Nellore cattle adapted either for 9 or 14 d to high-concentrate diets.

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This study was designed to evaluate the length of the adaptation period to high-concentrate diets on total tract digestibility of DM, NDF and starch of Nellore (NE) and 1/2 Angus x Nellore (AN) cattle. The experiment was designed as completely randomized block with 2 × 2 factorial arrangement, replicated 6 times (3 animals/pen), in which 72 22-mo-old yearling bulls [36 NE (319.2 ± 18.5 kg), and 36 AN (307.9 ± 29.5 kg)] were fed in 24 pens for 89 d according to the treatments: NE adapted for 9 d; NE adapted for 14 d, AN adapted for 9 d, and AN adapted for 14 d. Measures over time were taken on d 10, 15, and 20 of the experimental period. Each of the adaptation diets containing 62%, 70%, and 78% concentrate was fed for 3 d to cattle adapted for 9 d. For cattle adapted for 14 d, the adaptation diets containing 62%, 70%, and 78% concentrate were fed for 5 d, 4 d, and 5 d, respectively. The finishing diet contained: 66.5% cracked corn grain, 14.0% sugarcane bagasse, 16.0% cottonseed meal, 1.5% supplement, 1.2% urea, and 0.8% limestone (DM basis). Diet samples were collected just after morning delivery (0830h) on d 8, 9, 13, 14, 18, and 19 of experimental period, and composite samples were made per pen for d 8 and 9, 13, and 14, and 18 and 19. Samples of orts and feces were collected just before morning (0800h) meals on d 9, 10, 14, 15, 19, and 20 of the experimental period, and a composite samples were made per pen for d 9 and 10, 14, and 15, and 19 and 20. Fecal samples were collected from the same animal in each pen, which was chosen randomly. No significant ($P > 0.10$) biotypes and adaptation length main effects were observed for DM and starch digestibilities. A significant ($P = 0.01$) interaction between biotype, adaptation length, and day of collection was observed for NDF

digestibility, where no differences were detected ($P > 0.10$) across treatments on d 10 and 20; however, on d 15 the NDF digestibility was greater for AN adapted in 14 d (53.9%) and NE adapted in 9 d (53.1%) when compared with AN adapted in 9 d (41.3%) and NE adapted in 14 d (35.1%). Thus, cattle should be adapted for 14 d regardless of biotype, because no differences in digestibility were detected on d 20, and because longer periods of adaptation are safer.

Key Words: adaptation, digestibility, feedlot

0239 Effect of OmniGen-AF® supplementation on the metabolic profile of growing beef cattle.

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To examine the effect of OmniGen-AF® (OG) supplementation on serum indicators of growth and development in growing beef cattle, healthy 8-mo old purebred Angus cattle were randomly assigned to 0 (control; 4 heifers, 2 bulls, and 2 steers) or 56 g/hd/day OG (OG; 4 heifers, 3 bulls, and 2 steers). Cattle were housed in a freestall barn with straw bedding and fed via Calan Broadbent system a diet including grass hay, alfalfa hay, and ground corn once per day. Blood was collected via jugular puncture on d 0, 3, 5, 7, 10, 14, 21, 28, 35, and 49 of supplementation and 1, 3, 7, 10, 14, and 21 d after supplementation and analyzed for serum concentrations of glucose, insulin, leptin, and haptoglobin. Using a repeated-measures-in-time design in PROC MIXED, we examined changes in serum parameters from baseline during the 49 d of supplementation and separately during the 21 d after supplementation. We hypothesized that OG supplementation alters carbohydrate metabolism during the supplementation period. We observed sex-specific effects of OG supplementation on serum indicators of carbohydrate metabolism and growth. During the supplementation period, serum glucose concentrations increased in control bulls and steers compared with male OG-supplemented cattle ($P = 0.01$), whereas no treatment effects were observed for heifers ($P = 0.80$); those gender-specific treatment group differences were also observed after supplementation. During the supplementation period, serum leptin concentrations decreased in female controls compared with female OG-supplemented cattle ($P < 0.01$). No treatment group differences for serum leptin were observed for bulls and steers combined ($P = 0.54$) or after supplementation irrespective of gender. Changes in insulin concentrations were not different between treatment groups ($P = 0.29$); however, insulin concentrations were lower during but not after supplementation in OG-supplemented cattle compared with controls, when baseline insulin concentrations were used as linear covariate ($P = 0.01$). During but not after the supplementation period, haptoglobin concentrations decreased in OG-supplemented bulls ($P = 0.03$) and increased in OG-supplement steers ($P = 0.06$) compared with their sex-specific controls. No differences in serum haptoglobin between treatment groups were observed in females or during supplementation withdrawal. These data suggest no consistent effects of OG supplementation on the metabolism of growing beef cattle.

Key Words: beef cattle, metabolism, OmniGen-AF

0240 Dietary melatonin and growth responses in feedlot heifers.

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Two trials were conducted to determine if feeding melatonin (MEL) to growing beef heifers altered feedlot performance or carcass composition. Trial 1 was initiated on October 22 while Trial 2 commenced on April 15, and both utilized black-hided, non-implanted heifers ($n = 90$ per trial) which were blocked by initial BW (380 kg, Trial 1; 300 kg, Trial 2). Heifers were assigned to a pen (6 hd/pen) within block and pen was randomly assigned 1 of 3 treatments which provided 0, 20 or 100 mg MEL $\cdot$ hd^{-1} $\cdot$ d^{-1} for Trial 1, while Trial 2 treatments provided 0, 100 or 200 mg MEL $\cdot$ hd^{-1} $\cdot$ d^{-1}. Heifers were fed twice daily at 0700 and 1100 h a basal diet that contained (DM basis) 15% corn silage, 70.9% cracked corn, 5.8% DDG, 5.0% wheat midds, 1% urea, and the residual was micro ingredients which included MGA (NEg = 1.46 Mcal/kg, CP = 12.9%). Melatonin supplements were made monthly for each treatment by diluting MEL powder into finely ground corn and were fed at 0.45 kg as-fed $\cdot$ hd^{-1} $\cdot$ d^{-1} as a replacement for cracked corn at the 1100 h feeding. Slaughter occurred by block, and carcasses were chilled for 48 h before data collection. Pen (experimental unit) data were analyzed using the MIXED procedure of SAS and orthogonal contrasts were used to assess linearity (-0.5345, -0.2673, and 0.8018 for Trial 1, and -1, 0, 1 for Trial 2). In Trial 1, a positive linear effect for G:F (0.156, 0.160, and 0.169) and calculated dietary NEg (1.36, 1.41, and 1.45 Mcal/kg) was observed ($P \leq 0.02$) for the 0, 20, and 100 mg treatments, respectively. Positive linear tendencies ($P \leq 0.09$) were detected for ADG (1.84, 1.88, and 1.95 kg/d) and HCW (354, 355, and 361 kg), while all treatments had similar rib-eye ether extract percentages ($P = 0.41$) in Trial 1. In Trial 2, feeding 200 mg MEL increased HCW vs. 0 mg (348 vs. 342 kg, $P = 0.05$) and 100 mg HCW = 343 kg. No differences in 12th rib fat depth or marbling score were recorded ($P \geq 0.13$) in either trial. Results indicate that feeding MEL to non-implanted feedlot heifers may increase gain efficiency and HCW with no effects on carcass composition.

Key Words: melatonin, feedlot, heifers

0241 Dietary melatonin and growth responses in implanted feedlot steers. M. R. Schaefer* and D. M. Schaefer, *University of Wisconsin, Madison.*

Two trials were conducted to determine if feeding melatonin (MEL) to growing beef steers altered feedlot performance or carcass composition. Trial 1 was initiated on October 23 while Trial 2 started on March 19, both utilized black-hided steers (n = 90 per trial) which were blocked by initial BW (325 kg, Trial 1; 410 kg, Trial 2). Steers were assigned to a pen (6 hd/pen) within block and pen was randomly assigned 1 of 3 treatments which provided 0, 100 or 200 mg MEL per animal/d. All steers received a single implant of 120 mg trenbolone acetate and 24 mg estradiol on d 28 (Trial 1) or d 0 (Trial 2). Steers were fed once daily at 0800 h a basal diet that contained (DM basis) 15% corn silage, 70.9% cracked corn grain, 5.8% dried distillers grains, 5.0% wheat midds, 1.4% limestone, 1% urea, and the residual was micro ingredients (NEg = 1.46 Mcal/kg, CP = 12.9%). Melatonin supplements were made monthly for each treatment by diluting MEL powder into finely ground corn and were fed at 0.45 kg as-fed per animal/d as a replacement for cracked corn. On d 154 in Trial 1, three steers per pen in the lightest 2 blocks were restrained between 1400 and 1600 h to collect blood and urine samples. Data were analyzed using the MIXED procedure of SAS with treatment as a fixed effect while block and trial were recognized as random effects, and an orthogonal contrast was used to compare the 0 vs. 200 mg treatments. No growth responses were different across the treatments ($P \geq 0.19$). Feeding MEL increased ($P \leq 0.01$; 0 vs. 200 mg) 12th rib fat depth (1.2 vs. 1.4 cm) and yield grade (2.9 vs. 3.3), tended ($P = 0.10$) to increase HCW (379 vs. 386 kg); however, it did not alter marbling score (563 vs. 566; $P = 0.74$). Plasma serotonin levels were similar across treatments; however, urine 6-hydroxymelatonin-sulfate increased ($P = 0.01$) in MEL fed steers (5, 217, and 253 ng/ml urine). Dietary MEL may increase HCW in steers; however, the additional weight accumulation might be attributed to more fat gain as implied by the increased rib fat depth.

Key Words: feedlot, melatonin, steers

0242 Use of the residual retained energy as a measure of efficiency in growing Nellore cattle bulls. A. M. Castilhos*[1], A. M. Jorge[1], C. L. Francisco[1], M. E. Z. Mercadante[2], S. F. M. Bonilha[2], C. M. Pariz[1], D. C. M. Silva[1], and R. H. Branco[2], *[1]Universidade Estadual Paulista-FMVZ, Botucatu, Brazil, [2]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho, Brazil.*

This study used 357 Nellore bulls (212 + 38 kg BW; 279 + 29 d of age) to evaluate the effect of a new efficiency measure (residual retained energy) on feedlot performance and economic viability of the cattle production system. GrowSafe automated feeding system (GrowSafe Systems Ltd., Airdrie, AB, Canada) and individual pens were used to record DMI. Residual retained energy (RRE) was calculated as difference between net energy required for gain (NEFG) and the retained energy (RE) for animal. Net energy required for gain was estimated as (DMI– feed required for maintenance) * diet NE_g. Retained energy for animal was predicted by equation of the NRC (2000). Other efficiency measures as residual feed intake (RFI), residual intake and BW gain (RIG), and residual BW gain (RG) were used. Residual feed intake was calculated as the residuals from the regression of total DMI on $BW^{0.75}$ and ADG. Residual gain was calculated as the residuals from the regression of total ADG on $BW^{0.75}$ and DMI. Residual intake and BW gain was determined from linear combination into RFI and RG. Animals were classified for each efficiency measure as Low (< 0.5 SD mean), Medium (within ± 0.5 SD), and High (> 0.5 SD mean) groups. Carcass characteristics [LM area and back fat thickness (BF); 12th–rib] were evaluated using ultrasound measures. Economic value included was profit ($/bull.d^{-1}). Feedlot performance variables were ADG (kg/d), DMI (kg/d), and final BW (kg). Data were analyzed using PROC MIXED in SAS. For feedlot performance, High group had greater ($P < 0.001$) final BW and ADG compared with other groups. No group effects ($P = 0.94$) were detected for DMI. For carcass characteristics, no group effects ($P = 0.50$) were detected for BF. However, High group had greater LM area ($P = 0.001$) than other groups. High group demonstrated better efficiency values for the three measures evaluated (RFI, RIG, RG; $P < 0.001$), and greater profit ($P < 0.001$) compared with other groups. In conclusion, the residual retained energy proved to be a new measure of efficiency able to identify more productive and profitable animals on herd, without detriment to the degree of finish of the carcass.

Key Words: efficiency measure, Nellore cattle, profit, retained energy

Table 0242.

	RRE			
Variable	Low	Medium	High	SEM
Final BW, kg	301.91^{c}	326.92^{b}	367. 24^{a}	7.75
ADG, kg/d	0.93^{c}	1.03^{b}	1.16^{a}	0.19
DMI, kg/d	6.95	6.93	6.89	0.03
RFI	0.57^{a}	0.06^{b}	-0.62^{c}	-0.45
RIG	-0.61^{c}	0.01^{b}	0.75^{a}	0.09
RG	-0.05^{c}	0.08^{b}	0.14^{a}	0.02
LM area, cm^2	53.87^{b}	57.00^{b}	60.34^{a}	2.52
BF, cm	1.77	1.57	1.65	0.18
Profit, $/bull.d^{-1}	0.33^{c}	0.50^{b}	0.78^{a}	0.05

$^{abc}P < 0.05$

0243 Effects of rumen-protected PUFA supplementation to late-gestating beef cows on performance and physiological responses of the offspring.

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Our objective was to evaluate the effects of PUFA supplementation to beef cows during late gestation on performance and physiological responses of the offspring. On d 0 of the experiment, 96 multiparous, non-lactating, pregnant Angus × Hereford cows at the end of their second trimester of gestation were stratified by BW and BCS, and divided into 24 groups of 4 cows/group. Groups were randomly assigned to receive (as-fed basis) 452 g of soybean meal per cow daily in addition to 1) 200 g/cow daily of rumen-protected PUFA mix based on eicosapentaenoic, docosahexaenoic, and linoleic acids (PF) or 2) 200 g/cow daily of rumen-protected fatty acid mix based on palmitic and oleic acids (CON). Groups were maintained in 2 pastures (12 groups/pasture) with ad libitum access to water and alfalfa hay. However, groups were segregated 3 times/wk and offered treatments (Mondays, Wednesdays, and Fridays) from d 0 until calving. Within 12 h after calving, calf BW was recorded. Calves were weaned on d 280, and preconditioned for 45 d. Blood samples were collected from all calves on d 280, 282, 285, 288, and 293 to evaluate plasma haptoglobin concentration. Supplementing beef cows with PF did not ($P \geq 0.24$) impact cow BW change or pre-calving BW, as well as cow BCS change and pre-calving BCS. No treatment effects were detected ($P \geq 0.14$) for calf birth BW, calving rate, percentage of male calves born, and kg of calf born per cow assigned to the experiment. At weaning, no treatment differences were detected ($P \geq 0.24$) for weaning rate, calf weaning BW (205-d adjusted or not), and kg of calf weaned per cow assigned to the experiment. Calves from CON cows were older at weaning ($P = 0.03$) than PF cohorts. No treatment effects were detected ($P \geq 0.22$) for calf preconditioning ADG, BW, and percentage of calves treated for BRD symptoms. Nevertheless, a treatment × day interaction was detected ($P = 0.03$) for plasma haptoglobin concentration, which was greater for calves from CON vs. PF cows on d 282. In summary, PF supplementation to late gestating beef cows did not impact overall cow and offspring productive parameters, but reduced offspring acute-phase protein reaction elicited by weaning.

Key Words: beef cows, offspring, PUFA, supplementation

0244 Effects of injectable trace mineral supplementation on yearling bull growth, carcass characteristics, testicular development and semen quality attributes.

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The study objective was to evaluate effects of injectable trace mineral supplementation on growth, carcass characteristics, testicular development and semen quality in yearling Angus bulls. Bulls (446 kg ± 35, SD) were blocked by age into 4 pens of 15, and randomly assigned to receive Multimin 90 (MM) or a saline injection (CON; $n = 30$ per treatment) at 1 mL/68 kg BW and fed a common finishing diet for 73d. Breeding soundness exams (BSE) and scrotal circumference measurements were conducted on d 53 on all bulls. Liver and blood mineral concentrations ($n = 14$/treatment) were determined on d 1 and 53, and semen mineral concentrations were also determined on d 53. Bulls were harvested on d 74, and testicles were assessed for testicular density and histology, and carcass data collected after a 48-h chill. Data were analyzed using MIXED or GLIMMIX procedures of SAS with the fixed effect of treatment and bull as the experimental unit. Days of age (BSE, testicular data) and initial mineral concentrations (plasma, liver) were used as covariates. No differences due to treatment were observed in ADG, carcass characteristics, testicular density or histology ($P \geq 0.27$). Results from BSE indicate no differences in scrotal circumference, testicular tone, morphology, or pass/fail percentages ($P \geq 0.30$) between treatments; however, overall motility ($P = 0.07$) tended to be lesser in MM-bulls. Based on reference ranges, d 1 liver mineral concentrations were considered adequate in all bulls. Day 53 liver and plasma mineral concentrations were similar between MM and CON treatments ($P \geq 0.15$). Treatment did not affect whole semen mineral concentrations ($P \geq 0.18$), or Se, Zn, and Mn concentrations ($P \geq 0.48$) of seminal plasma. However, seminal plasma Cu concentrations were greater in MM bulls ($P = 0.04$). Spermatozoa concentrations of Se and Zn ($P \geq 0.27$) did not differ due to treatment; however, spermatozoa Cu tended ($P = 0.07$) to be lesser and spermatozoa Mn concentrations were decreased ($P = 0.03$) in MM-bulls. Interestingly, spermatozoa Mn concentrations were negatively correlated with morphology ($r = -0.41$, $P = 0.04$). These data suggest supplementing bulls adequate in mineral status with MM does not affect growth, carcass characteristics or semen attributes. However, semen mineral concentrations may be related to semen quality and more work is needed to clarify the importance of mineral distribution in semen fractions on semen quality.

Key Words: bulls, semen quality, trace minerals

0245 Effect of α tocopherol acetate and ascorbic acid on performance, carcass traits, and incidence and severity of liver abscesses in finishing cattle.
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Liver abscesses (LA) in cattle negatively affect feedlot performance by decreasing ADG, feed intake, and G:F. Abscessed livers are condemned and abdominal adhesions associated with LA can result in extensive carcass trimming during harvest, further compounding adverse economic impact. Given pending regulatory changes pertaining to the use of in-feed antibiotics in cattle production, there is growing interest in alternatives to antibiotics for LA control. The objective of this study was to evaluate use of a combination of the antioxidants, ascorbate and α tocopherol acetate, for mitigation of LA in feedlot cattle. Yearling crossbred heifers (n = 390; initial BW 481 ± 9.4 kg) were blocked by previous treatment and allocated randomly to 24-dirt surfaced feedlot pens (10 m × 35 m) with 13 to 14 heifers/pen. Heifers were weighed, implanted with TE-200 implants, and placed into feeding pens. Finishing diets consisted of 60% steam-flaked corn, 30% wet corn gluten feed, 8% alfalfa, and 2% supplement (DM basis) and provided 300 mg/d monensin, no tylosin, and either 200 IU/d α tocopherol acetate (CTL) or 2000 IU/d α tocopherol acetate plus 500 mg/day crystalline ascorbate (AOX). Heifers were fed once daily ad libitum for 94 d, then weighed and transported 450 km to a commercial abattoir for harvest. The HCW and incidence/severity of LA were determined the day of harvest, and carcass traits were evaluated following 32 h of refrigeration. Compared with CTL, feeding AOX tended to decrease DMI (10.66 vs. 10.31 kg/d; P = 0.08) and improve G:F (0.1204 and 0.1254; P = 0.12), but did not impact ADG, incidence of LA (25.6 vs. 23.5% for CTL and AOX, respectively), HCW (828.4 vs. 830.5 kg for CTL and AOX, respectively), or other carcass traits (P > 0.20). In conclusion, feeding antioxidants is not a viable alternative to decrease incidence of liver abscesses in finishing cattle.

Key Words: antioxidant, feedlot, liver abscess

0246 Feed intake and production efficiency of beef cows.
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The objective of this study was to determine the relationships between DMI and growth as heifers and cows and calves weaned, weight of calf weaned, and milk production. Cows born in 1999–2001and sired by industry AI bulls (Angus, Hereford, Simmental, Limousin, Charolais, Gelbvieh, and Red Angus) and with Angus, Hereford, and MARC III (composite) dams were randomly mated to F_1 bulls from these same crosses (with the exception of MARCIII dams) resulting in heifers (F_1^2) that were 2-, 3-, and 4-breed crosses. Heifers (F_1^2) born in 4 consecutive years (2004–2007) were retained and bred to produce four successive calf crops, calving first at 2 yr of age. Individual feed intake and BW gain were measured for an 84-d period between weaning and first breeding on F_1^2 heifers born in years 2005–2007 (n = 220, 249, and 218, respectively). At 5 yr of age, F_1^2 cows were not bred. Twenty-one d after weaning, F_1^2 cows (n = 158, 179,154, and 131, respectively, for birth years 2004–2007) were individually offered 120 kcal ME/kg $BW^{0.75}$·d^{-1}in Calan gates for 112 d, and then given ad libitum access for an additional 98 d. Milk production at approximately 100 d after calving was measured using a 16-h weigh-suckle-weigh at 2- and 5-yr of age. Heritability and genetic correlations were estimated with MTDFREML. The heritability estimates were Heifer DMI (0.69) Heifer ADG (0.49), Cow DMI (0.48), Cow ADG (0.46), and 5-yr-old milk production (0.41). There were positive genetic correlations between heifer DMI and heifer ADG (0.89), cow DMI (0.65), cow ADG (0.73), average weaning weight of calves (0.52), and total calf weight weaned (0.23). There were positive genetic correlations between cow DMI and average weaning weight of calves (0.28), and total calf weight weaned (0.21). In conclusion, there are genetic correlations between DMI and total weight of calf weaned; also, heifer intake does offer some opportunity to select for intake in mature cows. Selection for reduced DMI may have a negative effect on total BW of calf weaned. USDA is an equal opportunity provider and employer.

Key Words: cows, feed intake, production efficiency

0247 Effects of concurrent selection for residual feed intake and average daily gain on fertility and longevity in black Angus beef females.
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During an individually fed feed efficiency test, traits including ADG, DMI, G:F, residual feed intake (RFI), and residual gain (RG) are evaluated. Almost invariably, ADG and RFI are the only traits in this list that are not correlated. Previous data would suggest that RFI does not affect fertility; however, a selection index that incorporates RFI and improves fertility has not been well defined. Thus, the objective was to determine if concurrent selection for RFI and ADG may identify beef heifers that have improved fertility and longevity in the beef herd. Yearling feed efficiency testing and subsequent production data were collected on 540 purebred, Black Angus heifers from 14 contemporary groups over 6 yr. These data were unbiased in that heifers were retained based on fertility, irrespective of feed efficiency performance indicators. Cattle that were both above contemporary group average for ADG as well as below contemporary group average for RFI were categorized as PASS, and all other heifers were categorized as FAIL. The MIXED and GLIMMIX procedures of SAS were used to analyze continuous and binary variables, respectively.

The model included heifer category as the main effect and included contemporary group as a random effect. Across the dataset, ADG and RFI were not correlated ($P = 0.64$). Yearling pregnancy rates did not differ ($P = 0.14$) between PASS (87.2%) and FAIL (82.3%), nor did the proportion of heifers that became pregnant in the first 21 d of the breeding season ($P = 0.69$). Pregnancy rate as a 2-yr-old tended to be greater ($P = 0.07$) in PASS (85.7%) compared with FAIL (75%). Moreover, the proportion of females that remained in the herd at 3, 4, and 5 yr of age was greater ($P \leq 0.05$) in PASS than FAIL. It should be noted that PASS did not differ from FAIL for phenotypic birth BW, weaning BW, yearling BW, or yearling height ($P \geq 0.53$). Furthermore, nonparent EPDs for calving ease maternal, scrotal circumference, milk, and rib-eye area did not differ between PASS and FAIL ($P = 0.42$). However, PASS tended to have a greater nonparent marbling EPD than FAIL (0.409 vs. 0.375, respectively). These data indicate that dual selection for ADG and RFI may identify beef heifers that have improved fertility and longevity without impacting growth and maternal EPDs.

Key Words: feed efficiency, fertility, residual feed intake

0248 Efficacy of a novel intranasal Zn solution on health and growth performance of high risk, newly received stocker cattle. M. M. Foster*, E. B. Kegley, J. G. Powell, J. L. Reynolds, J. A. Hornsby, D. L. Galloway, J. J. Ball, and J. Zhao, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville.*

The objective of this study was to determine if using an intranasal Zn solution would impact health and growth performance of high-risk stocker cattle. Upon arrival from regional sale barns, male beef calves ($n = 239$; 3 arrival dates [block]; initial BW = 276 ± 2.4 kg) were identified with individual ear tags, vaccinated with clostridial and 5-way modified live bovine respiratory viral vaccines, dewormed, branded, and castrated (if necessary). In addition, nasal swabs were collected from 24 calves (12/treatment) in block 2 and cultured for bacterial pathogens on d 0, 1, 2, and 7. Calves were stratified by arrival gender and BW into 2 treatments: Zn treated, 3 mL of a solution containing 32.4 mg of Zn administered intranasally, or control, in which calves were not treated. Calves were penned without fenceline contact to calves on the other treatment in replicated 0.42-ha grass pastures (24 pens), and cattle had ad libitum access to bermudagrass hay along with receiving a grain supplement to meet or exceed their nutritional requirements. Rectal temperatures were taken on d 0, 1, 7, and 14 after arrival. Calves were observed daily for signs of morbidity and a Clinical Illness Score (CIS 1 [normal] to 5 [morbid]) was recorded. Cattle that scored > 1 on the illness score and had a rectal temperature greater ≥ 40°C were treated with an antibiotic per a preplanned treatment protocol. If rectal temperature ≥ 40°C persisted past first antibiotic post-treatment interval, cattle were re-treated according to pre-planned protocol. Body weights were similar across treatments throughout the duration of the study ($P \geq 0.22$). Calves treated with Zn had a lower ADG from d 7 to 28 and d 14 to 28 compared with the control ($P < 0.01$). Control calves tended to be treated with 3 antibiotics more often than Zn treated calves ($P = 0.06$). Overall treatment antibiotic costs did not differ across treatments ($P = 0.64$). There were no differences ($P \geq 0.10$) for rectal temperature of calves across treatment. The prevalence of bacterial pathogens were not different across treatments ($P \geq 0.24$) except the presence of *P. aeruginosa* which tended to be greater in the control compared with the Zn treated calves ($P = 0.08$). From the results of this study, calves treated intranasally with Zn showed no differences in overall performance and minimal differences in morbidity compared with the control.

Key Words: bovine respiratory disease, morbidity, Zn

0249 Performance and net energy in High and Low RFI beef cattle on restricted intake. K. C. Dykier and R. D. Sainz*, [1]*University of California, Davis.*

To determine how beef cattle with known residual feed intake (RFI) phenotypes would perform under restricted feeding, 36 weaned Angus cross beef calves (24 steers and 12 heifers) were selected from a group of 98 calves that had been previously phenotyped for RFI. High and Low RFI animals (24 steers and 12 heifers) were subjected to a 52-d feeding trial with intake limited to 1.5% of BW. Feed offered and refused were measured daily, BW was taken at 14-d intervals, and ultrasound measures (LM area and subcutaneous fat over the 12th–13th ribs) were taken at the beginning, middle and end of the trial. After 52 d of intake restriction, RFI groups had similar BW, ADG, DMI, RFI and G:F. Fat gain, protein gain, and estimated recovered energy (RE) were similar between groups, although High RFI cattle had 0.26 cm more subcutaneous rib fat than Low RFI ($P = 0.01$). High RFI cattle also had more rib fat at the start of restricted feed trial. RFI groups did not differ in estimated heat energy (HE) or maintenance requirement (NEm; $P > 0.10$). Heifers had lower HE than steers ($P < 0.01$). All cattle had lower ADG, RE, NEm and HE in response to limited feed. Overall HE was reduced from 0.26 Mcal/kg$^{0.75}$ on ad libitum feeding to 0.16 Mcal/kg$^{0.75}$ on the restricted level of intake. The difference in HE from ad libitum to restricted feeding was −47 and −28% in High and Low RFI cattle, respectively ($P < 0.01$). Estimated NEm requirement was reduced from 0.095 to 0.073 Mcal/kg$^{0.75}$ overall, with a difference of −39% and +14% ($P < 0.01$) in High and Low RFI cattle, respectively. Estimated NEm requirement changed by −32% and +7% ($P = 0.004$) in heifers and steers, respectively. These results indicate that when limited, both High and Low RFI cattle lower their maintenance requirement and heat production to similar levels, although High RFI cattle had higher HE and NEm during ad libitum

Table 0249.

Table 1. Performance and net energy of RFI groups in response to diet restriction.

	RFI		Sex			P value		
Trait	High	Low	H	S	SD	RFI	Sex	RFI x Sex
Initial BW, kg	454.4	440.2	443.2	456.2	49.2	0.42	0.31	0.80
Final BW, kg	507.2	487.9	487.3	507.8	57.0	0.35	0.32	0.73
ADG, kg/d	1.015	0.917	0.940	0.993	0.210	0.87	0.49	0.51
DMI, kg/d	5.98	6.10	5.50	6.57	0.463	0.49	< 0.001	0.92
Gain:feed	0.171	0.152	0.171	0.152	0.035	0.14	0.15	0.63
RFI, kg/d	-0.242	-0.121	-0.717	0.354	0.464	0.47	< 0.001	0.94
Ribeye area, cm^2	80.19	80.54	76.79	83.94	7.74	0.90	0.014	0.41
12^{th}-13^{th} rib fat, cm	1.26	0.97	1.18	1.05	0.212	0.001	0.099	0.069
Fat gain, kg/d	0.37	0.28	0.32	0.33	0.18	0.15	0.79	0.15
Protein gain, kg/d	0.12	0.12	0.12	0.13	0.04	0.92	0.60	0.59
Fat:protein in gain	3.33	2.23	2.91	2.65	2.34	0.08	0.66	0.10
RE, Mcal/d	4.16	3.32	3.64	3.84	1.60	0.13	0.73	0.16
RE, Mcal/$kg^{0.75}$	0.043	0.036	0.039	0.040	0.014	0.16	0.85	0.11
HE, Mcal/d	13.68	14.86	12.76	15.78	2.38	0.07	< 0.001	0.25
HE, Mcal/$kg^{0.75}$	0.147	0.163	0.141	0.169	0.028	0.13	0.007	0.37
NEm, Mcal/$kg^{0.75}$	0.065	0.081	0.063	0.082	0.03	0.10	0.063	0.20

feeding. Furthermore, heifers may be better equipped than steers to adapt maintenance requirement and heat production in response to limited feed.

Key Words: efficiency, net energy, residual feed intake

0250 Effects of the EPNIX® beef program on feedlot performance in diets containing no Monensin or Tylosin. V. B. Holder[*1], J. S. Jennings[2], and R. S. Swingle[3], *[1]Alltech Inc., Nicholasville, KY, [2]Texas A&M AgriLife Research and Extension Center, Amarillo, [3]Cactus Feeders, Amarillo, TX.*

This study was conducted to compare growth performance, health and carcass characteristics of beef steers fed diets containing EPNIX® products (Alltech Inc., EPNIX) with steers fed control (CON) diets formulated using conventional sources of trace minerals and common feed additives. One thousand six hundred eighty crossbred steers (Initial BW = 347.9 ± 23.7 kg) were used in a randomized complete block design with 2 treatments (CON and EPNIX) and 12 pens per treatment. Pen was the experimental unit. CON diets contained trace minerals from mostly inorganic sources plus monensin and tylosin. EPNIX diets contained organic trace minerals, yeast and bacterial preparations, but not monensin or tylosin. Both treatments were fed diets containing ractopamine hydrochloride at the end of the feeding period. EPNIX products tended to increase DM intake (9.95 vs. 10.12 kg/d, $P = 0.086$), but there were no differences between treatments in final BW, ADG or feed efficiency ($P \geq 0.145$). Carcasses from steers on the EPNIX treatment were 6.4 kg heavier (409.7 vs. 416.1, $P = 0.015$) than CON steers and dressed yield was 0.5 units higher (64.4 vs. 64.9%, $P < 0.001$). Final BW adjusted to a common dressed yield was higher for EPNIX steers ($P \leq 0.038$), as was carcass-adjusted ADG ($P \leq 0.033$). Carcass adjusted feed efficiency did not differ between treatments. Differences in health parameters between treatments were not remarkable. Marbling score and quality grade distributions were not remarkably different between treatments ($P \geq 0.019$). Calculated yield grade was lower (leaner) for EPNIX than CON carcasses (3.30 vs. 3.15, $P = 0.049$) due to heavier carcass weight and larger LM muscle area (92.5 vs. 96.3 in^2, $P < 0.001$). Liver abscess prevalence was higher for steers on EPNIX relative to CON (13.6 vs. 26.5%, $P < 0.001$), but measures of liver abscess severity did not differ between treatments. Differences in meat quality parameters were not remarkable. These results demonstrate that cattle may be fed successfully with EPNIX® products fed in lieu of monensin and tylosin, although liver abscess prevalence would be a concern. The increased dressed yield and heavier carcass weights for steers on the EPNIX treatment suggests a possible role of EPNIX products to improve carcass weight transfer.

Key Words: antibiotics, carcass

0251 Natural dry matter intake fluctuation impacts performance, feeding behavior and rumen morphometrics of feedlot cattle: 10 yr of data assessment. G. D. Cruz[*1], I. C. Pereira[2], D. D. Millen[3], M. D. Arrigoni[2], C. L. Martins[2], and C. F. Costa[2], *[1]Cargill Animal Nutrition, Elk River, MN, [2]São Paulo State University (UNESP), Botucatu, Brazil, [3]São Paulo State University (UNESP), Dracena, Brazil.*

This study aimed to evaluate the impact of natural DMI fluctuation on performance, carcass characteristics, feeding behavior,

blood metabolic profile and rumen morphometrics of feedlot cattle. All 10 experiments used for this analysis were conducted at the feedlot research station (São Paulo State University, Botucatu, Brazil campus) from 2006 to 2015. Data were collected from 838 yearling bulls fed high-concentrate diets in group pens (3 or 4 animals per pen; $n = 238$ pens). Pens were considered the experimental unit for this study. Daily DMI fluctuation was calculated for each pen as the difference in intake between consecutive days. Daily DMI fluctuation was expressed as variation according to the following formula: DMI fluctuation in kilograms/DMI of the previous day in kilograms × 100. The final data from each pen represented the average daily DMI fluctuation for the entire feeding period. Based on the overall median of DMI fluctuation of 5.62%, cattle were classified into two groups: high- or low-fluctuation. All data analysis was performed in R using a mixed model approach where pens and years were random variables and fluctuation group was considered as fixed. The low and high fluctuation groups presented a DMI fluctuation average of 4.79% and 6.74%, respectively. Low fluctuation group performed better than high fluctuation one, with greater ADG (1.45 kg vs. 1.39 kg; $P = 0.05$), DMI (9.16 kg vs. 8.89 kg; $P = 0.06$), total weight gain (143 kg vs. 137 kg; $P = 0.08$), LM area daily gain (0.18 cm^2 vs. 0.16 cm^2; $P = 0.03$), and lower shear force (4.71 kg vs. 5.41 kg; $P = 0.03$). In terms of feeding behavior, low fluctuation group spent more time ruminating (341 min vs. 322 min; $P = 0.04$), less time resting (893 min vs. 917 min; $P = 0.06$) and visited the water trough less often (6.6 visits vs. 7.4 visits; $P = 0.04$). No effects of DMI fluctuation was observed ($P > 0.10$) on blood metabolic profile, rumenites incidence and rumen morphometrics. This multiannual evaluation illustrates the severe impact of an apparent small DMI intake fluctuation on feedlot performance and raises even more awareness to bunk management and proper nutrition.

Key Words: feedlot, intake fluctuation, performance

0252 Effect of total replacement of trace minerals with Bioplex® proteinated minerals on the health and performance of lightweight, high-risk feedlot cattle.

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This study was conducted to compare growth performance, health and carcass characteristics of lightweight beef steers fed diets containing traditional trace mineral supplementation (CON) with steers fed diets containing only proteinated forms of Zn, Cu, Co and Mn (BIOPLEX). Eight hundred one lightweight crossbred beef steers (Initial BW = 139 ± 4.3 kg) were used in a randomized complete block design with 2 treatments (CON and BIOPLEX) and 12 pens per treatment. Pen was the experimental unit. CON diets contained trace minerals from mostly inorganic sources. BIOPLEX diets were reformulated to replace all supplementary sources of Zn, Cu, Co, and Mn with proteinated forms of these minerals (Bioplex®, Alltech Inc.). Diets were formulated to provide equal total mineral concentrations in the ration. There were no significant differences between treatments in dry matter intake, gain or feed efficiency. Numerical improvements in both average daily gain and dressing percentage resulted in a tendency for increased hot carcass weight in BIOPLEX diets (357.2 vs. 366.0 kg, $P = 0.10$). Morbidity was not affected by treatment but mortality was reduced by 57% on the BIOPLEX treatment (4.78 vs. 2.05%, $P = 0.03$), driven by a 69% reduction in mortality due to respiratory causes (3.28 vs. 1.02%, $P = 0.016$). Carcass composition, quality and yield grades were unaffected by treatment. In this study, total replacement of the trace minerals Zn, Cu, Co and Mn with proteinated forms reduced mortality from respiratory disease and tended to improve carcass weight. Total replacement with proteinated forms of trace minerals may play a role in supporting the production and health of high risk, light weight feedlot cattle.

Key Words: carcass, chelate, respiratory

0253 The effect of frequency of supplementing rumen protected unsaturated fatty acids on blood serum fatty acid profiles in beef heifers and lactating cows.

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The objective of this study was to determine frequency of supplementation of rumen protected fat (RPF; ESSENTIOM) influences circulating serum fatty acids (FA) in beef heifers and lactating cows. In experiment 1, 12 early gestation beef heifers were supplemented 0.5 kg corn gluten feed (CGF) daily during a 2-wk adaptation period. During the last 3 d of adaptation, blood samples were collected immediately before supplementation, then 8 and 16 h post-supplementation daily. Each heifer was then randomly assigned to one of 3 supplementation frequency treatments of RPF (3, 5, or 7 d/wk) for 3 wk in a Latin square design with 3 periods, with each treatment receiving the same amount of RPF and CGF per wk (1 and 2.7 kg respectively). Blood samples were collected during the final 3 d of each supplementation period as in adaptation period. In experiment 2, 18 Angus crossbred cows in early lactation were supplemented 4.54 kg CGF weekly either at 3, 5, or 7 d/wk during a 2-wk adaptation period. Blood samples were collected during the last 3 d of adaptation as in experiment 1. For the subsequent 3 wk, RPF was added to the CGF supplement so that each supplementation frequency received 1.59 kg/wk of RPF. Blood samples were collected during the last 3 d of supplementation as in experiment 1. Serum FA profiles on a random subsample of 8 heifers in experiment 1

and all animals in experiment 2 were determined via GC and values were analyzed using the MIXED procedure of SAS. In experiment 1, serum concentrations of C18:2 and total FA were increased during supplementation compared with during adaptation (trt*time, $P \leq 0.04$). However, there were no differences between supplementation frequencies within a day*time period. In experiment 2, serum concentrations of C18:2 and total FA were increased with RPF supplementation compared with adaptation (trt*time, $P \leq 0.01$). There was a tendency ($P < 0.1$) for the 7 d/wk frequency to have greater concentration of C18:2 and total FA for some of the first 24 h of the sampling period compared with the other 2 frequencies in experiment 2. These results demonstrate that supplementation of RPF during early gestation or lactation increased serum FA profiles of beef heifers and cows. However, these increases in serum FA may be altered dependent on the frequency of RPF supplementation in lactating cows but not heifers.

Key Words: rumen protected fat, serum fatty acids, supplementation frequency

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0254 Economic viability of supplementation during the rainy season for growing water buffaloes.

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The aim of this study was to evaluate the economic viability of the use of supplementation during rainy season for growing water buffaloes. Twenty buffaloes [Murrah water buffalo, non-castrated males; 10 ± 1 mo of age; 206 ± 29 kg initial body weight (BW)] in growing phase on rotational stocking system (*Urochloa brizantha* cv. Xaraés; 3.36 ha) were used. Animals were randomly assigned by BW and divided into two treatments to receive supplementation (0.6% BW; corn, urea and mineral salt; $n = 10$) or not (control; $n = 10$). Body weight was measured at the beginning and the end of the rainy season (180 d of experiment) to determining total gain (TG) and average daily gain (ADG). Economic viability was demonstrated by the items: cost/steer, cost/kg gain, income/steer, profit/steer, and profitability per hectare. Data were analyzed with PROC MIXED in SAS. No treatment effects ($P = 0.64$) were detected for initial BW (202.45 vs. 208.75 kg for supplement and control treatments, respectively). Supplement treatment had greater final BW ($P = 0.03$), TG ($P < 0.01$), ADG ($P < 0.01$), cost/steer ($P = 0.03$), income/steer ($P < 0.01$) and profit/steer ($P < 0.01$) than control treatment (338.63 vs. 301.86 kg for final BW; 136.18 vs. 93.11 kg for TG; 0.76 vs. 0.52 kg for ADG; \$225.77 vs. \$196.83 for total cost/steer; \$317.42 vs. \$217.03 for income/steer; \$91.65 vs. \$20.20 for profit/steer, for supplement and control treatments, respectively). Supplement treatment showed lower cost/kg gain ($P = 0.01$) than control treatment (\$3.10 vs. \$4.06, respectively). For profitability per ha, supplement treatment had higher value ($P < 0.01$) than control treatment (\$1221.58 vs. \$267.39, respectively). For stocking density, supplement treatment tended ($P = 0.06$) to have higher rate than control treatment [6.77 vs. 5.47 AU/ha (1 AU = 450 kg of BW), respectively]. In conclusion, supplementation strategy during the rainy season is a viable and profitable option for water buffaloes in growing phase. Supported by FAPESP #2014/06446–3.

Key Words: economic viability, supplementation, water buffalo.

0255 Subclinical ketosis prevalence in Nellore beef cows during the breeding season in Brazil did not affect pregnancy rate.

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Ketosis is a metabolic disease that affects the cattle production, therefore causes significant effects on the animal's metabolism and consequently decrease of animal production. Animals with negative energy balance may be committed by ketosis, with the subclinical form as the most common manifestation. The aim of this study was to evaluate the prevalence of subclinical ketosis (SK) in Nellore beef cows during the breeding season. Ninety-six females, 50 multiparous, and 46 primiparous, housed in a rural company in the state of Minas Gerais, Brazil, were evaluated between January and May of 2015. All cows were managed on a pasture system, composed of *Brachiaria brizantha*, with free access to water and mineral supplementation. For all animals, a protocol for estrus synchronization was performed, resulting in all animals being inseminated on the same day. Before insemination, blood levels of β-hydroxybutyrate (BHBA) were recorded by sampling a drop of blood from the tip of the tail, and adding the sample to a Optium Xceed portable device (Abbott Diabetes Care, Doncaster, Australia) for measurement of BHBA. Animals with BHBA concentration above 1200 mmol/L in the blood were classified as with SK. Visual inspection was also done to assess body condition score (BCS), using a scale of 1 to 5 as recommended by Spitzer (1986). After 60 d from the artificial insemination, animals were tested for pregnancy status. Prevalence of subclinical ketosis was on average 34% (33/96), being 32.61% (15/46) in primiparous and 36% (18/50) in multiparous. There was no effect of SK on the pregnancy rate ($P > 0.05$) for both primiparous and multiparous cows. The overall pregnancy rate was 35.41% (34/96), being 36.36% (12/33) in animals with SK and 34.93% (22/63) without SK ($P > 0.05$). In primiparous cows, the pregnancy rate was 10.8% (5/15) in animals with SK and 19.5% (9/31) in animals without SK, but in multiparous, the pregnancy rate was 14.0% (7/18) in animals with SK and 26.0% (13/32) without SK. There was an effect of the BCS on

the occurrence of SK ($P < 0.001$), in which animals with BCS above 3 had 21.42% (6/28) of SK and animals with BCS below 3 had 39.70% (27/68). In conclusion, the prevalence of SK observed in Nellore beef cows in Brazil was high, but did not affect pregnancy rate. As expected, animals with lower BCS had higher prevalence of SK.

Key Words: subclinical ketosis, pregnancy rate, Nellore cows

0256 Effects of breeding system of origin (natural service or artificial insemination) on pregnancy rates, distribution of calving, and calf weaning weights of commercial beef cow herds in North Dakota.

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Objectives of this study were to compare pregnancy rates, calving distribution, and calf weaning weights of commercial beef cows exposed to two different breeding systems. Producers recruited ($n = 10$) had never implemented estrus synchronization and AI into their reproductive management plan. Within each herd, cows were randomly assigned to one of two breeding system treatments: (1) only exposed to natural service herd bulls (NS; $n = 1{,}122$) or (2) exposed to ovulation synchronization and fixed-time AI followed by natural service bulls (TAI, fixed-time AI; $n = 1284$). Production, performance and profit outcomes were evaluated within/across herds for each breeding system. Females exposed to TAI were exposed to 7-d CO-Synch + CIDR protocol with fixed-time AI at 60–66 h after CIDR removal. Clean-up bulls were placed in breeding pastures 1 d after AI and remained with females until the end of the producer defined breeding season. Presence of a viable fetus was determined at least 45 d after the conclusion of the breeding season. At parturition, birth date was recorded. No differences ($P = 0.54$) were observed in the proportion of females pregnant at the end of the breeding season between NS (93.1%) and TAI (93.2%) treatments. Cows in the TAI treatment calved 7.8 d earlier ($P < 0.001$) in the calving season compared with NS cows. A greater proportion ($P < 0.01$) of TAI cows (44.8%) gave birth in the first 21 d of the calving season compared with NS cows (26.0%). From d 22 to 42 a greater proportion ($P < 0.01$) NS cows (41.6%) gave birth compared with TAI cows (28.2%), and a greater proportion of NS cows (23.7%) gave birth from d 42 to the end of the calving season compared with TAI cows (17.2%). A treatment x calving group interaction was present for weaning weight. Greater ($P < 0.01$) weaning weights were observed for calves born from TAI cows in the first 21 d of the calving season (269.3 ± 1.82 kg) compared with NS born calves (257.6 ± 2.65 kg). Weaning weights of calves born to TAI and NS cows in the second 21 d and from d 42 to the end of the calving season were similar ($P = 0.17$). Use of TAI in commercial beef herds increased the number of calves born earlier in the calving season and increased the weaning weights of calves.

Key Words: AI, beef cattle, breeding systems, natural service

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0257 Resynchronization for sequential timed artificial insemination.

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Increasing the number of pregnancies resulting from AI has a positive impact on the profitability of a beef cattle operation. However, subsequent AI after timed insemination is currently limited by distribution of return to estrus for non-pregnant females precluding a second timed insemination. The objective of this study was to determine if resynchronization in beef cattle for a second timed AI, without knowledge of individual female pregnancy status to the first timed insemination, is a viable management tool. Beef cows ($n = 140$) and heifers ($n = 45$) were allotted to 2 study groups: (1) single synchronization and timed AI (SS; $n = 67$ cows, 22 heifers) and (2) consecutive synchronization and timed inseminations (RS; $n = 73$ cows, 23 heifers). Both groups were simultaneously subjected to the 7-d CO-Synch + CIDR protocol for the initial timed insemination. Briefly, CIDR®s were inserted on d −9 with an injection of GnRH. On d −2, CIDRs were removed and an injection of $PGF_2\alpha$ was administered. Timed AI and an injection of GnRH occurred on d 0. For RS, CIDR®s from the first synchronization protocol were re-inserted on d 14. The CIDR®s were removed on d 21 and estrus detection patches were applied. All cattle with activated estrus detection patches were re-inseminated 72 h after CIDR removal (d 24). Pregnancy was determined via trans-rectal ultrasonography on d 54 to identify cows that conceived to the first or second insemination (based on fetal size) or failed to conceive. Interactions of parity, AI technician, or sire with treatment on pregnancy rate were not detected. Pregnancy rate to the first timed AI did not differ ($P = .49$) between SS and RS groups (66% (59/89) and 61% (59/96), respectively). Re-synchronization yielded 15 additional AI pregnancies, resulting in overall RS AI pregnancy rate of 77% (74/96). Overall pregnancy rate to AI tended ($P = 0.10$) to be greater in the RS than SS group (77% vs. 66%, respectively). This method of resynchronization for a second timed AI may be a useful management tool to increase pregnancy rates during a breeding season. Additionally, it would accommodate scheduling AI technicians where they might not otherwise be available to breed on natural return to estrus. Further analysis of the economic viability of this particular

approach is warranted.

Key Words: beef cattle, estrous synchronization, timed AI

0258 Impact of diet on the behavior of limit-fed beef cows in drylots. C. L. Daigle*[1], J. R. Baber[1], J. E. Sawyer[2], and T. A. Wickersham[1], *[1]Texas A&M University, College Station, [2]Department of Animal Science, Texas A&M University, College Station.*

Providing cattle with opportunities to interact with their environment while in feedlots may impact time allocation and influence space use. Mid- to late-gestation cows ($n = 96$) were stratified by body weight, BCS, age, and days in gestation and randomly assigned to one of 12 pens (8 cattle/pen; 4 pens/treatment). Each pen was randomly assigned to one of three treatments: HAY (cattle had ad libitum access to Bermudagrass hay), HC (limit-fed concentrate in the morning and forage 12 h later), and TMR (limit-fed a total mixed ration once in the morning). Limit-fed treatments, HC and TMR, were fed a diet of wheat straw (35%), cracked corn (29%), dried distillers' grains (27%), and premix (9%) formulated to contain 1.58 Mcal NE_m/kg and fed to deliver 80% of NRC predicted NE_m requirements. After cattle had been exposed to these treatments for 105 d, behavioral observations recorded the number of cattle performing each posture (stand, lie, walk) and behavior (feed, drink, ruminate, rest), as well as the number of cattle within 1 m of the feed bunk using 10-min instantaneous scans. A Generalized Linear Mixed model (PROC MIXED) evaluated the impact of treatment on cattle posture and behavior. Least squared means with a Tukey-Kramer adjustment identified differences among the 3 treatments. Treatment did not impact the number of cattle standing, walking, lying, or drinking ($P > 0.05$). More cattle were observed feeding in HAY ($t_9 \leq 13.7$, $P < 0.01$) compared with HC and TMR (2.76 vs. 0.18 and 0.39). More cattle rested in HC and TMR ($t_9 > -12.7$, $P < 0.01$) than HAY (5.72 and 5.63 vs. 3.20). More cattle ruminated in HAY than TMR (1.18 vs. 0.64; $t_9 = 3.2$; $P = 0.03$), and HC tended to ruminate more than TMR (0.98 vs. 0.64; $P = 0.09$). More cattle were observed resting in HC and TMR than in HAY (6.02 and 6.17 vs. 3.45; $t_9 \leq -12.6$, $P < 0.01$), and HAY spent more time less than 1 m of the feeder than cattle in HC or TMR (3.46 vs. 1.23 and 1.05; $t_9 \leq 3.5$, $P < 0.05$). Cattle provided with hay ad libitum rested less and engaged in more feeding and ruminating. By spending more time at the feeder, hay-fed cattle may use pen space more intensely than others which could impact pen management.

Key Words: behavior, diet, drylot

0259 Newborn beef calves benefit from supplementation of vitamins D and E. C. D. Nelson[1], M. Poindexter*[2], J. L. Powell[2], J. V. Yelich[2], S. L. Bird[3], and R. L. Stuart[4], *[1]University of Florida, Gainesville, [2]Department of Animal Sciences, University of Florida, Gainesville, [3]University of Minnesota, Grand Rapids, [4]Stuart Products Inc., Bedford, TX.*

The objective of this study was to determine the effects of injectable vitamins A, D, and E on fat-soluble vitamin status of beef calves. Sixteen Angus calves from a herd in Minnesota and 17 Angus and Brangus calves from a herd in Florida born in March were randomly assigned to receive no treatment or subcutaneous injection of VITAL-E® Newborn (Stuart Products Inc.; 50,000 IU retinyl-palmitate, 50,000 IU vitamin D_3, and 500 IU *RRR*-α-tocopherol/mL of product). Minnesota calves received either no treatment (CON, $n = 8$) or 5 mL subcutaneous injections of VITAL E-Newborn (ADE, $n = 8$) within 24 h of birth and serum samples were collected at 0, 2, 7, 50, and 210 d of age. Florida calves received either no treatment ($n = 7$) or 4 mL of VITAL E-Newborn ($n = 9$) within 24 h of birth and serum samples were collected at 0, 25, 50, and 180 d of age. Serum retinol concentrations were not affected by treatment, but retinyl-palmitate was greater at 2 d of age in the Minnesota ADE vs. CON calves (646 ± 204 vs. 20 ± 1 ng/mL). In contrast, serum 25-hydroxyvitamin D (25(OH)D) concentrations of the Minnesota ADE calves increased from 8.4 ± 1.3 ng/mL at birth to 61.7 ± 3.6 ng/mL at d 7, compared with 5.5 ± 1.3 at birth and 9.8 ± 4.6 at d 7 in CON calves ($P < 0.001$). Serum 25(OH)D of Florida ADE calves increased from 9.9 ± 3.3 ng/mL at birth to 36.2 ± 3.9 ng/mL at d 25, compared with 5.4 ± 3.5 and 19.7 ± 4.8 ng/mL in CON calves ($P < 0.05$). Serum 25(OH)D was still elevated at 50 d of age in ADE calves in both herds ($P < 0.01$; ADE = 38.8 ± 2.3 ng/mL vs. CON = 29.4 ± 2.5 ng/mL), but was the same at weaning near 50 ng/mL. Serum α-tocopherol increased in Minnesota ADE calves from 1.0 ± 0.5 μg/mL at birth to 6.8 ± 0.5 and 5.3 ± 0.5 μg/mL at d 2 and 7, respectively, compared with 0.6 ± 0.5, 1.3 ± 0.5, and 2.4 ± 0.5 μg/mL in Minnesota CON calves at 0, 2, and 7 d of age, respectively ($P < 0.001$). Serum α-tocopherol was similar between Florida ADE and CON calves with averages near 0.8 μg/mL at birth and 2.5 μg/mL at 25 d of age. In conclusion, supplementation of newborn beef calves with VITAL-E Newborn increases serum 25(OH)D and α-tocopherol concentrations and overcomes deficiences in vitamins D and E of the young calf.

Key Words: beef calves, fat-soluble vitamins

0260 Functional SNP in a polygenic disease induced by high-altitude in fattening Angus steers using systems biology approach. A. Cánovas[*1], R. Cockrum[2], D. Brown[3], S. Riddle[3], J. M. Neary[4], T. N. Holt[5], J. F. Medrano[6], A. Islas-Trejo[6], R. M. Enns[7], S. E. Speidel[7], K. Cammack[4], K. R. Stenmark[8], and M. G. Thomas[7], *[1]University of Guelph, ON, Canada, [2]Virginia Polytechnic Institute and State University, Blacksburg, [3]University of Colorado, Denver, [4]Colorado State University, Fort Collins, [5]College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, [6]University of California, Davis, [7]Department of Animal Sciences, Colorado State University, Fort Collins, [8]University of Denver, CO.*

High-altitude (> 1800m) disease is a challenging problem in beef and dairy cattle. The disease is consequential of hypoxia-induced right ventricular (RV) heart failure as per vascular inflammation of the pulmonary artery (PA) and hypertension. The disease has moderate to high heritability ranging from 0.2 to 0.4; however, minimal information exists of the genes involved. The transcriptomes of six tissues (i.e., left and right ventricle, pulmonary artery, aorta, muscle, and lung) were examined in samples harvested from fattening-yearling Angus steers phenotyped to be of low or high pulmonary arterial pressures (LPAP and HPAP; n = 10/group). Tissue specific splice variants were identified in RV (n = 555), aorta (n = 547) and PA (n = 152; $p < 0.01$ FC > 2) between LPAP and HPAP animals. Most of the splice variants are located in key regulators genes with roles in angiogenesis and cardiomyopathy (NFATC1), movement of leukocytes and neutrophils (OLR1, PLAUR), failure of heart (CTGF), hypertrophy of heart ventricle (TREM1, GATA2) and vascularization (SYVN1). Besides, several SNP variants segregated specifically in either the LPAP or HPAP animals. Among them, 139 SNP were located in key regulator genes involved in the adaptation of high altitude disease. These approaches helped identify splice variants corresponding to key regulator genes in a polygenic disease induced by high-altitude in Angus cattle. The identification of functional SNP associated with high-altitude disease by combining structural and functional genomic data will help to develop more robust approaches for genetic selection in beef cattle.

Key Words: beef, health, genomics, systems biology, RNA-sequencing, functional SNP

0261 Factors affecting timing and intensity of calving season of beef cow-calf producers in the Midwest. C. E. Andresen[*1], P. J. Gunn[1], and L. L. Schulz[2], *[1]Department of Animal Science, Iowa State University, Ames, [2]Department of Economics, Iowa State University, Ames.*

Despite demonstrated market incentives to adopt controlled calving seasons, many producers still have herds that calve somewhat broadly throughout the year. We postulate this observed management behavior is related to a variety of factors. Primary data, collected through a coordinated survey effort with U.S. Department of Agriculture's National Agricultural Statistics Service, were used to quantify factors that affect producers' decisions regarding timing and intensity of calving season. Descriptive statistics were generated using the surveymeans procedure of SAS, and the surveyreg procedure was used to conduct a regression analysis. Of the survey respondents, 88% were commercial producers and 12% were seedstock producers or operated a combination seedstock/commercial operation with an overall average of 63 beef cows. Ninety-seven percent, 50%, 33%, and 26% of farms calve in the spring (March, April, May), summer (June, July, August), fall (September, October, November), and winter (December, January, February), respectively. Twenty-two percent observed a calving season exclusively in the spring. Sixty-six percent of respondents indicated calving season was dictated by weather, 34% because of labor availability, and 31% because of tradition. Least often reasons for calving season were market timing (16%), feed availability (8%), and other (4%). Producer-stated reasons for calving season explained 62% of the variation in timing and intensity of calving on an operation, whereas a model of producer demographic and operation characteristics explained 83% of the variation. These results highlight the importance of evaluating producer and operation characteristics in addition to producer input when making recommendations to enhance production efficiency and profitability. Furthermore, understanding the factors which impact calving season provides opportunities for improved Extension and research programming.

Key Words: beef, calving season, survey

0262 Effects of feeding NaturSafe on performance, carcass characteristics, and liver abscesses in finishing beef heifers at a commercial feedlot. M. F. Scott[*1], K. L. Dorton[1], D. L. Henry[1], C. R. Belknap[1], and B. E. Depenbusch[2], *[1]Diamond V, Cedar Rapids, IA, [2]Innovative Livestock Services Inc., Great Bend, KS.*

With the mandatory implementation of VFD on the horizon, as well as retailer and consumer demands for reduced antibiotic usage, cattle feeders are considering other technologies that can mitigate liver abscesses and maintain growth performance

when standard industry technologies are removed from the diet. In this study, cross-bred heifers (N = 1495; 359 ± 3.4 kg) were utilized in a randomized complete block design at a commercial feedlot to determine the effects of a *Saccharomyces cerevisiae* fermentation product (NaturSafe, Diamond V, Cedar Rapids, IA) on performance, carcass characteristics, and liver abscesses when monensin, tylosin, and direct fed microbials (DFM) were not included in the diet. Upon arrival, heifers were allowed ad libitum access to water and long-stemmed hay. During processing, they received a feedlot tag and growth implant, and were vaccinated and treated for parasites. Heifers were then blocked by arrival BW and randomly assigned to one of 2 treatments (10 pens/treatment, approximately 75 heifers/pen). Treatments consisted of a diet containing: (1) monensin, tylosin, and Bovamine Defend (positive control, PC) or (2) NaturSafe at 18 g/head/d without monensin, tylosin, and the DFM. Diets were fed twice daily with heifers receiving half of the daily dose of treatment in the TMR at each feeding. Pen BW were collected on d 0 and at harvest on d 125 and 146 (5 pens per treatment per day). Feed intake, morbidity and mortality were monitored daily. Cattle were vaccinated and implanted a second time approximately 74 d before harvest. Hot carcass weight, dressing percentage, quality grade, yield grade, percent kidney-pelvic-heart fat percentage, rib fat thickness, rib-eye area, marbling score and liver abscess scores were determined. Performance, carcass characteristics and liver abscess scores were analyzed using the MIXED procedure of SAS with pen as the experimental unit. Performance, carcass characteristics, morbidity and mortality were similar (P > 0.05) between treatments. Heifers fed NaturSafe had a numerically lower (P = 0.11) incidence of liver abscesses compared with PC (14.5% vs. 19.3%, respectively) with fewer (P = 0.02) livers condemned that had less severe (i.e., A-) abscesses (3.3% vs. 6.9%, respectively). Results from this study suggest that NaturSafe has the potential to reduce liver abscesses and maintain growth performance when standard industry technologies like monensin, tylosin, and DFM are removed from conventional production diets.

Key Words: *Saccharomyces cerevisiae*, fermentation product, cattle, performance

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0263 Inclusion of exogenous enzymes in creep feeding rations for nursing beef calves. J. M. Lourenço[*1], B. T. Campbell[2], N. DiLorenzo[3], and R. L. Stewart, Jr.[1], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, [2]DSM Nutritional Products, Parsippany, NJ, [3]University of Florida, North Florida Research and Education Center, Marianna.*

An in vitro experiment was performed to investigate if some exogenous enzymes customarily used in rations of monogastric animals would be effective when included in a creep feed (CF) for nursing beef calves. The chosen enzymes were included in experimental treatments both individually and in combination with other enzymes. The treatments consisted of: (1) Bermuda grass (BER); (2) a mixture of 75% Bermuda grass and 25% CF (BERCF); (3) BERCF enhanced with xylanase (XYL); (4) BERCF enhanced with β-1,3-glucanase (BGLUC); (5) BERCF enhanced with α-amylase (AMYL); (6) BERCF enhanced with a combination of xylanase, β-1,3-glucanase and β-1,4-glucanase (COMB1); or (7) BERCF enhanced with a combination of xylanase, β-1,3-glucanase, β-1,4-glucanase and α-amylase (COMB2). Two rates of inclusion of the enzymes were tested: the dose normally used in rations of monogastrics, and a dose 10 times greater (10x). Five replications per treatment were used. Incubations were performed for 24 h using rumen fluid collected by esophageal tubing from 6-mo-old nursing calves. Analysis of variance was conducted as a completely randomized design using fermentation bottle as the experimental unit with treatments and replications as factors. Digestibility of the ADF portion of the diet was lowest for BER, however, it was greater for BERCF, and it was maximal for BGLUC 10x (P = 0.02). Similarly, IVDMD was lowest for BER and highest for XYL 10x (P = 0.02). Production of acetate, propionate, and butyrate were all lowest for BER (P < 0.01). Total production of VFA was also minimal for BER, and it was greatest for COMB2 10x (P < 0.01). The acetate:propionate ratio was greatest for BER (P = 0.01). No differences were detected regarding molar proportion of propionate, however, molar proportion of butyrate was smallest for BER (P < 0.01). Total gas produced per g of incubated DM, and concentration of methane per L of gas were greatest for AMYL 10 (P < 0.01). Overall, the inclusion of the studied enzymes improved important traits such as IVDMD, ADF digestibility, and production of VFA. This indicates that nursing beef calves may benefit from the use of these enzymes, especially if they are included at rates greater than those found in diets of monogastric animals.

Key Words: creep feeding, exogenous enzymes, in vitro

0264 Body temperature and seminal characteristics in double and normally muscled senepol bulls in the tropics. I. Suero[1], E. Sanoguet[1], H. Sánchez[*1], J. Curbelo[1], A. Casas[1], T. Sonstegard[2], and M. Pagán-Morales[1], *[1]Department of Animal Science, University of Puerto Rico, Mayaguez, [2]Recombinetics Inc., St Paul, MN.*

Double muscled cattle present conformational differences in their carcasses that are highly attractive to the beef industry, including a greater yield of valuable muscles and lower adipose tissue accumulation. However, in the Puerto Rican Senepol cattle, which are highly adapted to the tropics, it is not known if such differences may affect thermoregulation or reproductive performance. Therefore, the present study compared rectal (RT) and scrotal [(ST); determined by infrared thermography at the proximal, medial, and distal regions of

the scrotum] temperatures, as well as sperm concentration, motility, and normality between 8 heterozygous double muscled (HM; MSTN NT821/WT) and 8 normally muscled (NM) Senepol bulls. All animals were homozygous SLICK (PRLR; chr20:39136558GC > G). Bulls were electro-ejaculated at d 55 and d 60 after a previous collection at d 1 (activation of spermatogenesis/sperm removal from epididymis) during a hot (HOT) and a cool (COOL) period with daily mean air temperature values of 30.0 and 28.8°C, respectively. Temperatures were recorded three times/d (0800, 1200, and 1500 h) during 5 d after d 1. Semen was analyzed using a Computer Assisted Sperm Analysis System (CASA) and a GLIMMIX procedure in SAS was used for the correspondent statistical analyzes. The HM bulls presented smaller scrotal circumferences ($P < 0.05$; HM: 36.12 cm vs. NM: 37.72 cm) and higher RT ($P < 0.05$; HM: 38.63°C vs. NM: 38.49°C) than the NM bulls. However, no differences in ST were observed between genotypes in any period ($P > 0.05$). Sperm concentration per cc of semen was lower in HM (460.04 x 10^6) than NM (837.32 x 10^6) in HOT ($P < 0.05$); however, no differences were observed in COOL ($P > 0.05$; 321.20 x 10^6 and 295.92 x 10^6 for HM and NM, respectively), with an imminent reduction in sperm concentration in both groups. In HM, the sperm motility was greater in COOL ($P < 0.05$), while total progressive sperm was greater in COOL for both groups ($P < 0.05$). The latter was also observed for normality ($P < 0.05$). The proportion of coil tail sperm was higher in HOT ($P < 0.05$) and HM showed more proximal cytoplasmic droplets overall in HOT (HM-HOT > NM-HOT > HM-COOL = NM-COOL). These results suggest that greater body temperatures could affect slick-double muscled Senepol cattle in terms of sperm concentration, maturation rate and motility, irrespective of the testicular size.

Key Words: motility, normality, sperm, Senepol

0265 Effects of summer and winter feeding of endophyte infected tall fescue seeds on average daily gain and activity of hepatic cytochrome P450 1A, 2C, 3A, aldo-keto reductase 1C, and uridine 5'-diphospho-glucuronosyltransferase in beef steers.

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The objective of this study was to investigate the effects of feeding endophyte-infected tall fescue seeds on ADG (kg/d) and activities of hepatic cytochrome P450 1A, 2C, 3A, aldo-keto reductase 1C, and Uridine 5'-diphospho-glucuronosyltransferase (UGT). Twelve Angus steers of 181 d of age and an average pre-weaning weight of 194.6 kg were blocked by initial BW at weaning. A control (KY32 or E–) and a treatment (KY31 or E+, 20 µg of ergovaline per kg of BW) were randomly assigned to animals within blocks ($n = 6$) by using Calan gates in two trials of 70 (summer 2015) and 56 d (winter 2016). Body weight was recorded on d 0 and every 14 d. Liver biopsies were collected before each trial and on d 3. Proteins in the S9 fractions were extracted into phosphate buffer and diluted to a concentration of 4000 µg/mL. Enzyme activity (RLU/min/mg of protein) was determined by a Promega Multi-Plus plate reader (Madison, WI) after incubation with specific substrates and detection reagents. Statistical analysis was performed by the GLIMMIX and FACTOR procedures of SAS 9.4 (SAS Institute Inc., Cary, NC) with statistical significance being determined at $P \leq 0.05$. In trial 1, E+ steers gained 0.323 kg/d less than E- steers ($P = 0.013$) between d 28 and d 70. Cytochrome 2C activity differed initially ($P = 0.042$) but did not on d 3 ($P = 0.675$). Cytochrome 1A and 3A activities were correlated ($r = 0.621$, $P = 0.042$). In trial 2, no treatment effect on ADG was found ($P = 0.435$). From d 28 to d 56, ADG increased consistently from 0.567 to 1.393 kg/d, whereas ADG remained similar ($P > 0.392$; 0.539 to 0.574 kg/d) in trial 1. Only initial UGT activity was 42% greater in E+ steers in trial 2. Cytochrome 1A and 2C activities were correlated ($r = 0.912$, $P = 0.002$). Other enzyme activities were similar in both trials ($P > 0.180$), and no treatment × d interaction on ADG was found ($P > 0.142$). Principal component analysis indicated that the activities of 1A, 2C, 3A, and 1C explained 65.88 to 66.41% of enzyme activity variances, whereas UGT activities explained the rest of the variances on d 3. Correlation coefficients of these two groups of enzymes with each principal component confirmed that they acted in separate pathways.

Key Words: beef, endophyte, tall fescue

0266 Relationships of neonatal beef calf birth weight and body size measures.

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Research investigating the effects of gestational nutrition or management on fetal development often use birth weight as the primary prenatal growth measure. Weight does not take skeletal size or shape into account and thus may not accurately assess many aspects of fetal growth. Our objective was to determine the relationship of weight and body size measures in neonatal beef calves. Calves were weighed within 16 h postnatal during a fall-calving ($n = 42$, Sim-Angus and Hereford) and spring-calving ($n = 47$, Sim-Angus) season. A flexible tape measure was used to record 5 body size measures for each calf. Crown to rump length (CRL) was defined as the length from poll to tailhead, whereas shoulder to rump length (SRL) was defined as the length from the neck-shoulder junction to tailhead, both following the spine. Heart girth was measured immediately posterior of the front legs and abdominal girth was measured at the umbilicus, both perpendicular to the spine. Cannon circumference was taken at the smallest point of 1 cannon bone. Ponderal index is used in human medicine to

assess body shape or tissue growth relative to skeletal growth. Calf ponderal index was calculated as birth weight (kg)/length $(cm)^3$ using either CRL (PI-CRL) or SRL (PI-SRL). Pearson correlations were determined for weight and body size measures. Birth weight had a weak positive correlation ($P \leq 0.06$) with CRL and SRL, moderate positive correlation ($P < 0.0001$) with heart girth and cannon circumference, and strong positive correlation ($P < 0.0001$) with abdominal girth. This suggests that birth weight is less related with body length than girth in neonatal calves. Birth weight had weak positive relationships ($P < 0.005$) with PI-CRL and PI-SRL, whereas CRL and SRL had strong negative relationships ($P < 0.0001$) with their corresponding ponderal index measures. Abdominal girth had a weak positive correlation with PI-CRL and PI-SRL, but heart girth was not correlated with either. Heart girth had a moderate positive correlation ($P < 0.0001$) with abdominal girth, CRL had a weak positive correlation ($P < 0.003$) with SRL, and PI-CRL had a weak positive correlation with PI-SRL. This suggests that length measures have more variation or potential for error. In summary, birth weight is weakly or moderately related to most body size measures in neonatal calves. Length, girth, and ponderal index measures can help to describe calf size and shape at birth, adding valuable information.

Key Words: calving, fetal growth, neonate

0267 Locomotor activity changes in the final 72 h prepartum in multiparous beef cows. S. M. Bolen[1], B. L. Vander Ley[2], K. N. Niederecker[1], and A. M. Meyer*[1], [1]*Division of Animal Sciences, University of Missouri, Columbia,* [2]*Department of Veterinary Medicine and Surgery, University of Missouri, Columbia.*

The objective of this study was to quantify changes in locomotor activity of multiparous beef cows during the final 72 h prepartum. IceQube activity monitors (IceRobotics, Edinburgh, UK) were placed above the left hind fetlock ($\geq$ 4 d prepartum) of 106 multiparous, spring-calving beef cows over 2 yr. Cows that were moved outside of their normal patterns during the 72 h prepartum were removed from the dataset, resulting in 63 cows to be used for analysis. Cows were housed in 18 × 61 m drylots during calving and allowed ad libitum access to hay or haylage in round bale rings placed in the drylots. Each cow's motion index, standing time, lying time, step count, and number of lying bouts were summed per hour using IceManager 2012 software. Motion index was calculated by the software using a proprietary algorithm. Hour 0 was defined as time of parturition (± 30 min). Data were analyzed by day (d −3 to d −1 prepartum), by 6-h period during the final 24 h prepartum, and by hour during the final 6 h prepartum using MIXED procedures of SAS. Motion index, standing time, step count, and number of lying bouts increased ($P < 0.001$), while lying time decreased ($P < 0.001$) on d −1 compared with d −2 or d −3 relative to parturition. In the 24 h immediately prepartum, the 6 h preceding parturition (−6 to 0 h) had greater ($P < 0.05$) motion index, standing time, step count, and number of lying bouts compared with the other 6-h periods before calving. There was no effect ($P = 0.19$) of 6-h period on lying time during the 24 h before parturition. Motion index increased ($P < 0.05$) from −6 to −4 h and remained steady from −4 h to 0 h. Cows had greater ($P < 0.05$) standing time and less ($P < 0.05$) lying time at 0 h compared with −5 and −6 h before parturition. Step count was greater ($P < 0.05$) from −3 to −1 h compared with −6 to −5 h. Number of lying bouts increased ($P < 0.05$) between −3 and −1 h and decreased ($P < 0.001$) from −1 h until calving. In conclusion, multiparous beef cow activity changes 4 to 6 h before parturition. These data suggest that electronic activity monitors can be used to recognize the earliest signs of parturition in beef cattle.

Key Words: activity, movement, parturition

0268 Impact of heifer development system on subsequent ADG and reproduction in two different breeding seasons. S. A. Springman*, H. R. Nielson, and R. N. Funston, *University of Nebraska, West Central Research and Extension Center, North Platte.*

A 4-yr study was conducted to determine the impact of heifer development system on subsequent growth and reproductive performance in 2 breeding seasons. In Exp. 1, March-born, crossbred (5/8 Red Angus, 3/8 Continental; $n = 225$) heifers were stratified by BW and randomly assigned to 1 of 2 post-weaning nutritional treatments (2 pastures·treatment^{-1}·yr^{-1}) from mid-January to mid-April. Heifers were offered ad libitum meadow hay (HAY) and 1.81 kg/d (29% CP, DM) supplement or allowed to graze meadow (MDW) and offered 0.45 kg/d supplement. Heifers were managed as a single herd before and following treatment. Heifers were synchronized with a single PG injection 5 d after being placed with bulls for a 45 d breeding season. HAY heifers had greater ($P = 0.01$) ADG during the treatment period than MDW heifers (0.77 vs. 0.51 ± 0.03 kg/d; HAY, MDW). At pregnancy diagnosis, HAY heifers tended to have greater BW compared with MDW heifers ($P = 0.06$; 377 vs. 367 ± 3 kg; HAY, MDW). Percent of mature BW before the breeding season was greater ($P = 0.02$) for HAY compared with MDW (58% vs. 55% ± 1%; HAY, MDW). Pregnancy rates were similar for HAY and MDW heifers ($P = 0.97$, 88 ± 4%). In Exp. 2, May-born, crossbred (5/8 Red Angus, 3/8 Continental; $n = 258$) heifers were stratified by BW and randomly assigned to HAY or MDW treatments. Similar to Exp. 1, heifers on HAY treatment had greater ($P = 0.01$) ADG during the treatment period (0.63 vs. 0.39 ± 0.03 kg/d; HAY, MDW), resulting in greater pre-breeding BW ($P = 0.02$) for HAY heifers compared with MDW heifers (320 vs. 305 ± 3 kg, respectively). At pregnancy diagnosis, BW was similar ($P = 0.16$) between treatments (368 vs. 356 ± 4 kg; HAY, MDW). Percent of mature BW before

the breeding season was greater ($P = 0.02$) for HAY (58%) compared with MDW (54%). Pregnancy rates were similar ($P = 0.44$) between treatments (72 vs. 68 ± 4%; HAY, MDW). Heifer development system did not impact pregnancy rate in the March or May replacement heifers; however, March heifer pregnancy rate was greater ($P < 0.01$) than May (87 vs. 70 ± 3%). The lower pregnancy rate in May heifers may be due to declining forage quality during the breeding season.

Key Words: beef heifer, calving date, heifer development

0269 Effect of castration method and analgesia on growth performance and carcass traits in feedlot cattle.

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Castration is a painful, yet routine management practice within the U.S. that is known to transiently decrease performance but the method of castration, provision of analgesia, or both may impact growth in feedlot cattle. Our objective was to determine the effect of castration timing (birth vs. feedlot entry), method (surgical vs. banding) and use of the analgesic meloxicam (**MEL**) on performance and carcass traits in feedlot cattle. This study was a randomized complete block design conducted over a 3-yr period. Single-source Angus × Hereford steer ($n = 42$) and bull ($n = 152$) calves were randomized at birth to 1 of 5 treatments arranged as a 2 × 2 + 1 factorial: (1) steers castrated near birth (**CON**), (2) bulls surgically castrated without MEL (**SUR**), (3) bulls surgically castrated with MEL (**SUR+MEL**), (4) bulls band castrated without MEL (**BAN**), and (5) bulls band castrated with MEL (**BAN+MEL**). Upon feedlot arrival (d −10), animals were blocked by initial BW (224 ± 4.5 kg) and assigned randomly to treatment pens ($n = 6$ pens/treatment). Oral MEL was administered at 1 mg/kg BW concurrent with castration on d 0. Individual BW was collected at weaning, d 0, 7, 14, 32, re-implant and on finishing to determine interim and overall ADG. Although BW was not affected by castration method or MEL, there was a tendency ($P = 0.10$) for CON animals to be heavier at d 32 and re-implant. From d 0 to 7, ADG was reduced for surgical (−0.42 kg/d) compared with band (0.43 kg/d) castration. Conversely, ADG was increased for surgical (1.74 kg/d) vs. band (1.46 kg/d) castration from d 14 to 32. Daily gain was increased for CON compared with castrated for all interim periods ($P \leq 0.02$) except re-implant to final ($P = 0.90$). There was also an overall improvement in ADG for CON ($P = 0.04$) and MEL ($P < 0.01$), but this was not influenced by method ($P = 0.80$). The CON had increased marbling score ($P = 0.03$) compared with castrated; whereas, backfat thickness was increased ($P < 0.05$) in SUR+M, but did not differ from CON ($P = 0.15$). Administration of MEL tended ($P = 0.08$) to increase yield grade. Castration near birth had long-term performance benefits compared with castration on feedlot arrival. Castration, regardless of method, transiently reduced ADG, but MEL administration improved overall ADG for both methods.

Key Words: analgesia, beef cattle, castration

0270 Evaluation of long-acting eprinomectin and a combination of moxidectin/oxfendazole administration post-weaning on immune status by Angus and Angus × Hereford crossbred replacement heifers over a 274-d grazing period.

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Internal parasite burdens have been reported to decrease animal performance and feed efficiency; however, little current research has evaluated the effects of burdens on the immune status in beef cattle. The objective of this study was to evaluate the effects of anthelmintic therapy on the immune status in replacement crossbred beef heifers. Beginning June 2, 2014, 83 fall-born Angus and Angus × Hereford replacement heifers were stratified by d −14 BW and fecal egg counts, and d of age. Heifers were then allocated randomly to 1 of 3 anthelmintic treatments consisting of: (1) control ($n = 28$; no anthelmintic administered; CON); (2) moxidectin/oxfendazole combination ($n = 28$; MO); or (3) long-acting eprinomectin ($n = 27$; LAE) for a 274-d grazing study. Heifers grazed in individual treatment groups on pastures, containing predominantly endophyte-infected tall fescue, for the duration of the project and were supplemented daily at 1% BW with corn gluten. Whole blood was collected via jugular vein on d 0, 14, 28, 84, 154, 168, 182, 234, and 274. On each d complete blood cell differentials were determined using a Cell-Dyn 3700 SL machine. Data were analyzed using the PROC MIXED of SAS for repeated measures. Two orthogonal contrasts were used and included: (1) comparing the mean of CON vs. the mean of treated heifers; and (2) comparing the mean of MO vs. LAE. Concentrations of white blood cells (WBC), lymphocytes, eosinophils, basophils, red blood cells (RBC), and platelets were greater ($P \leq 0.02$) from CON compared with treated heifers. The neutrophil:lymphocyte ratio (NEU:LYM) was greater ($P < 0.01$) from treated heifers compared with CON, and basophils were greater ($P = 0.01$) from MO compared with LAE; however, proportions of neutrophils and monocytes did not differ ($P \geq 0.54$) among treatments. A d effect was detected ($P < 0.01$) for WBC, lymphocytes, and monocytes. A treatment × d interaction ($P \leq 0.01$) was detected for neutrophils, NEU:LYM, eosinophils, basophils, and platelets. A treatment × d tendency ($P = 0.08$) was detected for RBC, with RBC being highest for all cattle on d 0 and lowest on d 234 for LAE. Based on this study, anthelmintic therapy may positively impact immune status in replacement

beef heifers treated with various anthelmintics.

Key Words: immune status, long-acting eprinomectin, moxidectin/oxfendazole combination

0271 Modeling milk yield and calf performance of beef suckler cows on pasture-based systems.

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Milk production of beef suckler cows is the main factor determining live weight of calves at weaning. However, the milk yield of beef suckler cows in Ireland is declining due to a reduction in the proportion of replacements sourced from the dairy herd and an emphasis on breeding for terminal traits. Correspondingly, calf weaning weights are also declining. Additionally, in suckler beef systems where grass, both grazed and conserved, forms a major part of the feeding system, beef suckler cows have to cope with seasonal changes in feed resource availability over the annual production cycle. The aim of current study was to develop a dynamic model to evaluate how the dynamics of milk production effects on the growth performance of beef suckler calves, within a pasture-based production system. A dynamic Grange Suckler Cow-Calf Model (dGSCCM) was developed that simulates energy partitioning, milk production and calf performance of two contrasting beef suckler cow genotypes; Charolais (C) and Charolais x Holstein-Friesian (CF). The parameter coefficients and equations used in the model were derived from published literature and established databases. The performance of cows and calves were determined by the genetic potential, physiological status, and availability of feed. The milk production profile of both beef suckler cow genotypes were generated through Irish data fitted to the lactation curve of Wood. The average daily milk yield for first and second parity was 7.35 and 8.70 kg for C and 11.12, and 13.10 kg for CF, respectively. Corresponding weaning weights at 240 d of age were 282 kg and 301 kg for C and, 332 kg and 355 kg for CF. Sensitivity analysis was performed by changing milk yield ± 20%. It showed that calf weaning weight is highly sensitive to cow milk production; each additional kg in daily milk yield increased weaning weight by 10.2 kg for CF in second parity to 14.3 kg for C in first parity. The model provides a basis for the evaluation of the growth response of beef suckler calves based on dynamics of milk production of their dams.

Key Words: calf live weight, dynamic modeling, lactation curve, pasture-based systems

0272 Dry and wet conditions during the prepartum forage growing season affect offspring feedlot performance and carcass composition in beef cattle.

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We hypothesize that dry and wet conditions during the prepartum forage growing season impact cow nutrient availability during pregnancy, resulting in altered fetal growth and development, and affecting subsequent feedlot performance and carcass composition. Steers (n = 7439) and heifers (n = 2380) finished in southwestern Iowa feedlots through the Tri-County Steer Carcass Futurity Cooperative were used for a retrospective analysis. Cattle were born in the Midwest (Iowa, Missouri, Indiana, Illinois, and Minnesota) in February, March, or April of 2002 to 2013. Feedlot performance and carcass data were measured for each animal. Palmer Drought Severity Index (PDSI) values were obtained for each dam during the prepartum forage growing season (April through October) on a monthly basis. Conditions were classified as dry (mean PDSI value ≤ -2.00), normal (mean PDSI value > -2.00 and < 2.00), or wet (mean PDSI value ≥ 2.00) during this period. Data were analyzed using the MIXED procedure of SAS with PDSI drought classification, birth year, feedlot, and calf sex included as fixed effects. Feedlot delivery BW was greatest ($P < 0.01$) for calves born to dams in the wet class, intermediate ($P < 0.01$) for normal, and least ($P < 0.01$) for dry. Feedlot ADG was greater ($P < 0.01$) for calves from cows in the dry class compared with normal and wet, suggesting compensatory growth. Calves born to dams in the normal class had a greater ($P = 0.02$) number of days on feed than wet. Calculated yield grade was improved ($P < 0.01$) for calves from normal and wet classes compared with dry, partially because calves born to cows in the normal class had greater ($P \leq 0.01$) LM area than dry and wet. Calves born to cows in the dry class had the most ($P < 0.01$) 12th rib fat and marbling, normal were intermediate ($P \leq 0.03$), and calves from wet had the least ($P \leq 0.03$). Despite this, drought classification did not affect ($P \geq 0.39$) final pre-slaughter BW, HCW, or dressing percent. In conclusion, prepartum forage growing season precipitation likely impacts offspring post-weaning growth and carcass characteristics by altering nutrient intake of cows throughout gestation due to grazing during the growing season and consumption of stored forage in winter. More research is necessary to investigate the impacts of dry and wet conditions during specific periods of fetal development on subsequent calf performance.

Key Words: developmental programming, drought, post-weaning

0273 Modeling body condition score at calving by past body condition and forage allowance in grazing beef cow on rangelands. M. Claramunt[*1] and P. Soca[2], [1]*Centro Universitario de la Regiãn Este, Universidad de la Repãblica, Treinta y Tres, Uruguay,* [2]*Facultad de Agronomia. Universidad de la Republica, Paysandu, Uruguay.*

Body condition score at calving affects the length of postpartum anoestrus, probability of pregnancy and the response of temporary suckling restriction and flushing on reproductive performance. Body condition score could be manipulated by forage allowance (FA). Therefore, modeling the effect of FA on BCS could provide valuable information for beef cow managers. The objective was to study the relationships between FA and BCS at middle gestation (BCSm) and calving (BCSc) of primiparous beef cow grazing located in native pastures. We used data from an experiment that evaluated the effect of 2 levels of FA on productivity of primiparous beef cows grazing rangelands. The experiment took place in Facultad de Agronomía, Uruguay. Eighty cows were assigned to a completely randomized experiment of 2 FA in spatial replication on 2 blocks during 2 yr. The annual FA averaged 2.5 and 4 kg DM/kg BW for low (L) and high (H) FA, respectively. Cow BW and forage mass were measured monthly and used to adjust FA using the "put and take" method. The experiment started in autumn −150 d postpartum (dpp) and finished 190 dpp. The BCS at −150 dpp (early gestation [BCSe]) was recorded. The BCS was recorded by a visual scale (1–9 points). We used a seasonal value FA before BCS was recorded (FAm and FAc), calving date in Julian days (CD) and the previous BCS and FA to explain BCSm and BCSc. Models were obtained by multiple regressions and variables were selected by Stepwise. An increase in BCSe and FAm improved BCSm (BCSm = 0.16 + (0.66*BCSe) + (0.43*FAm) + (−0.07*(FAm-2.89)^2); r2 = 0.63; $P < 0.01$; Mean = 5; RMSE = 0.43) and BCSc was increased as a result of the increase in BCSe and BCSm (BCSc = 0.28+ (0.18*BCSe) + (0.62*BCSm) + (0.008*CD; r2 = 0.57; $P < 0.01$; Mean = 4.4; RMSE = 0.2). Models have a good explanation capacity and highlight the effect of prepartum BCS and FA on BCSc. Forage allowance indirectly affected BCSc by its positive effect on BCSm. These models could be employed by beef herd managers to control or predict the BCSc and reproductive performance.

Key Words: body condition score, forage allowance, modeling

0274 Growth Potential of Dhanni cattle under rain-fed conditions of Punjab, Pakistan. G. Bilal[*1], M. Moaeen-ud-Din[1], and A. Zurwan[2], [1]*PMAS-Arid Agriculture University, Rawalpindi, Pakistan,* [2]*PMAS-Arid Agriculture University, Rawalpindi, Pakistan.*

The objective of the present study was to investigate growth potential of Dhanni cattle (a local humped cattle used for light draft) for possible utilization as potential beef cattle in arid or rain fed region of Attock, Punjab, Pakistan. Data on live weight of cattle ($N = 185$: 105 male, 80 females; age ranged from 1 to 375 d) were recorded in the field from 30 registered farmers raising purebred Dhanni cattle. The overall production system consisting of grazing (from 0800 to 1700 daily) with little or no supplementation. Mostly farmers weaned the calves between 6 and 8 mo of lactation probably due to low milk yield of Dhanni cows. Age of cattle was divided into 11 monthly classes with the last class having d 301 to 375. Data were analyzed using PROC MIXED of SAS (University Edition). The model included fixed effects of age at of cattle on test-day and sex; random effects of herd and residual. Males had slight higher weights (73.94 ± 1.81) than females (71.77 ± 1.97), but overall effect of sex was statistically nonsignificant ($P = 0.33$). Estimates of herd and residual variances were 18.15 and 206.35, respectively. Live weight of cattle varied with age ($P < 0.0001$). The least squares estimates of means of live body weight (kg) for monthly age classes 1 (1–30 d), 2 (31 to 60 d) and so on to 11 (301–375 d) were 24.86 ± 2.60, 39.31 ± 3.18, 51.68 ± 4.62, 61.86 ± 2.90, 72.27 ± 3.67, 75.49 ± 3.65, 80.19 ± 3.93, 81.97 ± 5.04, 97.45 ± 4.25, 98.80 ± 6.12 and 117.49 ± 5.41, respectively. Overall, cattle showed a daily growth rate of 268.50g from 1 mo to approximately 12 mo of age. The data shows potential of Dhanni cattle for raising as a beef cattle using current genetic and genomic selection tools.

Key Words: Dhanni cattle, growth potential, field condition

BEEF SPECIES SYMPOSIUM: IMPROVING WELFARE OF BEEF CATTLE

0275 Assessing and improving welfare in cow calf systems. C. B. Tucker*, *University of California, Davis.*

To date, animal welfare assessment, particularly independent audits, have focused on intensive animal agriculture. As public and corporate interest in farm-to-plate animal welfare assurance grows, extensive animal agriculture, such as cow-calf operations, may begin to be audited as well. The extensive nature of cow-calf systems presents both opportunities and challenges from an auditing perspective. Cow-calf operations lend

themselves toward animal welfare auditing from two perspectives: direct inspection of animals (animal-based measures) and evaluation of practices or records (management-based measures). Looking at the animals directly during a ranch visit allows assessment of several key welfare concerns, namely stockmanship, animal behavior during handling, long-term effects of forage availability (e.g., body condition), and some health conditions like lameness, pinkeye and injury. An investigative approach to assessing management practices provides information about welfare concerns, including pain management during common procedures, weaning practices, and antibiotic use (a proxy for incidence of health problems such as bovine respiratory disease). When available, direct inspection of ranch records can also provide information about frequency and causes of mortality. The more challenging aspects of animal welfare assessment on cow-calf operations are related to how cattle are kept, or facility-based measures, including: water access and quality, access to dry, protected lying areas, shade and shelter. Assessing the animal welfare implications of transport are also a challenge. These environmental factors are known to be important, yet change on a regular basis, thus are difficult to audit. In addition, there are other logistical challenges including the size of the cow-calf sector (757,000 U.S. ranches) and, in some cases, limited availability of days/year and facilities to directly observe cattle. Despite these challenges, there is tremendous potential to provide valuable feedback to ranchers and their customers and ultimately improve animal welfare in the cow-calf sector.

Key Words: cow-calf, welfare, assessment

0276 Best management practices for weaned calves for improved health and well-being. C. R. Krehbiel*, B. K. Wilson, C. J. Richards, and D. L. Step, *Oklahoma State University, Stillwater.*

Morbidity and mortality from Bovine Respiratory Disease (BRD) in newly weaned calves continues to be the most significant health problem facing the beef cattle industry. BRD accounts for over 50% of all cattle treated for sickness, and several studies have documented the economic impacts of BRD on profit outcomes of calves. Direct costs attributable to BRD include death loss, treatment and labor costs, and prevention costs. BRD has been shown to impact growth performance and feed efficiency, days on feed, carcass merit and market value, and can decrease the returns of individual cattle from $50 to $250. Best management practices for weaned calves vary depending on factors such as season of year calves are purchased, calf genetics, length of time in the marketing/transport process, previous management/vaccination, among other factors. Calves purchased directly from a ranch have fewer health problems. In general, the longer an animal is in the marketing chain, the more health problems will be encountered. Calves that have spent several days in the marketing channel may develop clinical BRD before or very soon after arrival at the feedlot; whereas, cattle with less time in the marketing chain may get sick later (2 to 4 wk), due to the length of time it takes for BRD to develop. On or before arrival, calves should be given a risk score (High, Medium, Low) that relates to the quantity of stress they have encountered and the probability they will develop BRD. High-risk calves normally will have been recently weaned, have received no vaccinations, have not been castrated or dehorned, have been commingled and have moved through at least one auction market. Low-risk calves will come from a single source and will have gone through a value added/preconditioning program that includes vaccination, castration, dehorning, weaning, and adaptation to a feed bunk. Variation exists within risk category, and groups of calves from auction markets can have few health problems, while some groups of preconditioned calves have high incidence of BRD. Cattle managers must be willing and able to make changes in management to meet the needs of the individual loads of cattle. To improve health and well-being, the beef cattle industry should move toward lowering the risk of receiving calves. This presentation will review the best management practices for weaned calves based on risk category for improved health and well-being.

Key Words: bovine respiratory disease, health and well-being, weaned calves

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277 Dairy cow culling: Best practices and industry trends. J. Walker*, *Dean Foods, Dallas, TX*

We all know that the best time to find a new career is while you still have your current one. And every dairy farmer should know that every dairy cow should have two careers, a MILK cow and a BEEF cow. While the proportion of animals sent to slaughter unfit for transport is extremely low, considering the number of cows slaughtered every year, the number of cows shipped that are unfit for transport becomes a significant welfare concern. There have been significant efforts on the part of the beef industry in the form of the Beef Quality Assurance programs to address the issue, yet there seems to remain a gap in performance in the dairy sector when it comes to dairy cattle condition at slaughter. The underlying cause of this gap is multifactorial, and the key to the solution is understanding the fundamental disconnect between dairy farmers and the beef supply chain. If progress is going to be made, we must first understand the drivers at the farm level. Milk price, milk production, feed cost and cull cow prices appear to be the primary drivers. Additional drivers include an apparent disconnect between the processor and the supplier and language barriers. Stakeholder engagement from farm to plant is essential to bridge the gap and improve the welfare of cattle sent to slaughter. Once the bridge is built, education, training and accountability will be the necessary drivers to secure change needed to demonstrate to consumers and customers alike that the welfare of cattle continues to be an industry priority.

Key Words: dairy, cull, welfare

0278 Welfare assessments of low stress handling in finishing feedlot cattle. K. S. Schwartzkopf-Genswein*, *Agriculture and Agri-Food Canada, Lethbridge, AB.*

Over the past 10–15 yr low stress handling for beef cattle and the techniques used to achieve it have gradually increased in use and understanding. The goal of low stress handling is to facilitate ease of animal movement as well as improve animal and handler safety. Its use is particularly important when handling finishing feedlot cattle that are heavy (> 300 kg) and more prone to injury, exhaustion, heat stress and lameness particularly at marketing when cattle are sorted, loaded/unloaded. Much excellent information is written and available on websites regarding specific techniques. The goal of this talk is to provide a brief over view of relevant low stress handing techniques for finishing cattle with a main focus on how and if these techniques reduce stress both physiologically and behaviorally. Studies assessing the effects of noise, light, visibility of the handler, facility design and prod use on indicators of cattle stress, as well as performance and meat quality have shown significant relationships between these variables. Overall, these studies help to validate the use of low stress techniques. Continued research is required to document the effects that low stress handling has on animal health, welfare and economics in the feedlot industry.

Key Words: low stress, handling, feedlot, finishing cattle

279 Evolution of animal welfare at packing plants. L. N. Edwards-Callaway*, *JBS USA, Greeley, CO.*

Animal welfare and humane handling have become integral components of slaughter plant operations over the past several decades. In the early nineties, Dr. Temple Grandin, a world-renowned animal scientist who revolutionized animal handling within the livestock industry, worked with the North American Meat Institute (NAMI) to publish the *Recommended Animal Handling Guidelines for the Meat Packing Industry*, which since its inception has served as the gold standard for animal handling at packing plants. Many commercial slaughter facilities address the proper treatment of animals through standard operating procedures, verification and monitoring programs, founded on the NAMI guidelines, in addition to applicable federal regulations. In the mid-1990s, Dr. Grandin was commissioned by the USDA to develop an objective system to evaluate the critical control points of animal handling at packing facilities. A HAACP-type (Hazard Analysis Critical Control Point) approach to evaluating animal handling was developed and adopted by NAMI and ultimately the meat industry as the voluntary standards for proper humane handling at slaughter facilities. By the end of the ’90s, major corporations such as McDonald’s began requiring animal handling audits at beef and pork supplier slaughter plants. With their purchasing power, these major food companies were able to drive improvement in animal handling performance at the packing facilities that supplied them. Within the past several years, many federally inspected plants have implemented a “systematic approach” to humane handling, which is a voluntary HAACP-based program described by the USDA Food Safety Inspection Service (FSIS) as a program that assesses critical control points of animal handling, develops appropriate programs and facilities to minimize stress and discomfort to animals and monitors performance continually. The meat industry has professionalized animal handling by supporting additional training and certifications specific to working with and processing animals, building a strong culture of animal care with the animal handlers at their facilities. As the number of plants reaching “excellent” levels on animal handling audits have continued to increase, the meat industry looks for novel ways to continually make progress (e.g., implementing the use of remote video auditing to monitor and train employees). There has been more focus in recent years on the condition of animals arriving at facilities and the impacts that has on how they must subsequently be handled. Animal handling continues to be a priority for all segments of the value chain.

Key Words: animal handling, auditing, slaughter

BIOETHICS SYMPOSIUM

0280 How was that chicken raised? Ethics and deliberating conscientiously about animal welfare standards. R. X. Anthony*, *University of Alaska, Anchorage.*

How was that chicken raised? Ethics and deliberating conscientiously about animal welfare standards

Whose or which animal welfare standards should be framing and guiding deliberations and practices so that they actually contribute to higher level of animal welfare? Animal welfare standards should first and foremost produce positive outcomes for the health and welfare of farm animals. However, the development and implementation of these standards do not always meet this mark. Global trade and commercial factors and the lack of governance structures and local science can result in less than desirable outcomes for animals. Farmers must contend with governmental regulations that are legally binding and a variety of private standards ranging from assurance and certification schemes and programs, voluntary codes of practice and standards of excellence from advocacy organizations. The plethora of standards can lead to “psychic numbing” and the moral psychology of denial among both farmers and consumers and can impede the discharge of good animal husbandry practices. Here, I explore the promise and shortcomings of employing wide reflective equilibrium (WRE, Daniels, 1996) to address these conditions. WRE can

help to produce coherence among conflicting sets of beliefs and values held by a moral agent or groups of moral agents, such as farmers and consumers who must consider "wicked problems," i.e., problems that are seemingly intractable in nature and which breed error, ignorance, confusion, transference of responsibility and learned helplessness. The development and implementation of animal welfare standards produce "wicked problems" that are complicated by social, economic and environmental constraints, empirical deficits and political struggle among different stakeholders in the food system. Implications of WRE for personal morality and public policy will be discussed.

Key Words: animal welfare, bioethics, ethics and deliberation

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0281 Farm animal welfare: Three essential ingredients from an international context. A. De Paula Vieira*, *Positivo University, Curitiba, Brazil.*

The animal food chain is characterized by an array of values that represent the interests of different stakeholders. These values are reflected in policies, practices, branding, and media. They highlight market share and profitability, food safety, quality assurance, traceability, sustainability, good governance, and trustworthiness. Animal welfare value is informed by animal welfare science, which brings the perspective of the animal into focus. This presentation will highlight (1) the centrality of animal welfare science and technology in innovating for animals' needs; (2) the importance of local contexts and engaging stakeholders in discussions when implementing substantial changes; and (3) the roles of shared value, well-informed communication and development of tools for monitoring, e-government and education, respectively.

(1) Animal welfare science is central in ensuring that policymakers, producers, consumers, retailers and industry agents continue to make the interests of farm animals a priority as the global system anticipates new challenges. Animal welfare scientists are essential in multidisciplinary teams to design new apparatuses, articulate the proper role of care for farm animals, and in transferring knowledge to producers.

(2) Engaging with all interested parties at the local level is key to contextualize the needs and challenges faced by animal producers in their home countries as they strive to be responsible custodians of their animals, promote respectable livelihoods and enhance food security and efficient use of resources, and minimize food loss and waste. Local producers and professionals such as animal welfare scientists should be given training and greater visibility as strategic collaborators for their significance in promoting animal welfare and "co-branding."

(3) There is increasing aspiration by consumers that animal production reflects common goals such as greater transparency and reflexivity by all in the food system, humaneness and social justice. Here, it is paramount that animal welfare scientists become conduits of innovation. Technology such as e-government platforms together with public policies will be crucial as the production sector embraces robust sustainability pathways and produces "responsible commodities" in the information age.

To sustain financial success and promote social benefit, animal value chains must consider the structure of their respective operations, be open to perform structural changes that is informed by the best science available and have strong ethical grounding, adopt new practices, design and model business and production processes that are personalized to their customers, and innovate their products and services to meet contextualized local and global expectations.

Key Words: farm animal welfare, sustainability, food chain

0282 Breaking down communication barriers to connect with stakeholders. R. Beck*, *The Center for Food Integrity, Gladstone, MO.*

The science is clear on antibiotics, animal housing, GMO feed, the global demand for protein, etc.—so why does it seem consumers don't understand or agree with any of it? The gap between consumer expectations and perceived industry performance presents grand challenges for those trying to stick to the science, but presenter Roxi Beck will lay the foundation for a big solution that serves to decrease that gap. In this session, attendees will:

(1) Gain an understanding of what U.S. consumers believe about animal agriculture and associated issues (animal care, antibiotics, GMOs, etc.)

(2) Expand awareness of why consumers distrust agriculture and the food system

(3) Review the Center for Food Integrity's peer-reviewed and published model to build consumer trust

(4) Learn effective approaches that allow stakeholders (including consumers) to consider complex and controversial science in their decision-making process

(5) Walk away with a toolbox of approaches and methods that complement CFI research to have meaningful stakeholder conversations

Key Words: consumers, industry performance, trust

ADVANCES IN BOVINE RESPIRATORY DISEASE

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283 Genetic approaches to selection for resistance to bovine respiratory disease. J. E. Womack*, *Texas A&M University, College Station.*

Advances in genomics, molecular genetics and genotyping technology offer unique opportunities to identify genetic

variation associated with complex traits, including host resistance to infectious diseases. The Bovine Respiratory Disease Consortium is a team of scientists and educators who are exploiting these technologies to identify genomic elements underlying resistance to the bovine respiratory disease complex and translating research findings for application by the beef and dairy industries. Genome-wide association studies (GWAS) in both dairy calves and beef feedlot cattle have been conducted, and numerous associated loci have been identified. Promise for successful translation to genomic selection and effective breeding of resistant animals comes from our discovery of higher than expected heritabilities and some loci with reasonably large effects. Challenge of animals with single BRD associated pathogens and subsequent RNA-seq and pathway analyses complement the GWAS studies and helps provide candidate genes for causal variation underlying susceptibility. Work is underway to identify optimal clinical criteria to identify BRD for use in EPDs and translation into predicted transmitting abilities for susceptibility. This program also includes development of educational courses and a study of economic impact of BRD to both beef and dairy industries. A comprehensive extension component of the project includes outreach at every level as evidenced through the project website (http://www.brdcomplex.org).

Key Words: bovine respiratory disease complex, complex traits, disease resistance, genomic approaches

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0284 Differential gene expression in cattle challenged with single pathogens of the bovine respiratory disease complex.

L. J. Gershwin[*1], A. Vaneenennaam[1], J. F. Taylor[2], J. Kim[2], R. L. Toaff-Rosenstein[3], H. L. Neibergs[4], and J. E. Womack[5], *[1]University of California, Davis, [2]University of Missouri, Columbia, [3]University of California, Berkeley, [4]Department of Animal Sciences, Washington State University, Pullman, [5]Texas A&M University, College Station.*

Bovine respiratory disease complex (BRDC) is an important infectious cause of mortality and morbidity in cattle. BRDC develops when stressed cattle are infected with one of several viruses followed by one or more bacterial pathogens. To evaluate the host response to each of these pathogens, we measured global transcript abundance using RNA sequence analysis, comparing infected steers with normal controls after single pathogen infections. At maximum clinical signs, steers were euthanized for necropsy and collection of lung, bronchial, nasopharyngeal, and retropharyngeal lymph nodes, and pharyngeal tonsils for RNA sequencing. Viral agents used for the challenge were: bovine respiratory syncytial virus (BRSV), infectious bovine rhinotracheitis (IBR), and bovine viral diarrhea virus (BVDV). Bacteria used to challenge included: *Mannheimnia hemolytica*, *Pasteurella multocida,* and *Mycoplasma bovis*. Differential expression of genes coding for non-specific defense innate immunity and the acute phase response was found among all pathogen infections. These included pattern recognition receptors, mucins, and host defense peptides; more specific immune response genes were differentially expressed in individual pathogen infections. Adaptive immune system pathways for both T and B cells were activated in BRSV infection. In general viral infections elicited a greater number of differentially expressed genes than bacterial pathogens. Tissues were compared and found to contain both differentially expressed genes shared among all tissues examined and specific to tissue type. Overall data obtained will have important implications for design of better therapeutic modalities; and will help further elucidate the complex pathogenesis of BRDC.

Key Words: BRDC, infection, RNA

0285 Genome-wide association study of bovine respiratory disease complex in U.S. feedlot cattle.

C. M. Seabury[*1], H. L. Neibergs[2], J. F. Taylor[3], and J. E. Womack[4], *[1]College of Veterinary Medicine, Texas A&M University, College Station, [2]Department of Animal Sciences, Washington State University, Pullman, [3]University of Missouri, Columbia, [4]Texas A&M University, College Station.*

Bovine respiratory disease complex (BRDC) is the leading natural cause of morbidity and mortality among feedlot cattle, and is responsible for substantial economic losses during commercial beef production. The primary objective of the present study was to estimate the heritability of two related BRDC traits in U.S. feedlot cattle (binary case-control; clinical severity scores), and identify quantitative trait loci (QTL) associated with differential susceptibility to BRDC. All beef cattle (Angus, Red Angus, Taurine Crossbreds, Charolais, Hereford) were sampled from commercial feedlots in Colorado (CO) and Washington (WA), with BRDC phenotypes assigned using the McGuirk diagnostic scoring system. Similar numbers of heifers (928) and steers (934) were genotyped using the Illumina BovineHD BeadChip, which included 932 BRDC cases, and 930 controls. Genome-wide association analyses were performed using a linear mixed model (EMMAX) with genomic relationship matrix (G), and accounted for the effects of month, season, breed, lot-pen, days-to-pull, sex, year sampled, and location in the combined cohort (CO+WA). Heritability estimates for the BRDC binary case-control and clinical score phenotypes ranged from 0.13–0.14 in CO, 0.25–0.20 in WA, and 0.20–0.22 in the combined cohort, respectively; thereby suggesting that a common set of susceptibility loci were likely to exist. QTL estimated to explain $\geq$ 2% of the variance in either of the BRDC phenotypes were detected in each individual population (CO, WA), whereas the most significant QTL detected for the combined cohort were estimated to explain $\geq$ 1% of the variance in both BRDC phenotypes. The genomic positions of several binary and clinical scores BRDC QTL

were found to overlap in all analyses (i.e., CO, WA, CO+WA); with the combined cohort producing overlapping QTL intervals (i.e., binary, clinical scores) on BTA1, BTA5, BTA8, BTA10, BTA13, and BTA27 thereby suggesting that genomic selection for reduced BRDC susceptibility in beef feedlot cattle is likely to help mitigate economic and production losses.
This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: beef cattle, bovine respiratory disease complex, genome-wide association study, genomic selection

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0286 Identification of causal variants underlying pathogen susceptibility and translation to genetic improvement.
J. F. Taylor*[1], H. L. Neibergs[2], C. M. Seabury[3], A. Vaneenennaam[4], J. E. Decker[1], J. L. Hoff[5], P. C. Tizioto[6], J. E. Womack[7], and R. D. Schnabel[1], *[1]University of Missouri, Columbia, [2]Department of Animal Sciences, Washington State University, Pullman, [3]College of Veterinary Medicine, Texas A&M University, College Station, [4]University of California, Davis, [5]Division of Animal Sciences, University of Missouri, Columbia, [6]Embrapa Southeast Livestock, São Carlos, Brazil, [7]Texas A&M University, College Station.*

We have developed populations of 2781 preweaned Holstein calves (CA and NM) and 1862 Angus, Red Angus, Taurine Crossbred, Charolais and Hereford heifers and steers (WA and CO) that are approximately equally represented as cases or controls that are being used to train models for the prediction of additive genetic risk of Bovine Respiratory Disease (BRD). Analyzing BovineHD genotypes for these populations revealed heritabilities for BRD risk in the range from 20–23% and revealed numerous large effect QTL, many of which are located in genomic regions that also harbor genes that are differentially expressed between Angus × Hereford controls and animals challenged with single pathogens of the BRD Complex. To enable selection for increased resistance to the pathogens responsible for BRD, we seek to develop estimates of genetic merit that are robust to the breed composition of the tested animals and to the extent of their relatedness to these training populations. To accomplish this requires the identification of the causal variants that have a large effect on risk of BRD that were detected in Genome-Wide Association Analyses (GWAA). The strategy that we have followed involves the development of a functional variant assay known as the GGP-F250 that includes variants likely to alter the function of proteins through frameshifts, amino acid substitutions or altering the sequences of 5' and 3' untranslated regions. Variant discovery was performed using whole genome sequences (WGSs) for 262 taurines and RNA sequence data for 153 taurine animals. Variants were validated using 1000 Bull Genomes project data for 1147 sequenced animals and WGS data on 35 indicine or indicine × taurine composite animals. Holstein training population animals have been genotyped with this assay and the combined data have been imputed to WGS variation (~11M variants with minor allele frequency > 5%) for the purpose of performing GWAA. The beef populations are likewise being imputed to WGS, and we seek to identify variants that are consistently associated with risk of BRD across populations for which the direction of allele effects is conserved across populations. These variants will be migrated to assays commercialized by Zoetis and GeneSeek that are routinely utilized by the beef and dairy industries to enable the translation of project results.

This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: BRD, GWAS, causal variants, estimated breeding values

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0287 Gene set enrichment analysis of bovine respiratory disease complex SNP data in feedlot cattle.
M. Neupane[1], J. F. Taylor[2], C. M. Seabury[3], J. E. Womack[3], and H. L. Neibergs*[1], *[1]Department of Animal Sciences, Washington State University, Pullman, [2]University of Missouri, Columbia, [3]Texas A&M University, College Station.*

Bovine Respiratory Disease Complex (BRDC) is responsible for annual deaths of more than 350,000 feedlot cattle and estimated losses of over $1 billion in the U.S. The objective of this study was to use gene set enrichment analysis of SNP data (GSEA-SNP) to identify pathways associated with susceptibility to BRDC in *Bos taurus* feedlot cattle. Cattle were sampled from commercial feedlots in Colorado and Washington, and cases were determined using the McGuirk diagnostic system. Approximately equal numbers of steers (933) and heifers (935) and cases (936) and controls (932) were genotyped with the Illumina BovineHD BeadChip and analyzed using an additive model with breed (Angus, Red Angus, Crossbred, Charolais and Hereford), days to pen removal, month and location as covariates in the genome-wide association analysis (GWAA). EIGENSTRAT principal component (PC) analysis was used to correct for population stratification using the first 10 PC resulting in $\lambda = 1.03$. GWAA was followed by GSEA-SNP utilizing 4388 pathways from Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes, Reactome, Biocarta and Panther. Haplotype block size was estimated and averaged across breeds to determine the size of the interval harboring each gene in which to search for a SNP that would serve as the proxy for the gene. The most significant SNP from the GWAA that was located within 7 kb of each gene was used as the proxy for each of the 19,723 genes mapped in the UMD 3.1 assembly. For each gene set, the significance value was calculated using the null distribution generated from 10,000 phenotype-based

permutations. Enrichment scores (ES) were calculated using running sum statistics. Five GO gene sets had normalized ES > 3 and were found to be associated with susceptibility to BRDC: GO:0005887 Integral Component of Plasma Membrane, GO:0031324 Negative Regulation of Cellular Protein Metabolic Process, GO:0005496 Steroid Binding, GO:0030162 Regulation of Proteolysis and GO:0008277 Regulation of G Protein Coupled Receptor Protein Signaling Pathway. No other gene sets were found to be associated with BRDC susceptibility. Of the 228 leading edge genes, 79 were differentially expressed between cases and controls and represent putative BRDC functional candidate genes which will be further investigated to determine how they may be best used in the selection of feedlot cattle that are more resistant to BRDC.

Key Words: GSEA-SNP, bovine respiratory disease complex

0288 Calculation of genomic predicted transmitting abilities for bovine respiratory disease complex in Holsteins. C. P. VanTassell*[1], G. Spangler[2], D. M. Bickhart[3], G. R. Wiggans[4], J. B. Cole[5], J. F. Taylor[6], H. L. Neibergs[7], C. M. Seabury[8], A. L. Van Eenennaam[9], and J. E. Womack[10], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]USDA-ARS, Beltsville, MD, [3]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [4]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [5]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [6]University of Missouri, Columbia, [7]Department of Animal Sciences, Washington State University, Pullman, [8]College of Veterinary Medicine, Texas A&M University, College Station, [9]University of California, Davis, [10]Texas A&M University, College Station.*

Bovine Respiratory Disease Complex is a disease that is very costly to the dairy industry. Genomic selection may be an effective tool to improve host resistance to the pathogens that cause this disease. Use of genomic predicted transmitting abilities (GPTA) for selection has had a dramatic effect on rates of genetic improvement in Holsteins, particularly for lowly heritable traits. Data were collected on 2682 calves located in California (n = 1978) and New Mexico (n = 705). DNA was extracted and animals were genotyped using the BovineHD BeadChip. A total of 22 individuals were excluded based on genotype call rate and breed designation other than Holstein. Of the remaining animals, 708 had unidentified sires, the remaining 1952 animals were the offspring of 578 sires which were identified by genotype matching. There were 38 bulls with at least 10 offspring, 343 with at least 2 progeny, and 235 bulls with a single offspring in the data set. A standardized scoring system considering animal body temperature, cough severity, nasal discharge, and eye discharge or ear scores was used to characterize the disease status of all calves according to the McGuirk classification system. Currently, GPTA are being calculated from these data using a heritability value of 0.20, which will be validated from the data. Estimated genetic marker effects will be compared with results from previous genome-wide association studies.

This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: BRD, genomic selection, predicted transmitting abilities

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0289 The value of genetic selection in reducing economic losses from bovine respiratory disease complex in beef cattle feedlots. J. S. Neibergs*[1] and H. L. Neibergs[2], *[1]Washington State University, Pullman, [2]Department of Animal Sciences, Washington State University, Pullman.*

The U.S. inventory of beef cattle has declined since its peak in the 1980s to levels present in the early 1960s. Low cattle inventories have contributed to record high prices since 2009. The increased cattle values have also resulted in a subsequent increase in economic losses from disease. Reducing losses due to disease has become increasingly important in managing thin profit margins at feedlots. The objective of this study was to develop a bio-economic model to evaluate the economic cost of bovine respiratory disease complex (BRDC) in beef feedlots and estimate the potential net economic gain from using selection approaches to reduce BRDC prevalence. Treatment cost, mortality, and harvest data from approximately 1000 heifers and 1000 steers with similar numbers of cases and controls were taken from two commercial feedlots and two commercial processing facilities at harvest. These data were used to develop a Reed-Frost epidemiological model that simulated BRDC prevalence in a population of cattle on feed. Treatment cost was computed as a function of days on feed and the prevalence of cases. Losses due to mortality, and carcass quality discounts were also included to estimate total economic losses. Based on market prices, and carcass discounts, the average economic loss per BRDC case was estimated. To estimate the potential net economic gain from selection, the rate of genetic gain was estimated using a 16.2% national BRDC prevalence rate obtained over a 15-yr period and an estimated heritability for BRDC susceptibility of 21% from the 2000 cattle evaluated in this study. An @ Risk model was used to estimate a 20-yr time frame of genetic selection with stochastic BRDC prevalence rates using historical USDA data. The model compared net economic gains for cattle feedlots that used selection to reduce BRDC and feedlots that approached reducing BRDC without selection. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the

USDA National Institute of Food and Agriculture.

Key Words: bovine respiratory disease complex, economics, epidemiology, genetics

0290 How might genomic information get translated into industry outcomes? A. L. Van Eenennaam*, *University of California, Davis.*

The 5-yr USDA-funded Bovine Respiratory Disease Complex Coordinated Agricultural Project (BRD CAP; USDA-AFRI 2011–68004–30367) aims to develop genetic markers associated with bovine respiratory disease (BRD) to enable the genetic identification of cattle that are less susceptible to BRD. Ultimately the aim of this project is to integrate predictive markers for BRD susceptibility into genetic tests and national cattle genetic evaluations. The research team is activity working to identify regions of the genome associated with BRD susceptibility in both dairy and beef cattle. Initial results have identified multiple genomic regions that were significantly associated with BRD susceptibility. Genomic selection has been introduced into dairy cattle breeding programs globally and within breed genomic estimated breeding values (GEBV) are published in a number of countries. Work is ongoing to integrate BRD information into dairy cattle evaluations at the appropriate economic weighting. However the incorporation of genomic information into beef cattle evaluations has been more problematic due to the presence of numerous breeds and the importance of crossbreeding in the commercial cattle population. Linkage disequilibrium between markers and quantitative trait loci (QTL) is not consistent across breeds, and so markers that were identified in one breed were frequently uninformative in other breeds. However, the sequencing of a large number of animals has opened up the possibility of identifying the actual SNP variations that are causing genetic variation. It is envisioned that by imputing the genotypes of reference animals collected by the BRD CAP up to full sequence and further fine mapping and analyses, the causative genetic variants associated with BRD susceptibility will be identified, and that inclusion of these markers on genotyping platforms will provide a reliable selection criterion to enable for the selection of both beef and dairy cattle that are less susceptible to BRD. There are several advantages associated with using causative SNP makers in selection panels including persistence of the marker effect across generations, and an increased likelihood that causative polymorphisms will be similarly associated with variation across multiple breeds. Ultimately, prospective marker panels will need to be tested in independent cattle populations to ensure they are predictive of BRD phenotype. Toward this end the BRD CAP is working in collaboration both breed associations and commercial feedlots to develop populations of BRD phenotyped animals. Ultimately selection against BRD susceptibility will depend on breeder inclusion of this disease trait in their breeding objective and selection decisions. See http://www.brdcomplex.org for more information.

Key Words: cattle, respiratory disease, extension

BREEDING AND GENETICS

0291 APY inverse of genomic relationship matrix–theory, analyses and questions. I. Misztal*, I. Pocrnic, D. Lourenco, and Y. Masuda, *University of Georgia, Athens.*

Genomic relationship matrix (GRM) can be inverted by Algorithm for Proven and Young (APY) based on recursion on a random subset of animals. While a regular inverse has a cubic cost, the cost of the APY inverse can be close to linear, allowing inexpensive computations with millions of genotyped animals. Theory proposed for APY assumes that optimal size of the subset (maximizing accuracy of genomic predictions) is due to a limited rank of GRM, which is a function of independent chromosome segments (Me) and subsequently of effective populations size (Ne). Simulation studies have shown that (1) the dimensionality is almost a linear function of Ne but for large Ne can be depressed by limited number of genotyped animals and SNP markers, (2) accuracy of predictions with APY inverse is higher than with a regular inverse, and (3) the distribution of independent chromosome segments is skewed. Tests using commercial data sets confirmed results by simulation. Comparisons of eigenvalue plots between simulated and commercial populations indicated an effective population size of 157 for Holsteins, 115 for Angus, 107 for Jerseys, 41 for broiler chicken and 30 for pigs. Experiences with the APY inverse raise a few questions. Can the rank provide information on the minimum SNP chip size that eliminates the polygenic component (or missing heritability)? Is the rank of GRM for a large two-breed population twice that of a single population? In simulation studies where QTL are on SNP markers, the best correlation of a simulated QTL effect is not with the actual SNP effect but with an average of adjacent SNPs. Is the optimum number (window size) of adjacent SNP a function of Ne and dictates the maximum resolution in GWAS? With all causative SNP are identified and their variances known, and appropriate weighted GRM (with APY inverse applicable) has the rank of the number of causative SNPs. Is the rank of weighted GRM with incomplete identification of QTLs (e.g., via GWAS or BayesB) smaller than that of a regular GRM? The APY inverse solves the problem of large-scale genomic computations and provides new insight into the genomic information.

Key Words: genomic selection, single-step GBLUP, APY inversion

0292 Dimensionality of genomic information and APY inverse of genomic relationship matrix. I. Pocrnic*[1], D. A. L. Lourenco[1], Y. Masuda[1], A. Legarra[2], and I. Misztal[1], [1]*University of Georgia, Athens,* [2]*INRA, UMR 1388 GenPhySE, Castanet-Tolosan, France.*

The objective of this study was to evaluate by simulation the dimensionality of genomic information in closed populations and its effect on genomic predictions using regular or sparse inverses of the genomic relationship matrices (GRM). Six datasets were simulated, representing populations with effective population sizes (Ne) approximately 20, 40, 80, 120, 160, and 200. Each population consisted of 10 non-overlapping generations, with 25,000 animals per generation and phenotypes available for generations 1 to 9. The last three generations were fully genotyped assuming genome length L = 30 Morgan, with 49,980 evenly allocated biallelic SNP markers and a total of 4980 biallelic and randomly distributed QTL affected the trait. The GRM was constructed for each population and analyzed for distribution of eigenvalues. The number of the largest eigenvalues explaining 90, 95, 98 or 99% of variation in GRM ranged from 814, 1611, 3701, 6253 (Ne≈20) to 5512, 9245, 15483, 20786 (Ne≈200), respectively. Genomic EBV (GEBV) were computed by single-step genomic BLUP (ssGBLUP) using either a direct inverse of GRM or a sparse inverse with the algorithm for proven and young (APY) that is based on recursion on a random subset of animals, where subset sizes were set to number of the largest eigenvalues explaining 90, 95, 98 or 99% of variation in GRM. APY inverse has approximately a linear cost as opposed to cubic for the regular inverse. Accuracies of GEBV for the last generation with APY inverse peaked at EIG98 and were slightly lower with EIG95, EIG99 or the direct inverse. In a situation with large number of SNP markers and genotyped animals, dimensionality of the SNP genomic information defined by the eigenvalues of GRM is approximately a linear function of effective population size, where most information is contained in about NeL largest eigenvalues, with no information beyond 4NeL. Genomic predictions with APY sparse inverse of GRM are more accurate and computationally inexpensive compared with regular inverse.

Key Words: genomic relationship matrix, genomic recursion, single-step genomic BLUP

0293 Accounting for discovery bias in genomic prediction. R. M. Thallman*[1], J. T. Parham[2], L. A. Kuehn[1], and J. P. Cassady[2], [1]*USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE,* [2]*South Dakota State University, Brookings.*

Our objective was to evaluate an approach to mitigating discovery bias in genomic prediction. Accuracy may be improved by placing greater emphasis on regions of the genome expected to be more influential on a trait. Methods emphasizing regions result in a phenomenon known as "discovery bias" if information used to determine influential regions is also used to predict genetic merit. Discovery bias causes genomic predictions to appear to be more accurate than they actually are. Generally, EBV of a population are conditional on as much information as possible and individual EBV are each conditional on exactly the same information. An analysis of simulated data (105 replicates) was conducted to test whether discovery bias could be reduced and true accuracy of prediction could be improved by relaxing the constraint that all EBV are conditional on the same information. In the default analysis, molecular breeding values (MBV) were computed from 2487 random SNP effects whose variances were estimated by REML. The 2600 phenotypes were simulated for non-parent animals only, which were progeny of 107 sires with number of paternal half-sibs per group ranging from one to 107. Corrected MBV (CMBV) were computed for each paternal half sib group by repeating the REML analysis on a data set that excluded records within that paternal half-sib group in an attempt to reduce discovery bias. True accuracy (correlation of MBV or CMBV with simulated breeding value) was lower for CMBV than for MBV. To recover the lost information without reintroducing discovery bias, a two-trait pedigree-based post-analysis was performed in which all 2600 phenotypes were fit as the first trait and the MBV (CMBV) were fit as the second trait. The solutions for the first trait are referred to as EBV and CEBV, respectively. True accuracy was greater for EBV than for MBV, suggesting the pedigree captured some genetic variance not accounted for by SNP. True accuracy was greater for CEBV than for EBV. Model derived accuracies were computed from prediction error variances of animals or functions of marker effects in the respective models. All model derived accuracies were greater than the corresponding true accuracies, indicating that discovery bias was present. Model

Table 0293.

	Model Derived Accuracy		True Accuracy		Discovery Bias
	Mean	SE	Mean	SE	Mean
MBV	0.960	7.11e-5	0.687	0.006	0.273
CMBV	0.954	7.59e-5	0.620	0.007	0.334
EBV	0.942	6.85e-5	0.716	0.006	0.226
CEBV	0.865	5.84e-5	0.721	0.007	0.144

MBV = Uncorrected molecular breeding value; CMBV = Corrected MBV; EBV = Uncorrected estimated breeding value; CEBV = Corrected EBV; Discovery bias = Model derived accuracy – True accuracy

derived accuracy was closer to true accuracy for CEBV than for EBV, indicating that the proposed correction was successful in reducing discovery bias, although it did not completely remove it. USDA is an equal opportunity employer.

Key Words: accuracy, discovery bias, genomic prediction

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294 Assessing genomic prediction accuracy for Holstein sires using bootstrap aggregation sampling and leave-one-out cross validation. A. Mikshowsky[1], K. A. Weigel[*2], and D. Gianola[3], *[1]University of Wisconsin, Madison, [2]Department of Dairy Science, University of Wisconsin, Madison, [3]University of Wisconsin, Madison.*

Since the introduction of genomic prediction for dairy cattle in 2009, genomic selection has dramatically changed many aspects of the dairy genetics industry and enhanced the rate of response to selection for most economically important traits. Young dairy bulls are genotyped to obtain their genomic predicted transmitting ability (GPTA) and reliability (REL) values. These GPTA are the main factor in most purchasing, marketing, and culling decisions until the bulls reach 5 yr of age and their milk-recorded offspring become available. At that time, daughter yield deviations (DYD) can be compared with the GPTA computed several years earlier. For most bulls, the DYD are similar to the initial predictions. However, for some bulls, the difference between DYD and corresponding GPTA is quite large, and published REL are of limited value in identifying such bulls. A method of bootstrap aggregation sampling (bagging) using genomic BLUP (GBLUP) was applied to predict the GPTA of 2963, 2963, and 2803 young Holstein bulls for protein yield, somatic cell score (SCS), and daughter pregnancy rate (DPR), respectively. For each trait, 50 bootstrap samples from a reference population comprised of 2011 DYD of 8610, 8405, and 7945 older Holstein bulls were used. Leave-one-out cross validation was also performed to assess the prediction accuracy when removing specific bulls from the reference population. The main objectives of this study were: (1) to assess the extent to which current REL values and alternative measures of variability, such as the bootstrap standard deviation (SD) of predictions, could detect bulls whose daughter performance will deviate significantly from early genomic predictions and (2) to identify factors associated with the reference population that can cause inaccurate genomic predictions. Correlations between bagged GBLUP predictions and 2014 DYD were lower than GBLUP predictions from the full reference population. The SD of bootstrap predictions was a useful metric for identifying bulls whose future daughter performance may deviate significantly from early GPTA for protein and DPR. Use of bootstrap predictions could prevent up to 50% of type I errors and roughly 10% of type II errors in sire selection decisions. The removal of certain reference population bulls indicated that testing set predictions for protein were robust overall, but some bulls negatively affecting prediction accuracy were identified.

Key Words: genomic prediction, bootstrap sampling, dairy cattle

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0295 The impact of call rate on genotype accuracy. D. C. Purfield[*1], M. C. McClure[2], and D. P. Berry[3], *[1]Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, Co. Cork, Ireland, [2]Irish Cattle Breeding Federation, Bandon, Ireland, [3]Teagasc, Moorepark, Fermoy, Co. Cork, Ireland.*

Data quality of single nucleotide polymorphism (SNP) arrays plays a key role in the accuracy and precision of downstream data analyses. The use of low quality genotypes can lead to false-positive results and impair the accuracy of genomic predictions. One such quality control measure commonly used is individual animal call rate, defined as the proportion of SNPs per individual where a genotype was called. Currently, no consensus exits on the minimum individual call rate that should be imposed, with threshold call rates per individual varying from 0.80 to 0.95 across studies. The objective of the present study was to determine the minimum individual call rate that could be applied without jeopardizing data quality. A total of 144,672 samples genotyped on a custom Illumina genotype panel on 143,827 dairy and beef cattle were available. The genotyping panel includes 14,371 SNPs on either the Illumina Bovine SNP50 or high density genotyping panels. All genotypes were called using the Illumina GenCall method. Lab-dates ($n = 4$) where > 15% of the samples genotyped had a call rate < 90% were not considered further. Of the remaining 142,433 samples, 493 animals had both a poor call rate (< 90%) and a subsequent high call rate (> 99%) after re-sampling and re-genotyping. The mean call rate for all samples was 98.77% (range: 15.81%-99.97%). The genotype and allele concordance rate among the genotypes available for all 493 animals with both a low and subsequent high call rate was estimated. Genotype and allelic concordance between low- and high-call genotypes increased as call rate increased (Table 1.). Low minor allele variants (i.e., variants with a minor allele frequency < 0.05) were imputed with greatest accuracy for samples with a mean genotype and allelic concordance of 99.24% and 99.55%. Imputation algorithms often correct for genotyping error, therefore to test if imputation improved concordance, all 493 low call rate samples were imputed using FImpute. A reference population of 140,268 animals with call rates > 90%, excluding the 493 high-call rate samples, was used. Imputation marginally increased concordance rates for all SNPs with a called genotype, but overall genotype concordance per class slightly decreased because missing genotypes were often incorrectly imputed as heterozygous genotypes. However, if a direct relative (i.e., sire, dam or progeny) was included in the imputation reference population, mean genotype

Table 0295.

Table 1. Genotype and allele concordance rates (CR) prior and post imputation for all 493 animals with a poor (<90%) and subsequent high call rate (>99%).

	Pre Imputation		Post Imputation			
Call rate class	Genotype CR	Allele CR	Genotype CR Called SNPs	Allele CR Called SNPs	Genotype CR All SNPs	Allele CR All SNPs
<40	38.36	62.35	38.61	62.38	39.42	63.22
40-50	47.08	68.57	47.33	68.62	44.74	67.15
50-60	58.59	76.59	58.89	76.67	53.68	73.54
60-70	79.31	89.51	79.66	89.65	73.21	85.92
70-75	86.06	93.01	86.29	93.08	81.71	90.51
75-80	93.47	96.73	93.64	96.79	90.77	95.26
80-85	96.83	98.41	96.93	98.46	95.56	97.72
85-90	98.44	99.22	98.47	99.22	98.08	99.01

and allele concordance for samples with a call rate between 85 and 90% increased to 98.13% and 99.04%, respectively.

Key Words: call rate, quality-control, genotype panels

296 Strategy for incorporating newly discovered causative genetic variants into genomic evaluations. G. R. Wiggans*[1], P. M. VanRaden[1], D. M. Bickhart[2], and M. E. Tooker[1], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

With sequence data available for an increasing number of dairy cattle, discovery of causative genetic variants is expected to be frequent. Current genomic evaluation systems require genotypes for all markers that contribute to an evaluation. A minimum number of animals with an observation for a new marker is required for accurate imputation. The SNP calls derived from sequence data from the 1000 Bull Genomes Project for 444 Holsteins were combined with SNP genotypes from bulls in the predictor population for U.S. national genetic evaluations to impute candidate variants from the full sequence. From this imputed data, the set of SNP used in genomic evaluation along with the newly discovered causative variants were selected and stored. Those genotypes replaced the original genotypes for the bulls when extracting genotypes for genomic evaluation. The time required for imputation is substantially reduced in routine evaluation by using the haplotype library and assignments from the previous evaluation. To create suitable prior information for the expanded SNP set, genotypes for approximately 100,000 animals (including the predictor bulls and many cows with genotyped progeny) were imputed without priors. This step took about 1 d; if the full set of animals had been used, it would have taken over a week. The accuracy of this approximation was tested using the December 2015 Holstein genomic evaluation of nearly 1 million animals. Genotypes from 978,987 bulls and cows were used to create the priors, which were used to impute the December 2015 Holstein genotypes. Of the nearly 60 billion comparisons, 97.7% were identical, 1% differed by 1 allele, and 1.2% differed by a missing allele. Efficient methods that result in higher concordance may be possible. Adding new highly informative markers to the evaluation process is expected to improve prediction accuracy. In addition, excluding other markers may further increase accuracy if they contribute more noise than value when highly informative markers are included. The procedure developed enables newly discovered causative variants to be added to genomic evaluation almost immediately, which saves the time previously required for a marker to be added to a new genotyping chip as well as the time required for sufficient animals to be genotyped with the new chip to achieve adequate imputation accuracy. With this strategy, the benefits from adding new markers to genomic evaluation can be realized sooner.

Key Words: causative variant, sequence data, genomic evaluation

0297 High density marker panels, SNPs prioritizing and accuracy of genomic selection. L. Y. Chang*[1], S. Toghiani[1], S. E. Aggrey[2,3], and R. Rekaya[1,3], *[1]Department of Animal and Dairy Science, University of Georgia, Athens, [2]NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens, [3]Institute of Bioinformatics, University of Georgia, Athens.*

Availability of high density (HD) SNP marker panels, genome wide variants and even sequence data create an unprecedented opportunity of dissect the genetic basis of complex traits and to enhance selection in livestock and plant species. The disproportional increase in the number of parameters in the genetic association model compared with the number of phenotypes has led to further deterioration in the statistical power, and increase in co-linearity and false positive rates. HD panels do not improve the accuracy of GS in any significant manner and could even lead to reduction in accuracy using both regression and variance component methods. As a result, HD panels at best they did not improve significantly the accuracy of genomic selection and at worst they led to a reduction in accuracy. This is true for both regression and

variance component approaches. To remedy this situation, either some form of SNP filtering or external information is needed. Current methods for prioritizing SNP markers (i.e., BayesB, BayesC) are sensitive to the increased co-linearity in HD panels which could limit their performance. In this study, the usefulness of F_{st}, a measure of allele frequency variation among populations, as an external source of information in genomic selection was evaluated. A simulation was performed for a trait with heritability of 0.4. Data was divided into three subpopulations based on trait distribution (top 5%, bottom 5% and in between). Marker data was simulated to mimic 770K SNP marker panel. A ten chromosome genome with 200K SNPs was simulated. Several scenarios with varying number of QTLs and their associated effects were simulated. F_{st} empirical cutoff values of 0.004, 0.008, 0.01, and 0.02 were used to prioritize markers resulting in 4579, 2288, 1745, and 650 selected SNPs, respectively. Using all 200K markers and no filtering, the accuracy of genomic prediction (correlation between true and predicted breeding values) was 0.48. When SNPs were pre-selected based on F_{st}, accuracy was 0.41, 0.48, 0.49, and 0.53 for F_{st} cutoff values of 0.004, 0.008, 0.01, and 0.02, respectively. It is clear that the accuracy obtained using all SNPs can be easily achieved using only 0.5 to 1% of all markers. These results indicated that SNP filtering using already available external information could increase the accuracy of genomic selection. This is especially important as next generation sequencing technology is becoming more affordable and accessible to animal and plant applications.

Key Words: SNP prioritizing, genomic selection, high density

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298 Selection of sequence variants to improve dairy cattle genomic predictions. M. E. Tooker*[1], P. M. VanRaden[1], D. M. Bickhart[1], and J. O'Connell[2], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]University of Maryland School of Medicine, Baltimore.*

Genomic prediction reliabilities improved when adding selected sequence variants from run 5 (July 2015) of the 1000 bull genomes project. High density (HD) imputed genotypes for 26,970 progeny tested Holstein bulls were combined with candidate sequence variants within or near genes for 444 Holstein animals. Variants with minor allele frequency (MAF) < 0.01, incorrect map locations, excess heterozygotes, or low correlations of sequence and HD genotypes for the same variant were removed. Individual genotype probabilities < 0.98 from Beagle and Mendelian conflicts between parents and progeny were set to missing. Test 1 included 481,904 candidate sequence SNP consisting of 107,471 exonic, 9422 splice, 35,242 untranslated regions at the beginning and end of genes, 329,769 SNP upstream or downstream of genes. Test 2 also included 249,966 insertions and deletions (indels). After merging sequence variants with 312,614 HD SNP and editing, Test 1 included 762,588 variants and Test 2 included 1003,453. Imputation quality was assessed by keeping 404 of the sequenced animals in the reference population and randomly choosing 40 animals as a test set. Their sequence genotypes were reduced to the subset in common with HD genotypes and then imputed back to sequence. Percentage of correctly imputed variants averaged 97.3% across all chromosomes in Test 1 and 97.2% in Test 2. Total time required to prepare, edit, and impute the sequence variants for 27,235 animals was about 5 d using < 20 processors. Computation of genomic predictions using deregressed evaluations from August 2011 for 33 traits and 19,575 bulls required about 3 d with 33 processors. Predictions were tested using 2015 data of 3983 U.S. bulls whose daughters were first phenotyped after August 2011. Many sequence variants had larger estimated effects than nearby HD markers, but prediction reliability improved only 0.6% points in Test 1 when sequence SNP were added to HD SNP, and only 0.4 higher than HD SNP in Test 2 when sequence SNP and indels were included. However, selecting the 17,000 candidate SNP with largest estimated effects and adding those to the 60,671 SNP used in routine evaluations improved reliabilities by 2.7% points (67.4% vs. 64.7%) on average across traits, compared with 35.2% parent average reliability. Accuracy of prediction can improve by adding selected sequence SNP to marker sets.

Key Words: causative variant, sequence data, genomic evaluation

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0299 Genomic prediction of crossbred performance. B. Harlizius*[1], M. S. Lopes[1], J. Vandenplas[2], C. A. Sevillano[2], and J. W. M. Bastiaansen[3], *[1]Topigs Norsvin Research Center, Beuningen, Netherlands, [2]Wageningen University, Netherlands, [3]Animal Breeding and Genomics Centre, Wageningen University, Netherlands.*

The majority of the commercial slaughter pigs are crossbred animals. However, breeding efforts have been mainly focused on increasing genetic progress of purebred populations. The aim of this work is to evaluate different strategies to improve genomic prediction of crossbred performance taking into account the breed origin of alleles in crossbred populations (breed-specific effects). Previous work showed that marker effects estimated in one breed cannot predict performance in another breed (across-breed prediction). This might be due to breed-specific effects caused by differences in linkage disequilibrium between the marker and the QTL, as well as differences in allele frequencies and in genetic background of the breeds. For prediction of crossbred performance, marker effects estimated in single-breed data showed some predictive value but training on crossbred data achieved higher accuracies, although the breed origin of alleles was ignored. In this study, prediction accuracies of breeding values from a traditional genomic selection model (GS) were compared

with prediction accuracies of breeding values from a model that accounts for breed-specific effects (BS). The population evaluated consisted of a two-way (Large White and Landrace) crossbred population. As both parents of all crossbred animals were known, the breed origin of alleles was easily determined after phasing of the data. The trait evaluated was gestation length (GL), for which a genetic correlation between purebred and crossbred performance (r_{pc}) of 0.90 was estimated. Prediction accuracy of BS breeding values was slightly greater than prediction accuracy of GS breeding values (0.53 and 0.52, respectively). Additional benefits of BS over GS are expected for traits with lower r_{pc} and when crosses of more distant purebred populations are evaluated. As a step further, a method based on long-range phasing for determining the breed origin of alleles in three-way crossbred data was developed. In a simulation study, the accuracy of breed of origin assignment was determined for 400 three-way crossbred animals with 95% correct assignments, 3% unassigned and < 2% incorrect assignments. Application of this method to real data, including 14,000 genotyped purebred animals and 1700 genotyped three-way crossbred animals, achieved 93% assignments of breed of origin of alleles without using pedigree information. Genotypic data from purebred animals was required to define the haplotypes of the three breeds contributing to the crossbreds. Currently, analyses are underway to use this breed origin information of the three-way crossbred population to estimate breed-specific effects for genomic prediction.

Key Words: pigs, crossbred performance, breed-specific effects

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0300 SNP filtering using Fst and implications for genome wide association and phenotype prediction. S. Toghiani[*1], L. Y. Chang[1], S. E. Aggrey[2,3], and R. Rekaya[1,3],[1]*Department of Animal and Dairy Science, University of Georgia, Athens,* [2]*NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens,* [3]*Institute of Bioinformatics, University of Georgia, Athens.*

Although genome-wide association studies (GWAS) detect single nucleotide polymorphism (SNP)-trait association, these SNPs explain only a small fraction of the variation. Genomic selection (GS), through the use of all available genetic information, tends to have a better dissection of the phenotypic variation, but its performance is still far from optimum. GWAS and GS are affected by lack of power is due to small sample size, large number of highly correlated markers, and the moderate to small effects of most QTLs. This situation could get even more complex with the continuous increase in marker density. Methods that internally try to prioritize SNPs (i.e., BayesB) tend to provide a certain relief when low to medium density panels are used but their advantages degrade with the increase of the number of markers. Thus, it is becoming a necessity to either perform a SNP filtering before conducting the association analysis or to enlist additional external sources of information. Knowledge of genetic diversity based on evolutionary forces is beneficial for tracking loci influenced by selection. F_{ST}, as measure of allele frequency variation among populations, provides a tool to reveal genomic regions under selection pressure. To evaluate its usefulness as an external source of information in association studies, a simulation was performed. A trait with heritability of 0.4 was simulated and three sub-populations were created based on the empirical phenotypic distribution (< 5% quantile; > 95% quantile and between 5 and 95% quantiles). Marker data was simulated to mimic 600K and 1 million SNP panels. Genetic complexity of the trait was modeled by the number of QTLs, their distribution, and magnitude of their effects. Using different empirical cut off values for F_{ST}, most QTLs were correctly detected using as little as 0.8% of SNP markers in the panels. Furthermore, the genomic similarity base on the selected SNPs was very high (> 0.80) for individuals with similar genetic and phenotypic values even that they have limited to no blood relationship. These results indicate that filtering SNPs using F_{ST}could be beneficial to GWAS and GS by focusing on genome regions under selection pressure. This could be relevant with the availability of next-generation-sequencing data. High functional genomic similarity based on selected markers indicates similarity in SNP signatures, regardless of blood relationships, and translates into high phenotypic correlation that could be used in decision making.

Key Words: GWAS, F_{ST}, genetic and phenotypic prediction

0301 A combined coalescence forward in time simulator software for pedigreed populations undergoing selection for complex traits. J. T. Howard[*1], F. Tiezzi[1], J. E. Pryce[2], and C. Maltecca[1], [1]*North Carolina State University, Raleigh,* [2]*Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia.*

The use of marker information in animal breeding has recently been an active area of research and has been incorporated in selection decisions and as a tool to control inbreeding across a variety of species. There is yet still much to be learned on the optimal way to use marker information to select animals and manage the genome of a population that is undergoing selection for complex traits that have a traditional quantitative basis (i.e., yield) and/or fitness basis (i.e., number of progeny). We have developed a combined coalescence and forward-in-time simulator for complex traits and populations. The simulator is performed in two stages. In the first stage whole-genome SNP data is read in ms format and is utilized to generate founder individuals and associated SNP marker panels ranging in size from thousands to millions of SNP. During this stage a wide variety of trait architectures can be generated with additive

and dominance effects for both a traditional quantitative trait and fitness along with genomic covariance among traits. The second stage generates new individuals across generations based on a variety of selection scenarios. The selection stage can be performed using a wide variety of relationship matrices including pedigree, independent markers, haplotypes, or run of homozygosity based haplotypes. Relationship matrices and their associated inverse are generated using computationally efficient algorithms based on updating matrices from previous generations. Complex population structures can be generated that allow for a differential contribution of gametes to the next generation as well as mating constraints. To demonstrate the program, we present a small application that mimics a dairy cattle and swine population to describe some of the metrics that are generated. Scenarios were generated based on a 12,000 SNP marker panel spread across 3 chromosomes and a population size of 650 animals (sires = 50; dams = 600) per generation. A scenario with selection on a quantitative trait occurring for 5 generations and breeding values estimated from pedigree or independent SNP had a running time for the dairy cattle scenario of 4.85 and 5.82 min, respectively. GenoDriver allows for a wide range of selection strategies to be evaluated in the presence of a fitness trait and is available at https://github.com/jeremyhoward/GenoDriver.

Key Words: genetic simulation, quantitative traits, genomic selection

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0302 Identifying and calling insertions, deletions, and single-base mutations efficiently from sequence data. P. M. VanRaden[*1], D. M. Bickhart[2], and J. R. O'Connell[3], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [3]University of Maryland School of Medicine, Baltimore.*

Whole-genome sequencing studies can identify causative mutations for subsequent use in genomic evaluations, but sequence alignment and variant identification are lengthy and sometimes inaccurate processes. Speed and accuracy of identifying small insertions and deletions (indels) of sequence can be improved by calling variants while aligning sequence reads. Previous algorithms separated alignment and calling steps, whereas program findmap stores previously known variants in memory, calls alleles for those variants, and identifies other potential new variants during alignment. The algorithm uses a string-pattern hash to store the reference genome in a rapidly accessed table. If both ends of a paired-end read do not align fully, the length of a potential indel within the read is calculated from the map location difference for two partial matches. The algorithm then finds the indel location and checks if the full read matches after accounting for the indel. Potential variants detected by findmap are checked and edited by program findvar for consistency across reads. New variants from findvar were compared with those from the Genome Analysis Toolkit (GATK) UnifiedGenotyper and from SamTools after Burrows-Wheeler Aligner (BWA) alignment. Detection accuracy was examined using reads simulated for 10 animals at 10X coverage from cattle reference map UMD3.1 with variants derived from run 5 (July 2015) of the 1000 bull genomes project that included 38,062,190 SNP, 532,179 insertions, and 1127,620 deletions. Half of variants were simulated as heterozygous, one-fourth as homozygous alternate, and one-fourth as homozygous reference. For homozygous alternate variants, findvar found 99.8% of SNP, 79% of insertions, and 67% of deletions; GATK found 99.4, 90, and 89%; and SamTools found 99.8, 12, and 18%, respectively. For heterozygotes, findvar found 99.1, 75, and 62%; GATK found 99.0, 90, and 88%; and SamTools found 98.2, 9, and 11%, respectively. False positives as percentages of true variants were 14, 0.4, and 0.3% from findvar; 12, 8.4, and 2.9% from GATK; and 37, 1.3, and 0.4% from SamTools, respectively. Read depth was 85.9 from findmap/findvar, 96.1 from BWA/GATK, and 84.4 from BWA/SamTools. With 10 processors, clock times were 106 h for BWA, 25 h for GATK, 11 h for SamTools, 3 h for findmap, and 1 h for findvar. The new software is freely available, with algorithms 10 to 30 times faster than current strategies for calling known and identifying new variants. Accuracy is improved by accounting for DNA variants while aligning sequence data.

Key Words: sequence alignment, variant calling, indel

0303 Issues in commercial application of single-step genomic BLUP for genetic evaluation in American Angus. D. A. L. Lourenco[*1], S. Tsuruta[1], B. D. Fragomeni[1], Y. Masuda[1], I. Pocrnic[1], I. Aguilar[2], J. K. Bertrand[1], D. W. Moser[3], and I. Misztal[1], *[1]University of Georgia, Athens, [2]INIA, Las Brujas, Uruguay, [3]Angus Genetics Inc., St. Joseph, MO.*

American Angus Association (AAA) has been using genomic information for genetic evaluations in a multistep approach since 2009. To improve accuracy while simplifying procedures, AAA is transitioning to single-step genomic BLUP (ssGBLUP) in the middle of 2016. Initial tests with ssGBLUP showed an increase in prediction accuracy of 25% for growth traits compared with traditional evaluations. Besides evaluation for growth traits, the goal of this study was to update the full pipeline for genetic evaluation with ssGBLUP methodology. The pipeline includes multi-trait models with linear and categorical traits, maternal effects, multibreed evaluations with external information, and a large number of genotyped animals but most of them with low EBV accuracy. Data included 9.7 M animals in the pedigree, 184,354 genotyped animals, and at most 8.2 M phenotypes for growth traits, calving ease (categorical), and carcass traits. The first issue during the implementation was the increasing number of genotyped animals. Single-step GBLUP requires the inverse of the genomic

relationship matrix (GRM), which had a high computing cost and required around 1 Tb of memory for this dataset. The algorithm for proven and young animals (APY) was used to approximate the inverse of the GRM. The number of core animals was set to 15,000, which was calculated as the number of eigenvalues of GRM explaining 99% of the variation. This algorithm reduced the memory usage to 40 Gb and required 10% of the computing time while slightly improving the accuracy. Another issue was the increase in computing time for calving ease evaluation, which uses a threshold model, from 12 h to 4.5 d. Resetting the preconditioned conjugate gradient iteration to solve the mixed model equations every 40 to 200 rounds helped decrease the time to 19 h. The inclusion of external EBV for Red Angus was required for evaluation of growth traits. We developed software to support genomic and external information, and the implementation of a genomic multibreed model increased the computing time only by 2.5 h. Current algorithm for approximation of accuracy of genomic EBV (GEBV) was too expensive for > 100,000 animals. A new algorithm was developed that does not require inverse of large GRM and accounts for multiple sources of information while avoiding double-counting. Correlations between accuracy from the new algorithm and true accuracy from PEV were higher than 0.85 for growth traits. Single-step GBLUP can be considered a mature methodology for commercial genomic selection in beef cattle.

Key Words: beef cattle, genomic selection

0304 Single-step GBLUP using APY inverse for protein yield in U.S. Holstein with a large number of genotyped animals. Y. Masuda*[1], I. Misztal[1], and P. M. VanRaden[2], [1]*University of Georgia, Athens,* [2]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The objective of this study was to provide initial results in an application of single-step genomic BLUP with a genomic relationship matrix (G^{-1}_{APY}) calculated using the Algorithm of Proven and Young (APY) to 305-d protein yield for U.S. Holsteins. Two G^{-1}_{APY} were tested; one was from 139,057 genotyped bulls with 12,895 core animals (APY140K) and the other one was from 764,029 genotyped animals with 12,913 core animals (APY760K). The predictor data set consisted of phenotypes recorded after 1989 and pedigrees limited to 3 generations back from recorded or genotyped animals. Genomic predictions (GPTA2011) were calculated for predicted bulls that had no recorded-daughters in 2011 but had at least 50 such daughters in 2015. We used the official daughter yield deviations published in 2015 (DYD2015) for the predicted bulls (N = 3797). We also used the official GPTA published in 2011 with a multistep method as a comparison, although official methods have improved since then. Coefficient of determination (R^2) and slope (b_1) were calculated from a linear regression of DYD2015 on GPTA2011. Using APY140K, the R^2 was 0.50 compared with 0.51 from the official GPTA. The b_1 was much better (0.98) compared with 0.81 from the official GPTA. With APY760K, the R^2 was 0.46 and b_1 was 1.08. Incorporating effect of a SNP related to DGAT1 increased R^2 to 0.51 for APY140K and 0.48 for APY760K. The decrease in R^2 with APY760K compared with APY140K could be due to inclusion of lower quality genotypes, or biases caused with the use of all genotypes with incomplete phenotypes. All the computations finished within 11 h including 4.2 h to set up APY-inverse with APY760K. Based on the linearity of the computation cost, using 1 million genotyped animals with the same model would require 14 h of computations. Single-step GBLUP can provide genomic predictions for all genotyped bulls and cows while accounting for pre-selection. Further research will determine the impact of various factors affecting the reliability such as validation methodology, weighting SNP markers, and quality of genotyped data.

Key Words: genomic evaluation, Holstein, ssGBLUP

0305 Heteroskedastic extensions for genome-wide association studies. Z. Ou*[1], R. J. Tempelman[2], J. P. Steibel[3,4], C. W. Ernst[3], R. O. Bates[3], C. Chen[3], and N. M. Bello[1], [1]*Department of Statistics, Kansas State University, Manhattan,* [2]*Michigan State University, East Lansing,* [3]*Department of Animal Science, Michigan State University, East Lansing,* [4]*Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

Bayesian multiple regression models based on genomic marker information are commonly used for genomic prediction and selection and are being increasingly utilized in genome-wide association (GWA) analyses to search for genomic regions associated with economical important traits in agriculture. These models jointly fit all markers, thereby circumventing the limitations of "one-marker-at-a-time" of traditional GWA inference. We have recently validated and tested extensions of genomic prediction models to account for residual heteroskedasticity, which is prevalent in livestock field data. Our objective was to evaluate the impact of not accounting for potential residual heteroskedasticity in GWA inference. Using simulated data scenarios that reflected a gradient of increasing residual heteroskedasticity, we fitted homoscedastic and heteroskedastic error versions of hierarchical Bayesian genomic prediction models assuming either normal (RR-BLUP) or heavy-tailed (BayesA) prior specifications on the effects of genomic markers. For each marker, we then constructed a posterior z-score using prediction error variance of the estimated marker effect to detect associations between genomic regions and phenotypes of interest. Under conditions of extreme heterogeneity of residual variances, heteroskedastic models showed an increase in power of up to 10% points for GWA discovery with little impact on false positive rate (i.e., change of 0 to 3% points), compared with the homoscedastic model counterparts.

Further, when heteroskedasticity was high, the absolute magnitude of the estimated signal for the most prominent QTL expressed as a posterior *z*-score was enhanced by 20% and 34% for heteroskedastic RR-BLUP and BayesA, respectively. The inferential advantages of heteroskedastic models over homoscedastic ones were particularly apparent under a BayesA specification. A data application involving three quantitative carcass and meat quality traits from a swine resource population representing high, mild and low levels of heteroskedasticity yielded proportionally enhanced differential detection signal for the heteroskedastic models relative to the homoscedastic ones, consistent with results from the simulation study. In conclusion, accounting for residual heteroskedasticity can be expected to enhance power in the identification of important genomic regions for traits of interest.

Key Words: genome-wide association, residual heteroskedasticity, genomic prediction model

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0306 Exploring the feasibility of using copy number variants as genetic markers through large-scale whole genome sequencing experiments.

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Copy number variants (CNV) are large scale duplications or deletions of genomic sequence that are caused by a diverse set of molecular phenomena that are distinct from single nucleotide polymorphism (SNP) formation. Due to their different mechanisms of formation, CNVs are often difficult to track using SNP-based linkage disequilibrium inference. This can result in decreased reliabilities of prediction for CNV causal mutations tracked by SNP genotyping arrays. To test if CNVs can serve as suitable genetic markers, we sequenced 75 individual bulls from eight different breeds and two subspecies of cattle (*Bos taurus taurus*: Angus, Holstein, Jersey, Limousin, Romagnola; *Bos taurus indicus*: Brahman, Gir, Nellore) to 11X coverage. We identified 1853 non-redundant CNV regions (CNVR) that comprise ~3.1% (87.5 Megabases) of the cattle genome, which represents an increase over previous cattle genome variability estimates (~2%). With the discrete genome copy number values identified in our analysis, we selected the top 1% (n = 80) of CNV sites found to be variable among the sequenced breeds by a modified F statistical measure to perform population structure analyses. We were able to distinctly separate breeds of cattle based on genomic copy number, suggesting that CNVs may have utility as genetic markers. Further analysis revealed that 77.5% (62/80) of our selected CNV windows could reliably be assessed for variability and that 54 of these loci were, in turn, located near tandem duplications. CNV genotyping remains a difficult endeavor and suffers from several obstacles related to their detection and mechanisms of formation; however, these initial results suggest that our current methods can be refined and may provide suitable utility for genomic evaluation in the future.

Key Words: sequence data, genetic markers, genotyping

0307 Use of marker × environment interaction whole genome regression model to incorporate genetic heterogeneity for residual feed intake, dry matter intake, net energy in milk, and metabolic body weight in dairy cattle.

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Feed efficiency in dairy cattle has gained much attention recently. Due to the cost prohibitive measurement of individual feed intakes, combining data from multiple countries is usually necessary to ensure a large enough reference population. It may then be essential to model genetic heterogeneity when making inferences about feed efficiency or selecting efficient cattle using genomic information. In this study, we constructed a marker × environment interaction model that decomposed marker effects into main effects and interaction components that were specific to each environment. We compared environment-specific variance component estimates and prediction accuracies of the interaction model analysis, an across-environment analysis ignoring population stratification, and a within-environment analysis on the feed efficiency data set. Phenotype traits included residual feed intake (RFI), dry matter intake (DMI), net energy in milk (MilkE), and metabolic body weight (MBW) from 3656 cows measured

in 3 broadly defined environments: North America (NAM), the Netherlands (NLD), and Scotland (SAC). Genotypic data included 57,574 single nucleotide polymorphisms per animal. The interaction model gave the highest prediction accuracy for MBW, which had the largest estimated heritabilities ranging from 0.37 to 0.55. The within-environment model performed the best when predicting the trait of RFI which had the lowest estimated heritabilities, ranging from 0.13 to 0.41. For traits (DMI and MilkE) which had intermediate estimated heritabilities (0.21 to 0.50 and 0.17 to 0.53), performance of the 3 models was comparable. Genomic correlations between environments were also computed using the variance component estimates from the interaction model. Averaged across all traits, genomic correlation was the highest between NAM and NLD, and was the lowest between NAM and SAC. In conclusion, the interaction model provided a novel way to evaluate traits measured in multiple environments in which genetic heterogeneity may exist. It offered the capability of estimating environment-specific parameters and performed either the best or nearly the best in the genomic prediction.

Key Words: genomic selection, interaction model, feed efficiency

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0308 Imputation of medium density genotypes from custom low density genotype panel in sheep.

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A custom low density genotype panel has been developed with 16,351 single nucleotide polymorphisms (SNPs), 12,118 of which are on the medium density Illumina Ovine50 Beadchip which has 51,135 SNPs. The objective of the present study was to quantify the accuracy of imputation from the low density to medium density panel in five different sheep breeds. Medium density genotypes were available on 2375 sheep from the breeds Suffolk (n = 566), Texel (n = 318), Vendeen (n = 461), Charollais (n = 559) and Belclare (n = 471). The youngest 75 animals per breed were used as the validation population; the 37,278 autosomal SNPs on the medium density panel that are not on the low density panel were masked for the validation population. Imputation was undertaken across the entire genome simultaneously using both family and population wide linkage (disequilibrium) information. Concordance rates and the correlation between the true and imputed genotypes were estimated for the validation animals which included the low density SNPs in the calculation. Across all genotypes, the correlation between the actual and imputed genotype was 0.983; the mean genotype (allele) concordance rate was 0.979 (0.989). The mean genotype and allele concordance rate per individual varied from 0.864 to 0.997 and from 0.929 to 0.999, respectively. The individual with the poor concordance rate was an outlier and the minimum genotype (allele) concordance rate excluding this individual was 0.920 (0.958). Mean genotype concordance rate per breed was 0.984, 0.972, 0.982, 0.969 and 0.989 for Belclare, Charollais, Suffolk, Texel and Vendeen, respectively. Imputation accuracy not accounting for pedigree was marginally better than when pedigree was accounted for in the imputation process. Imputation accuracy with a reference population of only the breed of animal to be imputed was also marginally better than when multiple breeds were included in the reference population; imputation accuracy of breeds not represented in the reference population were considerably worse. The low density panel is therefore a useful, lower cost, strategy to achieve genomics evaluations in these sheep breeds.

Key Words: imputation, sheep, genomic, low density

0309 Systematic profiling of short tandem repeats in the cattle genome.

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Short tandem repeats (STRs), or microsatellites (MS), are genetic variants with repetitive 2–6 base pair motifs in many genomes. Using high-throughput sequencing and experimental validations, we systematically profiled STRs in five Holsteins. We identified a total of 60,106 microsatellites and generated the first high-resolution STR map, representing a substantial pool of polymorphism in cattle. We observed significant STR overlaps with RefSeq genes and quantitative trait loci (QTL). We performed evolutionary and population genetic analyses using over 20,000 common dinucleotide STRs. Besides corroborating the well-established positive correlation between allele size and variance in allele size, these analyses also identified dozens of outlier STRs based on two anomalous relationships that counter expected characteristics of neutral evolution. And one STR locus overlaps with a significant region of a summary statistic designed to detect STR-related selection. Additionally, we showed that only 57.1% of STRs are located within SNP-based linkage disequilibrium (LD) blocks while the other 42.9% are not. Therefore, a substantial number of STRs are not tagged by SNPs in the cattle genome, likely due to STR's distinct mutation mechanism and elevated polymorphism. This study provides the foundation for future

STR-based studies of cattle genome evolution and selection.

Key Words: cattle genome, short tandem repeat (STR), whole genome sequencing (WGS)

0310 Assessing genetic diversity in Canadian beef cattle populations using Illumina BovineSNP50 chip.

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The main objective of this study was to utilize genomic profiles to assess genetic diversity within and between Canadian beef cattle populations to gain insights on population admixture and dynamics. Individuals (n = 2831) were genotyped for Illumina BovineSNP50 for 9 populations (Gelbvieh (GVH, n = 488), Charolais (CHA, n = 396), Angus (AAN, n = 492), Simmental (SIM, n = 404), Limousin (LIM, n = 205), Hereford (HER, n = 591), Hays Converter (HC, n = 208), Kinsella composites (KC, n = 15) and Lacombe Research Centre (LRC, n = 33). A total of 2828 individuals with 43,172 SNPs across 29 autosomes passed quality control and were used for further analyses. To study population structure between populations, a principal component analysis (PCA) was performed using SNP1101 software. Genomic inbreeding coefficients for each individual were estimated using 4 methods; VanRaden 2008 (F_v), Leutenegger 2003 (F_l), excess of homozygosity (F_h) and GCTA software (F_g) method implemented in SNP1101 software. The PCA analysis reported clear divergence between GVH, CH, AAN, SIM, LIM, HER and HC populations where 7 clusters were well defined, illustrated in Fig. 1. The KC and LRC populations are distributed between the other clusters confirming their genetic architectures as crossbred. The most genomically divergent breeds were CHA, AAN, GVH and HER. The correlations between inbreeding coefficients F_v with F_l and F_g were strong; 0.98 and 0.93, respectively. The average estimate of genomic inbreeding coefficients (F_v, Fl, and Fg) were highest for the HER ranged from 12.8 ± 0.1to 18.5 ± 0.2% followed by AAN ranged from 10 ± 0.1 to 12.7 ± 0.1%. In addition, the genomic inbreeding coefficients for composites/crossbreds ranged from 2.0 ± 1.0 to 4.0 ± 1.0% and from 1.0 ± 0.7 to 7.0 ± 1.0% for KC and LRC, respectively, where these inbreeding levels were low across all methods compared with purebred cattle. In conclusion, the genomic assessment of inbreeding using different methods indicated that HER and AAN breeds had the highest inbreeding level and thus inbreeding depression should be assessed for their traits at the genome level. Information on specific regions that are fixed for deleterious alleles allows directed introgres-

Fig 0310.

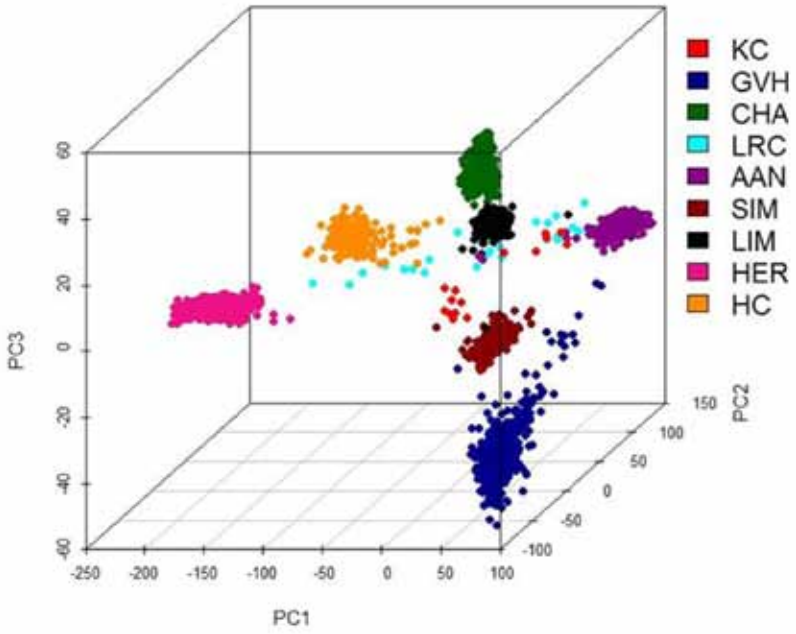

Figure 1. Population structures identified by principal component analysis. The plot shows the first three principal components (PCs) using Illumina BovineSNP50 (43,172 SNPs) across the 29 autosomes. KC is Kinsella composites, LRC is Lacombe Research Centre, GVH is Gelbvieh, CHA is Charolais, ANG is Angus, SIM is Simmental, LIM is Limousin, HER is Hereford, HC is Hays Converter.

sion between breeds to help address performance.

Key Words: genetic diversity, inbreeding, single nucleotide polymorphism, Canadian beef cattle

0311 Joint association analysis of additive and non-additive genomic effects for growth and carcass traits of beef cattle. E. C. Akanno*[1], M. K. Abo-Ismail[1,2], L. Chen[1], C. Li[1,3], J. Basarab[1,4], and G. Plastow[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Animal and Poultry Production, Damanhour University, Egypt, [3]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Edmonton, AB, Canada, [4]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, Canada.*

The biological dominance effects of genes have been suggested as one of the genetic mechanism explaining heterosis. We performed a joint association analysis using genotypes from Illumina BovineSNP50 (50K) BeadChip to evaluate the contributions of additive and dominance genomic effects to the variance of growth and carcass traits in beef cattle and to identify genomic regions that potentially harbor genes or quantitative trait loci underlying the variation. A total of 6794 multi-breed and crossbred beef cattle with phenotype and 50K genotypes were used. Traits studied included birth weight (BWT), weaning weight (WWT), pre-weaning daily gain (PDG), average daily gain (ADG), yearling weight (YWT), hot carcass weight (HCW), back fat thickness (BFT), rib-eye area (REA), marbling score (MS), lean meat yield (LMY) and yield grade (YG). Additive and dominance genomic relationships were created based on 42,610 single nucleotide polymorphism (SNP) markers that passed the quality control. The model used accounted for fixed contemporary group effects (herd, year, data source, and sex), covariates of genomic breed composition, age of dam, weaning age, age at start of feedlot test, and slaughter age, and random maternal and maternal permanent effect depending on the trait analyzed. A single SNP analysis that partitions the SNP effects into additive and dominance components was used for genome-wide association. The proportions of total phenotypic variance explained by additive and dominance effects for the studied traits are presented in Table 1. After applying a false discovery rate at a 5% significance level, a total of 66, 20, 2, 36, 66, 22, 9, 15, 10, and 3 SNPs were significantly associated with BWT, WWT, PDG, ADG, YWT, HCW, BFT, REA, LMY, and YG, respectively, for the additive component. For the dominance component, three SNPs (rs110564527, rs110361335, and rs41663796) and one SNP (rs43624164) were significantly associated with MS and WWT, respectively. The SNP rs110361335 located on chromosome 4 was found to be within *islet cell autoantigen 1* (*ICA1*) gene which is involved in insulin regulation. In addition, SNP rs43624164 on chromosome 10 found to be near the gene *ribosomal protein L10-like* (*RPL10L*) had significant additive and dominance effects on WWT. Although, the proportions of phenotypic variance explained by dominance were moderate for growth traits with known heterosis effects, the results of this study suggest that dominance effects are polygenic.

Key Words: beef cattle, dominance genetic effect, genomic prediction

0312 Investigation of genomic imprinting through allelic expression analysis of mRNA in chicken embryonic brain and liver. Z. Zhuo[1], S. J. Lamont[2], and B. Abasht*[1], *[1]Department of Animal and Food Sciences, University of Delaware, Newark, [2]Department of Animal Science, Iowa State University, Ames.*

Genomic imprinting refers to the epigenetic phenomenon that some autosomal genes are exclusively expressed from either the maternal or paternal allele whereas, based on Mendelian inheritance, expression of alleles are expected to be in

Table 0311.

Table 1. Proportions of phenotypic variance explained by additive and dominance effects in purebreds, crossbreds and overall populations[1]

	Purebreds (n = 2060)		Crossbreds (n = 4734)		Overall (n = 6794)	
Traits	Additive	Dominance	Additive	Dominance	Additive	Dominance
Birth weight, kg	0.54±0.053	0.21±0.066	0.56±0.034	0.10±0.043	0.51±0.026	0.08±0.028
Weaning weight, kg	0.21±0.052	0.25±0.081	0.34±0.031	0.03±0.039	0.30±0.024	0.06±0.027
Pre-weaning daily gain, kg/d	0.31±0.055	0.21±0.069	0.35±0.035	0.04±0.049	0.27±0.026	0.07±0.031
Average daily gain, kg/d	0.27±0.048	0.01±0.078	0.33±0.029	0.01±0.038	0.30±0.023	0.02±0.026
Yearling weight, kg	0.47±0.050	0.12±0.073	0.56±0.029	0.10±0.038	0.47±0.023	0.08±0.026
Hot carcass weight, kg	0.29±0.066	0.05±0.125	0.44±0.042	0.00±0.000	0.43±0.035	0.00±0.000
Back fat thickness, mm	0.48±0.070	0.00±0.000	0.23±0.039	0.01±0.070	0.31±0.036	0.01±0.054
Rib eye area, cm^2	0.40±0.069	0.11±0.133	0.40±0.041	0.00±0.000	0.41±0.036	0.00±0.000
Marbling score	0.32±0.066	0.00±0.000	0.35±0.041	0.13±0.067	0.32±0.035	0.00±0.000
Lean meat yield, %	0.45±0.070	0.03±0.125	0.30±0.040	0.03±0.067	0.37±0.036	0.05±0.053
Yield grade	0.43±0.071	0.10±0.129	0.32±0.041	0.05±0.068	0.39±0.036	0.03±0.053

[1]Purebred individuals have > 90% of their representative breeds (Angus, Hereford and Charolais); Crossbred individuals included beef-dairy hybrids, Beefbooster composite (www.beefbooster.com), and two and three way crossbreds involving Angus, Hereford, Charolais, Gelbvieh, Simmental, Limousine, and Piedmontese

equal amount and independent of their parental origin. DNA methylation in *cis*-acting manner is the major mechanism for genomic imprinting. Imprinted genes have been identified in several animal species and are frequently associated with embryonic growth and survival functions. Yet whether genomic imprinting exists in chickens is still debatable, as previous studies reported conflicting evidence regarding the topic. Albeit no genomic imprinting has been found in the chicken embryo as a whole, we investigated whether certain embryonic tissues exhibit genomic imprinting. In this study we interrogated the existence or absence of genomic imprinting in chicken embryonic brain and liver by examining the mRNA expression of parental alleles in an F1 generation. Eggs from two highly inbred chicken lines (Fayoumi and Leghorn) and their reciprocal crosses were collected and incubated for 12 d; then brain and liver were harvested from embryos for cDNA library preparation. To establish the genotypes of the inbred lines and the F1 hybrids and to minimize reference bias of RNA-seq sequence alignment, genomic DNA from inbred Fayoumi and Leghorn chickens was pooled separately and each pool was sequenced at 20X coverage. The SNP loci identified from DNA-Seq data were masked to create a customized reference genome (based on Ensembl Galgal4) for RNA-seq reads mapping. Of 65 million RNA-seq reads per sample generated using the Illumina HiSeq 2000 sequencer, 88% were mapped to the customized reference genome. The genome-wide ratio of mapped reads containing reference allele was reduced by 1.5% when comparing with the results from the original reference genome. Our analyses indicated that genomic imprinting is absent in chicken 12-d embryonic brain and liver. In genome-wide and chromosome-wide scales, we observed a balanced expression of maternal and paternal alleles. About 9.2% of the heterozygous loci showed allele specific expression independent of their parental origin (binominal test, p value $\leq$ 0.05). Certain alleles showed consistent expression pattern across all 8 F1 individuals indicating possible presence of *cis*-acting regulatory mutations or epigenetic modifications influencing expression of these alleles.

Key Words: genomic imprinting, chicken, RNA-seq

0313 Identification of causative genomic region for carcass weights of cattle. H. Chung*, *National Institute of Animal Science, Wanju, Korea (The Republic of)*.

The present analysis was designed to find causative genomic regions for carcass weights according to the recent requirements of farms. A total of 5000 Hanwoo cattle, which were registered in the national database, were slaughtered to measure carcass weights and extract DNA samples. Animals were genotyped with customized 56K Affymetrix SNP chips to identify genomic regions regarding carcass weight. The chip contained previously reported genetic variants, including QTL analyses from the literature reviews for meat quality traits from various cattle breeds in the world. Genome-wide association studies (GWAS) found significant genotypic effects for carcass weights in the genomic region (26254142 to 26274142 Mb) on the bovine chromosome 14 based on UMD3.1. To confirm significance for the identified SNP, 3700 animals were additionally slaughtered and genotyped, and as results, the 20 SNP presented extreme significant associations for carcass weights. The identified genomic regions with SNP may be used in marker-assisted selection programs to improve carcass weights in beef cattle.

Key Words: SNP, carcass weight, QTL

0314 Introgression of the Belgian Blue Myostatin variant into Nellore cattle: Effects of double muscling on birth weight and calving ease. G. Nogueira*[1], K. S. Paulussi[2], A. T. H. Utsunomiya[3], Y. T. Utsunomiya[3], A. Almeida[4], A. Tanuri[5], T. Santos[4], and R. Alonso[6], *[1]UNESP, Aracatuba-SP, Brazil, [2]UNESP, Araçatuba, Brazil, [3]UNESP Univ. Estadual Paulista, Jaboticabal, Brazil, [4]Deoxi, Aracatuba-SP, Brazil, [5]UFRRJ, Rio de Janeiro-RJ, Brazil, [6]Deoxi, Aracatuba-SP, Brazil.*

Introgression and backcrossing are powerful strategies to insert a specific segment of the genome expressing a desirable trait from a population to another and recover the original genetic background, respectively. The aim of this work is to present the effect of introgression of myostatin mutation on birth weight in Nellore cattle (*Bos indicus*). We evaluated 92 calves 15/16 Nellore, offspring of one purebred Nellore and two 7/8 crossbred (Nellore x Belgian Blue) bulls. All animals were genotyped to identify the ones carrying the myostatin mutation (BN– heterozygous for the mutation, NN– homozygous for the absence of mutation). The birth weight was analyzed in a mixed model framework, fitted by restricted maximum likelihood (REML) using lme4 package in R, including sex, biotechnology of reproduction (FTAI-fixed-time artificial insemination x FTET-fixed-time embryo transfer) and myostatin mutation as fixed effect and sire as random effect. Thirty-nine calves were identified as heterozigous for the mutation (BN) and 53 as homozygous for absence of mutation (NN). Heterozygous calves were born 4.92 ± 0.998 kg heavier (p-value = 1.6e-6) compared with the homozygous. No differences were found comparing FTAI (34.12 kg) and FTET (35.50 kg) (p-value = 0.126). Although not significant, males were born 1.76 ± 1.01 kg heavier than females (p-value = 0.083). Considering the random term of the mixed model, only 0.34% of the phenotypic variance was explained by sire effect. In summary, these results show that the effect of the myostatin mutation is the main factor regulating differences in birth weight. Despite to be expected, dystocia was not an issue in this study. Future analysis will comprise homozygous individuals for the presence of myostatin mutation (BB) and

its impact on birth weight and parturition.

Key Words: Nellore, double muscling, birth weight

0315 Genomic-polygenic and polygenic parameters and prediction trends for growth and reproduction traits in an Angus-Brahman multibreed population. M. A. Elzo*[1], R. Mateescu[1], M. G. Thomas[2], D. D. Johnson[1], D. O. Rae[1], J. D. Wasdin[1], M. D. Driver[1], and J. D. Driver[1], *[1]University of Florida, Gainesville, [2]Department of Animal Sciences, Colorado State University, Fort Collins.*

The objectives of this research were to estimate genomic-polygenic and polygenic parameters and to evaluate prediction trends as Brahman fraction increased from 0% to 100% in an Angus-Brahman multibreed population for 305-d yearling weight (YW), yearling reproductive tract score (RTS), age at first calving (AFC), and first calving interval (FCI) using single-step genomic-polygenic (GPM) and polygenic models (PM). Phenotype records were 1758 for YW, 381 for RTS, 1385 for AFC, and 985 for FCI. The pedigree file had 6845 calves, sires, and dams, and the genotype file contained 115,711 actual and imputed Illumina150k SNP markers from 1547 animals. The 4-trait GPM and PM included contemporary group, age of dam (YW only), sex of calf (YW only), direct heterosis, maternal heterosis (YW only) as fixed effects, and animal and residual as random effects. Genetic parameters were estimated using REML procedures and computed using AIREMLF90. Heritabilities were somewhat higher for GPM than for PM (0.47 vs. 0.45 for YW, 0.31 vs. 0.30 for RTS, 0.14 vs. 0.12 for AFC, and 0.31 vs. 0.29 for FCI). Genetic correlations were positive between YW and RTS (GPM: 0.55; PM: 0.60), negative between RTS and AFC (GPM: −0.22; PM: −0.55) and between AFC and FCI (GPM: −0.68; PM: −0.67), and near zero for all other trait pairs. The similarity between GPM and PM heritabilities and genetic correlations indicated that the 115,711 Illumina150k SNP markers added little additional information to that contained in the pedigree. Regression coefficients of breed group EBV means on Brahman fraction were negative ($P < 0.0005$) for YW, RTS, and FCI, and positive ($P < 0.0001$) for AFC as Brahman fraction increased. This indicated that heifers with higher Brahman percentages tended to be lighter and less mature as yearlings, older at first calving, and have shorter FCI than heifers with higher Angus percentages in this population. Regression coefficients of individual animal EBV on Brahman fraction showed similar trends, but were smaller, guaranteeing the existence of animals with high, medium, and low EBV across all Brahman percentages.

Key Words: cattle, genomic, reproduction

0316 Genome-enabled prediction of genetic values of growth traits using artificial neural networks. S. O. Peters*[1], M. Sinecen[2], M. G. Thomas[3], I. G. Imumorin[4], and K. Kizilkaya[2], *[1]Department of Animal Science, Berry College, Mount Berry, GA, [2]Adnan Menderes University, Aydin, Turkey, [3]Department of Animal Sciences, Colorado State University, Fort Collins, [4]Animal Genetics and Genomics Laboratory, Cornell University, Ithaca, NY.*

Data from Brangus heifers (3/8 Brahman-*Bos indicus* × 5/8 Angus-*Bos taurus;* n ≈ 743) registered with International Brangus Breeders Association were analyzed to predict genetic parameters of growth traits. Phenotypes included body weights collected at birth (birth weight), ~205 (weaning) and 365 (yearling) days of age. Genotypes were from BovineSNP50 (Infinium BeadChip, Illumina, San Diego, CA; 53,692 SNP). Artificial neural networks (ANN) have been used for marker-based genomic predictions of complex traits in animal and plant breeding. In this study, ANN was used to estimate the genetic values of growth traits of birth weight, weaning weight and yearling weight of Brangus heifers with all genome-wide marker data set and chromosome-base genome-wide marker data set. ANN provide nonlinear relationships between inputs and outputs with the interplay among variables learned adaptively. For the ANN model, 95% of the animals were randomly allocated to a training set, 5% to a test set. In the training phase of ANN with the scaled conjugate gradient method, 52,640 SNP as the genomic covariates of 706 individuals are linearly combined with a vector of weights. The resulting linear score were then transformed using an activation function to produce the output of ANN. Different ANN architectures were examined to assess the best predictive ANN. Up to 30 neurons in the hidden layer were tested for their influence on predictive quality. ANN models with 13, 15, and 1 neurons in the hidden layer were used for birth weight, weaning weight and yearling weight of Brangus heifers. ANN model including chromosome-base genome-wide markers achieved predictive correlations of $r = 0.96$ for birth weight using chromosome 23, $r = 0.94$ for weaning weight using chromosome 17 and $r = 0.92$ for yearling weight using chromosome 1. ANN model including all genome-wide markers achieved predictive correlations of $r = 0.93$ for birth weight, $r = 0.91$ for weaning weight and $r = 0.91$ for yearling weight. Results suggest that neural networks may be useful for predicting complex traits using high-dimensional genomic information.

Key Words: artificial neural network, genomic prediction, growth traits, SNP

0317 Molecular breeding values distribution in slick male and female Senepol cattle differing in musculature. C. L. González-Berríos*[1], A. Rivera-Serrano[1], A. Casas-Guérnica[1], T. Sonstegard[2], and M. Pagán-Morales[1], [1]*Department of Animal Science, University of Puerto Rico, Mayaguez, Puerto Rico,* [2]*Recombinetics Inc., St. Paul, MN.*

Recently, the polymorphisms responsible for double muscling [MSTN: exon 3 11bp indel (NT821)] and slick coat phenotype (PRLR: exon 10 cytosine indel) in Senepol cattle were described. However, the genomic implications of segregating animals according to PRLR and MSTN genotypes have not been elucidated for economically relevant traits (ERTs), especially in tropically adapted beef cattle. Thus, purebred Senepol cattle (males/females) were genotyped for both indel and molecular breeding values (MBV) were obtained through a commercially available marker panel (Igenity, Neogen Corp.). Three MBV categories were established: low (L), intermediate (I) and high (H) based on standard deviations of +1 (L), +2 (I) or +3 (H) from the average MBV for 12 ERTs. Statistical differences were determined using the Chi^2 test [sex, genotype (MSTN; PRLR) and double and triple combinations]. Genotypic proportions observed were: double muscle (DM): 6/NT821-NT821, 95/NT821-WT, and normal musculature (NM): 273 WT-WT ($P < 0.0001$) and slick coat (SC): 256/BB, 99/BA, and normal coat (NC): 4 = AA ($P < 0.0001$). Proportional differences were observed within BB for MBV-average daily gain between MSTN genotypes: NT821/WT: (11.76 H, 72.06 I, 16.18 L) and NM: (26.06 H, 53.72 I, 20.21 L) ($P < 0.05$). Also, within BB, differences in MBV categories distribution were: males: (20.90 H, 79.10 I, 0.00 L)/females: (33.33 H, 56.08 I, 10.58 L) and females: (16.93 H, 68.78 I, 14.29 L)/males: (4.48 H, 77.61 I, 17.91 L) for average daily gain and calving ease, respectively ($P < 0.05$). Significant differences in MBV-tenderness were observed within females for: NT821/WT (7.46% H, 68.66% I, 23.88% L) and NM: (14.22% H, 73.04% I, 12.75% L) ($P < 0.05$). Moreover, females BB ($n = 189$) significantly differed in MBV category distribution depending on musculature for: residual feed intake [NT821/WT: (26.83 H, 68.29 I, 4.88 L)/NM: (18.92 H, 60.14 I, 20.95 L), yield grade [NT821/WT: (24.39 H, 70.73 I, 4.88 L)/NM: (14.19 H, 66.89 I, 18.92 L)], backfat thickness [NT821/WT: (57.14 H, 38.10 I, 4.76 L)/NM: (27.70 H, 50.0 I, 22.30 L)], pregnancy rate [NT821/WT: (4.88 H, 78.05 I, 17.07 L)/NM:(25.00 H, 66.22 I, 8.78 L)] and Stayability [NT821/WT: (9.76 H, 63.41 I, 26.83 L)/NM: (18.24 H, 70.27 I, 11.49 L)] ($P < 0.05$). In the present study, a higher proportion of Senepol cattle with SC and NM were observed and intermediate MBV for all ERTs were predominant, with the exception of backfat thickness (NT821/WT-BB-Females). Therefore, genomic selection in slick Senepols segregating MSTN alleles are needed to improve their ERTs-MBV.

Key Words: slick, myostatin, Senepol

0318 PRUNE2 gene has a potential effect on residual feed intake in Nellore cattle. A. O. D. Lima[1], P. S. N. Oliveira*[2], P. C. Tizioto[2], A. L. Somavilla[3], W. J. S. Diniz[1], J. V. D. Silva[1], S. C. S. Andrade[4], C. Boschiero[5], A. S. M. Cesar[6], M. M. Souza[7], M. I. P. Rocha[1], J. Afonso[1], C. E. Buss[1], M. A. Mudadu[8], G. B. Mourao[5], L. L. Coutinho[6], and L. C. A. Regitano[9], [1]*Federal University of São Carlos, São Carlos, Brazil,* [2]*Embrapa Southeast Livestock, São Carlos, Brazil,* [3]*Universidade Estadual Paulista "Júlio de Mesquita Filho," Jaboticabal, Brazil,* [4]*Genetics and Evolutionary Biology Department-IB, University of São Paulo, Brazil,* [5]*Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil,* [6]*Animal Biotechnology Laboratory-ESALQ, University of São Paulo, Piracicaba, Brazil,* [7]*Federal University of São Carlos, Brazil,* [8]*Embrapa Pecuária Sudeste, São Carlos, Brazil,* [9]*Embrapa Southeast Livestock, São Carlos, Brazil.*

Residual feed intake (RFI) can increase the profitability of producers, reduce methane emission and land allocation to livestock production. However, this trait has late and costly measurements. Identifying gene expression changes combined with polymorphisms that affect residual feed intake variation is important for identify target regulatory polymorphisms that can be used in animal breeding programs. Diverse studies performed by our research group in a Nellore population, such as genome-wide association (GWA), association weight matrix (AWM) and RNA-seq analysis of liver tissue have been pointed *Prune homolog 2 (Drosophila) (PRUNE2*) as a potential candidate gene influencing feed efficiency. For this reason, we select this gene for a more detailed analysis considering haplotypes consisting of SNPs presented in the *Illumina Bovine HD Bead Chip.* For this, we used a population consisted of 591 steers with genotypes and RFI estimates available. After quality control filtering, performed by PLINK and Bioconductor/R, we used a total of 449.203 SNPs in our haplotype analysis. Genotype phasing and missing genotype imputation were performed using BEAGLE and the LDexplorer software was used for haplotype block recognition. After adjust the RFI estimates for fixed effects of contemporary group, which included type of pen, birth place, feedlot location and age of the animal effect as covariate, the genetic effects of haplotypes in *PRUNE2* gene was estimated by PLINK using a linear regression method. We identified 1 haplotype constituted of 4 SNPs: rs136298898 (C/T); rs133593644 (C/T); rs137799737 (A/C); rs132675549 (C/T), for which two out of 4 haplotype combinations had significant effect ($P \leq 0.05$) on RFI. Haplotype variation (1111) (p-value

= 0.0345) with 35.29% frequency was associated to lower RFI ($\beta = -0.0776$). On the other hand, haplotype variation (1112) (p-value = 0.0351) presenting 11.13% frequency was associated with high RFI ($\beta = 0.0846$). The *PRUNE2*gene has a potential role in biological processes, such as oxidation–reduction, metal ion and polyphosphate catabolic. Our findings indicated that this gene influence genetic variation of RFI, it is a strong candidate gene to be incorporated in Nellore breeding programs, nevertheless more studies considering this gene should be realized to understand better its biological role on feed efficiency in beef cattle.

Key Words: haplotype, feed efficiency, functional gene enrichment

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0319 A genome-wide association study for changes in dry matter intake due to temperature variation in an admixed beef cattle population. R. Ghebrewold[*1] and M. L. Spangler[2], *[1]University of Nebraska, Lincoln, [2]University of Nebraska, Lincoln.*

Environmental conditions, such as changes in ambient temperature, can cause changes in animal behavior and performance. In general it is believed that as ambient temperature increases, dry matter intake (DMI) of beef cattle decreases. However, our hypothesis was that the degree to which animals adjust their daily DMI due to changes in ambient temperature is partially controlled by underlying genetic effects. Consequently, the objective of this study was to estimate the genetic component of the regression of DMI on ambient temperature using an admixed beef cattle population consisting of various crosses of Angus, Simmental, and Piedmontese (n = 207). Ambient temperatures were received from a local weather station and DMI was collected via Calen gates. The feeding period averaged 155 d with a range of 114 d to 189 d depending on the management group. Individual animal regressions of DMI on ambient temperature were performed using either daily high or low temperatures over the entirety of the feeding period. Daily high temperatures (°C) averaged 15.07 with a range of −17.21 to 38.25. Daily low temperatures (°C) averaged 2.37 with a range of −28.33 to 15.26. The corresponding intercept and regression coefficient for each animal were used as phenotypes for a genome-wide association study (GWAS). Animals were genotyped with the BovineSNP50 Beadchip. Data were analyzed using GenSel software and a BayesC model fitting contemporary group (n = 4) and initial body weight (IBW) as fixed effects. A MCMC chain of 100,000 iterations was used with the first 40,000 samples discarded as burn-in. The proportion of SNPs having null effect (π) was set to 0.995. Posterior mean heritability estimates (SD) for the analysis when daily high temperature was considered in the regression were 0.64 (0.07) and 0.46 (0.08), for the intercept and slope, respectively. Similarly, posterior mean heritability estimates (SD) for the intercept and slope when the daily low temperature was considered in the regression were 0.69 (0.06) and 0.52 (0.07), respectively. These results suggest that changes in DMI due to changes in ambient temperature are under genetic control. Admittedly the population under study is small and admixed, suggesting that the genomic heritability estimates contained herein are potentially biased upward. However, the concept of applying this same procedure in larger populations warrants further investigation as a means of identifying animals that are less sensitive to environmental extremes.

Key Words: beef cattle, GWAS, feed intake

0320 An international effort to improve feed efficiency and reduce methane emissions in dairy cows through genomics. A. M. Wilson[*1], A. M. Butty[1], C. Baes[1], A. Cánovas[1], M. P. Coffey[2], E. E. Connor[3], M. De Pauw[4], B. Gredler[5], E. Goddard[4], G. Hailu[6], V. R. Osborne[7], J. E. Pryce[8], M. Sargolzaei[1,9], F. S. Schenkel[1], P. Stothard[10], E. Wall[2], Z. Wang[4], T. C. Wright[7,11], and F. Miglior[1,12], *[1]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [2]SRUC, Edinburgh, UK, [3]USDA-ARS, Animal Genomics and Improvement Laboratory, Beltsville, MD, [4]University of Alberta, Edmonton, Canada, [5]Qualitas AG, Zug, Switzerland, [6]Department of Food, Agricultural and Resource Economics, University of Guelph, ON, Canada, [7]University of Guelph, ON, Canada, [8]Department of Economic Development, Jobs, Transport and Resources, Bundoora, Australia, [9]Semex Alliance, Guelph, ON, Canada, [10]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [11]Ontario Ministry of Agriculture, Food and Rural Affairs, Guelph, ON, Canada, [12]Canadian Dairy Network, Guelph, ON.*

Increasing international demand for high quality dairy and meat products as well as greater awareness of climate change has put pressure on the livestock industry to deliver quality products while reducing its environmental impact. Enteric methane from cattle is a major contributor to greenhouse gas emissions and is a target of reduction through improving cow feed efficiency (FE) and reducing methane emissions (ME). The overall goal of this project is to produce genomic predictions for FE and ME that are ready for breeding application in the dairy cattle industry. Breeding for improved FE and less methane emitted will lower feed costs and reduce the industry's environmental footprint. Collecting phenotypes required for genetic improvement is presently very difficult and expensive, and to date, there has been limited to no direct selection for these traits in dairy cattle breeding. Recent genomic approaches provide the opportunity to finally select for these traits, but require a large reference population with accurate phenotypes. Data of individual feed intake and ME are being

collected from dairy cows and heifers, and whole DNA (Genome) and RNA (Transcriptome) sequence information will be used to identify new markers or mutations that influence the traits. The expanded Canadian database will be combined with international data from the United States, UK, Australia and Switzerland to create the world's first database to routinely validate genomic predictions for FE and ME. Milk spectral records will also be used to further develop predictions of FE and ME. In addition, research will be conducted to analyze the economic, environmental and social costs and benefits of the two traits, as well as the economic and social factors affecting the adoption of the technology at farm, industry and national levels.

Key Words: feed efficiency, methane emissions, dairy cattle

0321 Effect of diet energy level and genomic residual feed intake on dairy heifer performance.

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The objective of this study was to determine growth, feed intake, and feed efficiency of dairy heifers with different genomic residual feed intake (RFI) predicted as a lactating cow and offered diets differing in energy density. Post-bred Holstein heifers (128, ages 14–20 mo), were blocked by initial weight (high, medium-high, medium-low, and low weight) with 32 heifers per block. Each weight block was sorted by RFI (high, low) to obtain 2 pens of high and 2 pens of low predicted RFI for each block (8 heifers per pen). Low RFI heifers were expected to have greater feed efficiency than high RFI heifers. Dietary treatments were (1) a control diet with corn silage and alfalfa haylage (CON; 62.7% TDN, 11.8% CP, and 45.6% NDF, DM basis), and (2) a similar diet diluted with straw to reduce energy density (STR; 55.9% TDN, 11.7% CP, and 50.1% NDF, DM basis). Each treatment was randomly allocated to blocks to obtain a 2x2 factorial treatment arrangement of 2 RFI levels and 2 dietary energy levels. Diets were offered in a 120-d trial. Statistical analyses were performed using a MIXED procedure in SAS 9.3 with pen as experimental unit. Dry matter intake was affected by diet (11.0 vs. 10.0 kg/d for CON and STR, respectively; $P < 0.01$) but not RFI or the interaction of main effects ($P > 0.10$). Average daily gain was affected by the interaction of RFI and diet with low RFI heifers having higher gains than high RFI when fed STR (0.94 vs. 0.84 kg/d for low and high RFI, respectively, $P = 0.02$), but no difference for RFI groups when fed CON ($P = 0.25$). Feed efficiency was better for low RFI than high RFI heifers when fed STR (10.6 vs. 11.8 kg feed/kg gain for high and low RFI, respectively; $P < 0.01$), but no effect of RFI found when fed CON ($P > 0.10$). Body condition score increased when fed CON (3.8 vs. 3.5 for CON and STR, respectively; $P = 0.02$). Diet digestibility was greater for CON (58.4 vs. 50.8% DM digestibility for CON and STR, respectively; $P = 0.01$), which likely caused greater intake and gains for heifers fed CON. Based on these results, feed efficiency of heifers having different RFI is dependent on diet energy level with heifers having low RFI using the moderate energy (STR) diet more efficiently. The straw diet reduced intake and also maintained more desirable heifer weight gains.

Key Words: dairy heifer, residual feed intake, diet energy

0322 Genomic prediction for feed efficiency traits based on 50K and imputed high density SNP genotypes in multiple breed populations of Canadian beef cattle.

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Phenotypic data of difficult and/or costly to measure traits, such as feed efficiency, are usually available for a small number of beef cattle in each breed/population, resulting in low accuracy when within-breed/population genomic selection is attempted. Investigation of different strategies to combine data has the potential to improve the genomic prediction accuracy. In this study, we consolidated data of residual feed intake (RFI), average daily gain (ADG) and daily feed intake (DMI) from 7479 animals. These animals consisted of Canadian Angus ($N = 1158$), Charolais ($N = 707$), and four crossbred populations including Kinsella (UofAlberta, $N = 1487$), Elora (UofGuelph, $N = 746$), commercial animals PG1 ($N = 1885$) and TX ($N = 1496$). SNPs from the Illumina Bovine SNP50 Beadchip (50K SNP chip) and imputed Affymetrix high density (HD) (~428K SNPs) were employed to evaluate the genomic prediction accuracy at five-fold cross-validation using single-task Bayesian, simple data pooling Bayesian, and multitask Bayesian methods. The single-task Bayesian method estimates the SNP effects within a breed/population. The simple data pooling Bayesian method assumes the same SNP effect across breeds/populations and estimates the SNP effects based on the training data set that are simply combined from

all breeds/populations. The multitask Bayesian method estimates the SNP effects for each breed/population by also utilizing SNP effect information from other breeds/populations. The results showed that realized prediction accuracy of the single-task Bayesian method with the 50K SNP chip for RFI ranged from 0.22 ± 0.04 for Elora to 0.65 ± 0.03 for Angus. For ADG and DMI, the realized prediction accuracy of the single-task Bayesian ranged from 0.21 ± 0.03 for ADG in the Kinsella and TX populations to 0.57 ± 0.03 for DMI in Angus. The genomic prediction accuracies were improved by 0.02 to 0.17 with the simple data pooling Bayesian method except for RFI, in which the prediction accuracies were similar or slightly reduced by 0.02 to 0.07. The multitask Bayesian method yielded better prediction accuracy than the single-task Bayesian for most of the traits but did not perform better than the simple data pooling Bayesian method. Genomic prediction based on the imputed HD SNPs resulted in similar accuracies to that of the 50K SNP chip under all three methods. Further studies that include SNP functional information and/or intermediate phenotypes are underway to improve the genomic prediction accuracy for feed efficiency traits in Canadian beef cattle.

Key Words: beef cattle, genomic prediction, feed efficiency

0323 Use of multivariate statistical analyses to preselect SNP markers for GWAS on residual feed intake in dairy cattle. C. Dimauro[*1], E. Manca[2], A. Rossoni[3], E. Santus[3], M. Cellesi[4], and G. Gaspa[5], *[1]Università di , Italy, [2]Università di Sassari, Italy, [3]ANARB, Italian Brown Cattle Breeders' Association, Bussolengo (VR), Italy, [4]Università di Sassari, Italy, [5]Dipartimento di Agraria, University of Sassari, Italy.*

An index currently used to evaluate feed efficiency in cattle is the residual feed intake (RFI) whose heritability is around 0.20–0.40. Genome wide association studies (GWAS) can contribute to breeding programs aimed at improving RFI by detecting genomic regions and candidate genes that regulate it. However, the detection of significant SNP in GWAS with high density SNP platforms is often hampered by the severity of Bonferroni's *p*-value correction for multiple testing, due to huge number of tests. The pre-selection of markers could be an option to mitigate this problem. In the present research, a multivariate approach was used to select a pool of markers that could have any chances to be associated with RFI. Data consisted of 1092 Brown Swiss young bulls genotyped with the Illumina's 50K BeadChip. Animals were divided into two groups, according to RFI: high RFI (HRFI) for RFI > 0.5 standard deviations from the mean RFI; low RFI (LRFI) for animals with RFI < – 0.5 standard deviations from the mean. The two groups consisted of 266 and 280 animals, for LRFI and HRFI, respectively. Individuals that did not belong to the two groups were discarded.Three multivariate discriminant techniques were applied to data. The stepwise discriminant analysis was used to select 152 genome-wide most discriminant markers that were retained for the further analyses. The canonical discriminant analysis significantly separated the LRFI from the HRFI group, and the extracted canonical function was able to correctly assign 92% of animals to the correct group. Canonical coefficients associated to the 152 SNP in the canonical function were useful to rank markers according to their discriminant power. The ability of the selected SNP in depicting the RFI profile of calves was tested by developing a k-means cluster analysis that correctly classified 84% of individuals. For instance, a GWAS was also developed by regressing RFI phenotypes on SNP covariates. After *p*-values were corrected for multiple testing, no significant marker was obtained by using all original variables (41,183). When only the selected 152 SNP were used, 5 significant markers were obtained.

Key Words: SNP preselection, discriminant analysis, RFI

0324 Breed base representation in dairy animals of five breeds. H. D. Norman[*1], P. M. VanRaden[2], J. H. Megonigal[1], J. W. Dürr[1], and T. A. Cooper[2], *[1]Council on Dairy Cattle Breeding, Bowie, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

Inheritance of DNA from different dairy breeds can be determined by genotyping, just as individual ancestors such as parents, grandparents, or even great grandparents can be identified correctly in a high percentage of cases by genotyping even if not reported or reported incorrectly in pedigrees. Numbers of crossbreds in the U.S. dairy herd have increased by about 400% in the last decade. A procedure developed to determine the extent that alleles of various breeds appear in these crossbreds and in apparent purebreds was used to document breed composition in animals genotyped. The procedure constructed purebred reference groups (PRG) containing registered AI bulls (with milking daughters) chosen to represent 5 different breeds: Ayrshire (AY), Brown Swiss (BS), Guernsey (GU), Holstein (HO), and Jersey (JE). Any bull with an ancestor of another breed in his recorded 5-generation pedigree was excluded from the PRG. An exception was made for AY, for which other red breeds were permitted. The procedure was termed breed base representation (BBR) and estimated the similarity of alleles present in the 5 PRG to those of genotyped individuals. To measure BBR, the percentages of DNA contributed to a genotyped animal by each of the 5 breeds were calculated, summed, and then restricted to be between 0 and 100%. The more an animal's alleles resembled those in a PRG, the higher its BBR for that breed. The BBR help reveal the presence of either outcross bloodlines or crossbreeding, which are difficult to separate. Because animals vary even within breeds, the true source of the various breed alleles differs somewhat from BBR. Numbers of AI bulls in the reference populations in March 2016 were 442 AY, 5464

BS, 550 GU, 19,209 HO, and 3147 JE. Primary-breed BBR for those bulls were 97.2, 97.6, 97.8, 99.2, and 98.0%, respectively, which implies that they are purebreds; SD were 1.9, 1.2, 2.7, 1.2, and 1.0%, respectively. Mean primary-breed BBR were 94.8 for AY, 97.0 for BS, 97.8 for GU, 99.0 for HO, and 96.5% for JE for all genotyped males (201,283) and 95.0, 97.1, 96.9, 98.9, and 96.5%, respectively, for all genotyped females (994,949); SD ranged from 1.2 for males and 1.5% for females (HO) to 5.6 and 4.4% (AY), respectively. Genetic predictions for animals with crossbred genetics in their pedigrees could be obtained in the future by weighting marker effects from each breed by BBR.

Key Words: allele, genomics, purebred

0325 Estimation of the composition of four U.S. swine breeds using genomic data. S. A. Funkhouser[*1], R. O. Bates[2], C. W. Ernst[2], D. W. Newcom[3], and J. P. Steibel[2,4], *[1]Genetics Program, Michigan State University, East Lansing, [2]Department of Animal Science, Michigan State University, East Lansing, [3]National Swine Registry, West Lafayette, IN, [4]Department of Fisheries and Wildlife, Michigan State University, East Lansing.*

Lines of purebred pigs are essential for use in crossbreeding systems within the commercial industry. However, verification of breed purity can be challenging, and using color test matings to confirm white color in the Yorkshire or Landrace breeds is time-consuming and costly. Alternatively, advances in the availability and analysis of genomic data may enable rapid and precise determination of breed composition. Here, we have refined methods for determination of breed composition in U.S. populations of four swine breeds, and white color in Yorkshire or Landrace breeds using SNPs present on the GeneSeek Genomic Profiler for Porcine LD platform. These methods use a linear model in which unknown animal genotypes are regressed on a panel of allele frequencies, derived from reference Duroc, Landrace, Hampshire and Yorkshire purebred animals. Only SNPs that are not fixed across all reference animals and have a genotyping call rate of 90% or greater were used in the model. Model coefficients were constrained to be non-negative and to sum to 1.0, facilitating their interpretation as breed composition coefficients. By simulating 1000 admixed animals of known composition, a strong correlation was observed between the actual and estimated breed proportion of the simulated animals ($R^2 = 0.94$) so long as the actual breed of the simulated animals was reflected in the reference panel. Among a real dataset consisting of 920 Yorkshire sires, 95% of the animals were evaluated to have a Yorkshire breed proportion of 0.825 or greater. Determining that an animal may be highly purebred genome-wide does not preclude from failing a color test mating, in which alleles at particular genes such as *KIT* play a major role in color segregation patterns. Using seven SNPs flanking *KIT* (spanning chr8:43Mb– 44Mb), we have demonstrated that SNP haplotypes derived from the reference animals may be used to compute breed composition probabilities for a genomic segment flanking *KIT* of an unknown test animal. From the real Yorkshire sire dataset, 95% of the animals were estimated to have at least a 0.439 KIT-based breed composition probability of being a white breed. Dual use of genome-wide breed proportions and gene-based breed probabilities has great potential to inform swine breeders of the overall purity of an animal, as well as breed characteristics around particular key genes. Such knowledge may reduce the need to perform color test matings or other time-consuming and expensive procedures for breed verification.

Key Words: breed composition, swine, SNPs

0326 Genome-wide association study and accuracy of genomic prediction for teat number in Duroc pigs using genotyping by sequencing. C. Tan[*1,2], Y. Da[2], Z. Wu[3], D. Liu[3], X. He[2,3], N. Li[1], and X. Hu[1], *[1]State Key Laboratory for Agrobiotechnology, China Agricultural University, Beijing, [2]Department of Animal Science, University of Minnesota, St. Paul, [3]College of Animal Science, South China Agricultural University, Guangzhou.*

Swine teat number is related to a sow's ability to rear piglets to weaning age. The objective of this study was to identify genetic factors affecting swine teat number, evaluate the accuracy of genomic prediction, and evaluate the contribution of significant genes and genomic regions to the total genomic heritability and prediction accuracy using 84,151 autosome single nucleotide polymorphism (SNP) markers from genotyping-by-sequencing on 2936 Duroc boars. Heritability of teat number estimated using genomic restricted maximum likelihood estimation was 0.397 ± 0.033 for additive heritability and was 0.055 ± 0.027 for dominance heritability. Observed prediction accuracy calculated as the average correlation between the genomic best linear unbiased prediction and the phenotypic observations of validation individuals in a 10-fold validation study was 0.44 ± 0.04. Genome-wide association study (GWAS) and heritability estimates of individual SNPs identified a cluster of SNPs in or near the *PTGR2*, *FAM161B*, *VRTN* and *AREL1*genes in the 102.5–104.3 Mb region of chromosome 7 to have highly significant SNP effects on teat number. Fitting 10 SNPs in or near these four genes as fixed non-genetic effects in the model eliminated the significant effects in this region, reduced the additive heritability by 5.9% and reduced the prediction accuracy by 6.88%. Chromosomes 1, 2, 11, 12, 14, and 17 also had significant effects on teat number or substantial SNP heritabilities, and removal of those significant effects by fitting them as fixed non-genetic effects in the model reduced the prediction accuracy by 0.74–2.59% and reduced the total SNP additive heritability by 0–2.69%. The results indicated that swine teat number was

affected by genes with relatively large effects and that many more genes were also relevant to the accuracy in predicting teat numbers using the approach of genomic prediction.

Key Words: teat number, GWAS, genomic prediction, heritability

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0327 Genome-wide association study for supernumerary teats in Swiss Brown Swiss Cattle reveals LGR5 as a major gene on chromosome 5.

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Supernumerary teats (SNT) are any teats present on a cow's udder other than the regular four. In Swiss Brown Swiss cows, 19.9% carry SNT. Different stages of development of SNT are observed from rudimentary appendices to functional and possibly lactating teats. SNT may promote mastitis, impeach good placement of the milking machine and lower the market price of the animals. No genetic analysis of the trait has been done in this cattle population, although SNT have been routinely recorded with other conformation traits since 1995 in Switzerland. This study aimed to investigate the genetic architecture of this trait through genome-wide association studies (GWAS) performed with imputed whole-genome sequence.

Two trait definitions were used: Udder Clearance (UCT) considering whether a cow is carrier of any SNT or has a clear udder and Presence of Supernumerary Mammary Gland (PMG) opposing animal carrier of completely developed and possibly functional SNT with animals with a clear udder or carrier of a rudimentary SNT. Breeding values were estimated for Brown Swiss sires of at least 20 daughters with SNT records using an animal model including the random effects expert-by-year, farm-by-year and animal. The animal's dam life stage—heifer or cow—during its parity was fitted as a fixed effect in the same model. Single SNP regression using deregressed proofs of 1519 bulls with genotypes imputed to the variant list of the 5thRun of the 1000 Bulls Genome Project permitted discovery of three important regions on BTA5, BTA17 and BTA20 associated with the presence or the development of SNT.

Regions on BTA17 and BTA20 reached clearly lower *p*-values (10^{-7} vs. 10^{-4}) when associated to PMG than UCT, while variants on BTA5 were significantly linked to both trait definitions. No candidate genes on BTA 17 and BTA20 were found after functional analysis. On BTA5, however, the *leucine-rich repeat-containing G protein coupled receptor 5* (*LGR5*) can be considered as the major gene for our trait. Encoding a protein known as an up-regulator of the Wnt pathway and having an expression level impacting the mammary gland development, *LGR5* also carries a synonymous mutation that is highly associated to SNT.

To conclude, GWAS in the Swiss Brown Swiss population revealed *LGR5* on BTA5 as a candidate gene influencing the presence and development stage of supernumerary teats.

Key Words: dairy cattle, genome-wide association, supernumerary teats

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0328 Genomic and polygenic evaluations for milk and fat yields in Holstein upgraded Thai dairy cattle.

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The objectives of this study were to compare variance components, genetic parameters, prediction accuracies, and ranking of animals for 305-d milk yield (MY) and 305-d fat yield (FY) in a Holstein upgraded Thai dairy population using two genomic models and a polygenic model (PM). One genomic model utilized 7656 SNP (GM7K) and the other one used 74,144 actual and imputed 80K SNP (GM80K). Phenotypic and pedigree data were from 8361 first-lactation cows located in 810 farms that had their first calving between 1989 and 2014. Variance components and genetic parameters were estimated using REML procedures. Fixed effects were contemporary group (herd-year-season), calving age and heterosis. Random effects were animal additive genetic and residual. Estimates of variance components and heritabilities for MY and FY from GM80K were the highest, followed by those from GM7K, and PM had the lowest values. Correlations estimates between MY and FY were similar across models. The GM80K yielded higher prediction accuracies (38.8% for MY and 31.9% for FY) than GM7K (36.7% for MY, and 31.4% for FY) and PM (31.5% for MY, and 24.4% for FY). Different MY and FY EBV rankings existed across models. The highest rank correlations were between GM80K and GM7K (0.90 for MY, and 0.91 for FY), followed by those between GM80K and PM (0.84 for MY, and 0.83 for FY), and the lowest ones were between GM7K and PM (0.80 for MY, and 0.80 for FY). Animal rankings from GM80K should be preferred because its EBV had higher accuracy than EBV from GM7K and PM. Faster selection responses for MY and FY would be expected from GM80K than from GM7K and PM in this Holstein upgraded population.

Key Words: dairy cattle, genomic evaluation, imputation

0329 Genome-wide association study for loci associated with digital dermatitis and pododermatitis circumscripta in Holstein cattle. A. M. Oberbauer*[1], A. L. Danner[1], J. M. Belanger[1], T. R. Famula[1], and J. M. Heguy[2], [1]*Department of Animal Science, University of California, Davis,* [2]*UCCE Stanislaus and San Joaquin Counties, Modesto, CA.*

Estimates of dairy cattle lameness range up to 50% of individuals in a herd being lame at any one time. The economic costs associated with lameness include premature culling, treatment, reduced reproductive fertility, and decreased milk while there are welfare concerns associated with the pain caused by lesions. Two of the most common lameness disorders are digital dermatitis and sole ulcers (pododermatitis circumscripta). Though the etiology of the two conditions differs greatly, heritability estimates for digital dermatitis and sole ulcers have been determined to be 0.4 and 0.3, respectively, signifying moderate heritability and amenable to genetic selection programs designed to reduce prevalence. To determine loci associated with each condition, genome wide association studies (GWAS) were conducted. Using diagnostic hoof trimming records, as well as digital dermatitis and sole ulcer sire EBVs from two commercial dairy farms in California, blood samples were taken from 150 selected Holstein cows representing 56 cases and 94 controls. DNA extracted from each cow was genotyped with the Illumina BovineHD BeadChip. Derived SNP genotypes were filtered such that only SNPs having call rates ≥ 0.8, minor allele frequencies < 0.5, Hardy-Weinberg equilibria (HWE) p < 0.05, and Fisher's HWE p < 0.05 were included in the GWAS using Golden Helix SNP and Variation suite. Association testing using an additive, recessive, and dominant model for inheritance for each condition was performed using a correlation/trend test. Population stratification was corrected for using a principle component analysis. Haplotype block detection with linkage disequilibrium and association testing were also performed. Significant associations ($P <$ sup > genome < /sub > ≤ 0.05;-log 10≥ 1.3) were noted on chromosomes 3, 8, and 29 for digital dermatitis and a highly significant haplotype (Χ < sup > 2 < /sup > -log10 P ≥ 7.00, 95% CI) was noted on chromosome 29. Genome wide significance was reached on chromosomes 3 and 5 for sole ulcers though significant haplotype blocks were located on chromosomes 17, 25, and 28. An immune mediating candidate gene, *TIRAP*, on chromosome 29 was sequenced in three digital dermatitis cases and three controls, but no significant variations were noted. Future work will focus on further exploring the associated regions with the objective of identifying potential markers to aid in selecting breeding stock to reduce the incidence of both conditions.

Key Words: digital dermatitis, dairy cattle, genome-wide association

0330 Genome-wide associations study for somatic cell score in Russian Holstein cattle population. A. A. Sermyagin*, E. A. Gladyr', and N. A. Zinovieva, *L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation.*

The cattle health traits are one of the most important selection features but their improvement in short term is limited by low heritability. For the Russian Holsteins the utilization of fitness traits such as metabolic disorders, genetic diseases and especially udder health became the main goals. The developing new methods in dairy cattle have prompted us to find out associations between SNPs and sires' genomic enhanced breeding values (GEBV) for somatic cell score (SCS) to understand the additive genetic contribution to potential mastitis resistance. According to the first step for implementation of genomic selection in Russia we genotyped 256 bulls using Illumina BovineSNP50 BeadChip. The field records for somatic cell count (SCC) in the milk of 3419 first-calving daughters of 141 Holstein sires from 26 herds were included in the dataset. For sires with daughters' records we calculated the deregressed estimated breeding values (EBV) using BLUP AM. For the sires without SCC daughters' records we got the direct genomic values (DGV) calculated through GBLUP. The DGVs with the EBVs or parents' averages were combined using weight 0.8 to get GEBV as pseudo-phenotypes for common dataset. After quality check in Plink 1.9, the 41383 SNPs were taken for further analysis. The heritability coefficients for SCC and SCS were 0.202 and 0.142, respectively. We detected 10, 67, and 289 significant SNPs using Bonferroni ($P < 1.21 \times 10^{-6}$), permutation procedure (1×10^6 numbers per SNP) and FDR ($P < 0.05$) tests, respectively. The most of the closest and functional related genes involved for cellular, metabolic and immune functions were signed to SNPs: rs41981595 (*TRNAC-ACA*, $P = 2.7 \times 10^{-10}$), rs109696042 (*TCIRG1*, $P = 1.3 \times 10^{-7}$), rs109799695 (*ACO1*, $P = 1.6 \times 10^{-7}$), rs29026486 (*UQCC*, $P = 7.5 \times 10^{-7}$) and rs43298370 (*CERS6*, $P = 1.2 \times 10^{-6}$). Additive genetic variances for these genes ranged from 9.0 to 14.9%. The most of considerable polymorphisms were identified on chromosomes 2, 4, 8, 9, 13, 20, 21, and 29. Some SNPs without a clear causal mutation for SCS were identified (rs109186647, rs110041812, rs41633009, rs110507090 and rs41589293). Our knowledges of gene distribution and quantitative trait loci for SCC combined with the bulls' mating strategy allow decreasing the incidence of mammary gland infection in Russian Holstein population. Supported by the Russian Scientific Foundation, project number 15–16–00020.

Key Words: genome-wide associations, Russian Holstein cattle, somatic cell score

0331 Genome-wide association study of milk coagulation properties in dairy sheep. G. Gaspa[1], J. Serdino[1], M. G. Manca[1], S. Sorbolini[1], R. Negrini[2], C. Dimauro[3], and N. P. P. Macciotta[*1], *[1]Dipartimento di Agraria, University of Sassari, Italy, [2]Associazione Italiana Allevatori, Roma, Italy, [3]University of Sassari, Italy.*

The objective of this work was to seek genomic regions associated with milk coagulation (MCP) properties of ovine milk. A total 478 Sardadairy breed ewes were genotyped with the 60K SNP ovine beadchip (Illumina Inc., San Diego, CA). Individuals and SNPs with > 2.5% missing data were discharged. The remaining missing genotypes were imputed using BEAGLE 4.1 and checked for quality control (QC): SNPs that did not map on any chromosome, with minor allele frequency < 0.1% or statistically deviating from the Hardy-Weimberg equilibrium ($P < 0.01$) were removed. Individual milk samples from mid-late lactating ewes (45–249 d postpartum) added with preservatives (bronopol, 62,5 μL/100 mL) were analyzed to determine MCP by using Formagraph Instrument (Foss Electric A/S, Hillerød, Denmark) The three classical MCP were measured: rennet coagulation time (RCT), curd firming time (k_{20}) and curd firmness (a_{30}). Individual laboratory cheese yield (ILCY, % w/v) was also measured. A GWAS was performed with the GRAMMARgenomic control (GC) approach, that accounts for genetic substructure in the population, as implemented in the Genabel R package. MCP were pre-corrected for the systematic effects of flock-test date, days in milk, parity, lambing month, rack position and the random polygenic additive effect. The genetic (co)variance between animals was structured using the genomic relationship matrix. Environmental residual of the model were analyzed with a linear model including SNP genotype as covariate and statistical significance of the SNP effects were adjusted using the Bonferroni correction on the effective number of independent tests estimated on haplotype blocks bases. A total of 474 individuals and 47,202 SNPs pass the QC. Ten SNP passed the significance threshold in chromosomes 3, 7 10, 12, 13, and 25. Of interest s69172.1 (90,362,719 bp) in OAR7 was close to a QTL affecting fat and protein yield in Sheep. In chromosome 12 one SNP was both associated with RCT and k_{20} (OAR12_80896495.1) and another SNP (OAR12_39255725.1) affected significantly ILCY. Unexpectedly, no significant association were found on OAR6 where casein cluster maps.

Key Words: milk coagulation, GWAS, sheep milk

0332 Genetic markers identification and genotyping for resistance to internal parasites in sheep and goat infected with *Haemonchus contortus*. Z. M. Estrada Reyes[*1], A. L. Goetsch[2], T. A. Gipson[3], Z. Wang[4], M. Rolf[5], T. Sahlu[3], R. Puchala[3], S. Zeng[4], and R. Mateescu[1], *[1]University of Florida, Gainesville, [2]American Institute for Goat Research, Langston University, Langston, OK, [3]American Institute for Goat Research, Langston University, Langston, OK, [4]Langston University, Langston, OK, [5]Oklahoma State University, Stillwater.*

Gastrointestinal nematode infections (GNI) have a great economic impact for small ruminant production in humid areas. In these regions, *Haemonchus contortus* is the most important gastroenteric nematode. Unfortunately, the indiscriminate use of anthelmintic drugs to control GNI has generated resistance to these chemical compounds. Among the alternative strategies proposed, the genotypic and phenotypic variability of the small ruminants have encouraged the identification of the most resistant animals. To identify genetic markers associated with the control of nematode populations within the host, the detection of single nucleotide polymorphisms (SNPs) OLA-DRA20 gene was performed in sheep and goats experimentally infected with *H. contortus*. Animals from 3 different breeds of sheep and goat were used for the study during 3 yr of evaluation. Individuals were selected by using positive assortative mating of the most resistant individuals each year and received a complete diet (15% Crude Protein) ad libitum for the duration of the trial. Animals were treated with levamisole (7.5 mg/kg of live weight) 3 wk before the start of the trial. After deworming,

Table 0332.

Table 1. General Linear Model using SQRTFEC as dependent variable

Source	DF	Type III SS	Mean Square	F Value	Pr > F
Genotype	2	1504.089791	752.044895	3.57	0.0318
Species	1	503.004815	503.004815	2.39	0.1255
BREED(Species)	4	2451.739709	612.934927	2.91	0.0252
ADG	1	1609.890360	1609.890360	7.64	0.0068
MPCV	1	2003.812646	2003.812646	9.51	0.0026

Parameter	Estimate		Standard Error	t Value	Pr > |t|
Intercept	103.3585848	B	15.80079300	6.54	<.0001
Genotype AA	-10.6063506	B	4.07398853	-2.60	0.0106
Genotype GA	-9.7173711	B	4.83175843	-2.01	0.0469
Genotype GG	0.0000000	B	.	.	.
Species 1	8.1320130	B	6.54058182	1.24	0.2166
Species 2	0.0000000	B	.	.	.
BREED(Species) Dorper 1	7.6681621	B	5.61469332	1.37	0.1750
BREED(Species) Katahdin 1	5.1096637	B	5.59148000	0.91	0.3630
BREED(Species) St.Croix 1	0.0000000	B	.	.	.
BREED(Species) Kiko 2	-3.0964142	B	5.12691557	-0.60	0.5472
BREED(Species) LBoer 2	17.0954108	B	6.29246453	2.72	0.0077
BREED(Species) Spanish 2	0.0000000	B	.	.	.
ADG	-0.0855908		0.03096787	-2.76	0.0068
MPCV	-1.8844031		0.61112131	-3.08	0.0026

each experimental animal was infected with 10,000 L_3 of *H. contortus* per kg of body weight per oral route. Fecal samples were obtained to determine fecal egg count using the modified McMaster technique. Blood samples were collected from the jugular vein with sterile vacuum tubes with sodium heparin to evaluate blood package cell volume (PCV) and levels of IgA, IgM and IgG. DNA was purified from blood samples using DNeasy Blood & Tissue Kit (Qiagen). One SNP in the OLA-DRA20 segregating in this population was analyzed using High Resolution Melting assays and three genotypes were observed (AA, GA, GG). A GLM was fitted with MPCV, DMI, ADG, RFI, IgM, IgG, IgA levels and genotype as predictors and the square root of the mean of FEC as the response variable. According the results, the best significant predictors to fit the model were Genotype, Breed (Species), MPCV, DMI, ADG and genotype ($p < 0.05$). In conclusion, the polymorphism in the OLA-DRA20 gene could have an important role in the immune mechanisms against *H. contortus* infections in sheep and goats. Indeed, these results provided evidence that there is a significant effect among the square root of the mean of FEC and production traits between breeds within species.

Key Words: *Haemonchus contortus*, small ruminants, OLA-DRA20 gene

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0333 Genomic analysis of lactation persistency in four breeds of dairy cattle.

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The objectives of this study were to determine gains in reliability from the addition of genomic information to genetic evaluations for best predictions of lactation persistency in U.S. Ayrshire (AY), Brown Swiss (BS), Holstein (HO), and Jersey (JE) cattle, and to identify genomic regions with large effects on those traits. Data consisted of lactations initiated by calvings on or after January 1, 1997, stored in the national dairy database (NDDB) at the Council on Dairy Cattle Breeding (Bowie, MD). Persistencies were computed by multiple-trait best prediction for milk (PM), fat (PF), and protein (PP) yields. Genetic analyses were conducted on a within-breed basis using identical repeatability animal models and breed-specific (co)variance components. Traditional and genomic PTA and reliabilities were computed by GBLUP using the national genomic evaluation system. Gain in reliability from the addition of genomic information was calculated as the difference between the realized genomic reliability and the reliability of traditional PA using a cutoff study. Predictor populations consisted of animals with traditional genetic evaluations in April 2014, and validation sets included animals with traditional genetic evaluations in August 2009. Allele effects were converted to additive genetic standard deviations, and closestBed 2.17.0 was used to obtain a list of genes that contained SNP or were within 25 kbp of a genotyped SNP. Gene names and coordinates were those published in Cow Ensembl Release 79. Reliability gains averaged 8% in AY, 5% in BS, 12% in HO, and 12% in JE. The SNP ARS-BFGL-NGS-4939 at 1801,116 bp on BTA14, downstream of the *DGAT1* gene, had the largest effects on PM and PF in HO and PM in JE of any marker in the analysis. BovineHD1600000386 at 1554,597 bp on BTA16 had largest effect on PF and PP in JE, in a region previously reported to effect fat and protein yields and percentages. The SNP with the largest effects in AY were located on the X chromosome in regions reported to affect fat and protein yields and percentages in HO. The largest effect for PM in BS was in a region of BTA19 associated with MY in Chinese Holsteins, while the largest PF and PP effects were in regions of the X chromosome reported to affect fat and protein yield in U.S. Holsteins. Genetic correlations of yield with persistency range from −0.32 to 0.26, so loci with large effects on yield also can affect persistency.

Key Words: association analysis, best prediction, reliability

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0334 Genome-wide association study for tick count and infection level of *Babesia bovis* traits in Angus cattle.

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Tick and tick-borne diseases, including babesia (*B. bovis*), constitutes a major drawback to improve productivity of beef cattle in the tropics, especially for systems where *Bos taurus* cattle animals and their crosses are used. To identify highlight regions highly associated with the studied traits, genome-wide association studies (GWAS) were performed. Tick counts and blood sample were taken in two occasions from each of 355 Angus cattle at a farm located at Rio Grande do Sul State, Brazil. Blood samples were collected, in tubes containing EDTA for DNA extraction. *B. bovis* quantification was performed using both qPCR technique from genomic DNA of each animal with specific primers for this protozoary and the absolute quantification method. Animals were genotyped by using Illumina GeneSeek GGP Bovine 150K. Quality control criteria were: MAF < 2%, call rate < 92%, and animal call rate (with less than 90% of SNPs called). After edits, 144,924 SNPs and 350 animals were available. Fixed effects in the model included contemporary groups and effect of data collection period, as well as additive genetic direct and permanent environmental effects as random. Variance components and genetic parameters were estimated by Bayesian inference in a bivariate analysis using GIBBS2F90 software, and the effect of each SNP was estimated using methods Bayes C as implemented in the GS3 software. Also, it was

used de-regressed EBV. The mean h^2 were 0.207 and 0.059 for tick count (TC), and infection level of *Babesia bovis* (IB), respectively. The genetic correlations were 0.079 between TC and IB. Variances were calculated for windows of 1-Mb SNP. The results showed that the top 10 SNP windows for each trait explained a total of 51.45%, and 3.09% of genetic variance for TC, and IB, respectively. The 10 most significant markers for TC were located on chromosomes 4, 5, 6, 10, 12, 16, 19, 22, 29, and 30. The 10 most significant markers for IB were located on chromosomes 3, 5, 7, 8, 14, 20, and 24. There are others studies that indentified QTLs located in regions of top SNP associated with TC. Therefore, genomic regions identified may be important for the variation of tick count, but less important for infection level of *Babesia bovis* traits in Angus cattle. Acknowledgment: Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil.

Key Words: *Bos taurus,* GWAS

0335 Identification of loci associated with susceptibility to bovine paratuberculosis using imputed genotypes based on whole genome sequencing.

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Johne's disease or bovine paratuberculosis is a contagious bacterial infection in cattle caused by *Mycobacterium avium* ssp. *paratuberculosis* (*Map*). Previous genome wide association studies (GWAS) to identify loci associated with susceptibility to *Map* infection in Holstein and Jersey cattle have been performed using the Illumina BovineSNP50 BeadChip which consisted of approximately 54,000 SNPs in three released BeadChip versions. Although uniform SNP spacing was a design objective, a number of genomic regions were under-represented by markers. The objective of this study was to determine if there were loci associated with susceptibility to *Map* tissue infection located within these under-represented areas of the Bovine SNP50 BeadChip that would be identified using genotypes imputed to whole genome sequence (WGS). To do this, BovineSNP50 genotypes of 409 Holstein cows (162 cases and 247 controls) were first imputed using Beagle 4.1 to the density of the Illumina BovineHD BeadChip using 2703 previously genotyped Holstein cattle as a reference. The imputed BovineHD data were then imputed to WGS level (35,431,201 indels and SNPs) with FImpute using phased Run 4 WGS data for 1147 previously sequenced cattle from the 1000 Bull Genomes Project as a reference. Genotype quality control was performed using the same parameters as for the BovineSNP50 data and any SNP with a call rate < 90% or MAF < 1% was removed. After quality control, 16,063,342 indels and SNPs remained for analysis. A GWAS was performed with Efficient Mixed Model Association expedited (EMMAX) additive and allelic models and the most highly significant 500 loci were compared with the BovineSNP50 GWAS results. With the imputed genotypes, 13 and 5 new QTL were identified with the allelic and additive models, respectively, and 14 new QTL were identified by both models ($p = 4.17\text{x}10^{-6}$ to $p = 4.45\text{x}10^{-5}$). In addition, 81, 18, and 67 previously identified QTL were identified under the allelic, additive or by both models and were more precisely finely mapped using the imputed genotypes. In conclusion, imputation of BovineSNP50 data to WGS was effective for identifying new QTL and fine-mapping previously identified QTL.

Key Words: paratuberculosis, imputation, GWAS

0336 Joint SNP-haplotype analysis for genomic selection based on the invariance property of GBLUP and GREML to duplicate SNPs.

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Haplotype analysis of SNP markers in genomic prediction and estimation may utilize haplotype effects unaccounted for by single-SNP analysis, whereas haplotype analysis alone may not account for all single-SNP effects. The objective of this study was to establish a theoretical model by mathematical derivation and validation studies to show why haplotype analysis and the joint SNP-haplotype analysis may improve the accuracy of genomic prediction. We first modeled the genotypic value of a two-haplotype genotype as the summation of the single-SNP effects and the haplotype effects unaccounted for by the single SNPs within the haplotype block plus a potential loss of single-SNP effects of the haplotypes. Then we established an invariance property to duplicate SNPs. Assume that a set of SNP markers is duplicated r times in the mixed model. Genomic best linear unbiased prediction (GBLUP) of genetic values (additive, dominance and genotypic values) of individuals and SNP genetic variance components as well as the associated heritability estimates by genomic restricted maximum likelihood estimation (GREML) are invariant to the duplication of SNPs, and GBLUP of SNP additive, dominance and genotypic effects differ from those without duplicate SNPs by the square root of r. Based on this invariance property, adding single SNPs to the haplotype analysis would recover any loss of single-SNP effects of haplotype-only analysis and maintain the haplotype effects not utilized by single-SNP analysis without overestimating single-SNP effects. Validation studies using 6000 individuals with 423,131 SNPs from the Framingham Heart Study showed that heritability estimates under the joint SNP-haplotype model were lower than those from the haplotype-only model, confirming that adding SNPs to the haplotype model did not result in overestimation

of the total genetic contribution. In most validation samples, haplotype analysis was at least as accurate as single-SNP analysis, and the joint SNP-haplotype analysis had further improvement in prediction accuracy over the SNP-only or haplotype-only models. These validation results provided a confirmation of the benefit predicted by our theoretical model for the joint SNP-haplotype analysis of genomic prediction based on the invariance property of duplicate SNPs.

Key Words: genomic selection, haplotype, GBLUP, GREML, SNP

0337 Practical approximation of accuracy in genomic breeding values for a large number of genotyped animals. S. Tsuruta[*1], D. Lourenco[1], Y. Masuda[1], D. W. Moser[2], and I. Misztal[1], *[1]University of Georgia, Athens, [2]Angus Genetics Inc., St. Joseph, MO.*

Accuracy defined as the squared correlation between true and genomic EBV (GEBV) is required in genomic evaluations and it can be approximated by contributions from phenotypes, pedigrees, and genotypes. In single-step genomic BLUP, contribution from genotypes is based on inverses of genomic (G) and pedigree (A22) relationship matrices for genotyped animals. The objective of this study was to develop a less expensive formula to calculate accuracy in GEBV for a large number of genotyped animals. As alternative contributions from genotypes, we considered the mean square difference between off-diagonals for G and A22 (GmA22) and the number of genotyped animals or the number of effective SNP markers (ESM) as well as parent average accuracy (ACCPA). The ESM was calculated as the number of the largest eigenvalues of G explaining 99% of variation. The following three formulas were proposed: F1 = heritability × ESM × GmA22 × (1 + ACCPA); F2 = 1 + heritability × ESM × ACCPA × GmA22; and F3 = 1 + ACCPA. Phenotypes for birth weight (BW) and post weaning gain (PWG), pedigrees, and genotypes were provided by American Angus Association. The BW dataset consisted of 20K records and 91K animals with 20K genotyped animals. Two PWG datasets consisted of 30K records and 122K animals with 30K genotyped animals, and 35K records and 202K animals with 60K genotyped animals, respectively. The three formulas were compared with the accuracy calculated from prediction error variances (PEV) obtained from the inverse of the left-hand side of the mixed model equations. For direct GEBV on BW, correlations of PEV with F1 and F2 were the highest (0.86), but F1 was overestimated and the MSE was larger. For maternal GEBV on BW, correlations between PEV and F1 and F2 were the highest (0.85). For GEBV on PWG with 30K genotyped animals, correlations of PEV with F1 and F2 were the highest (0.82), but the MSE for F2 was larger. With 60K genotyped animals, correlations between PEV and F1 and F2 were also high (0.79 and 0.78, respectively), but F2 was underestimated and the MSE was larger. Both F1 and F2 gave reliable approximations of accuracy in GEBV. For each data set, the mean accuracy can be adjusted to reduce the bias. The new formula can calculate approximations of accuracy in GEBV for a large number of genotyped animals at a low cost.

Key Words: genomic breeding values, accuracy, Angus

0338 Comparison of transcriptome profiles in longissimus dorsi muscle between bulls and steers of Korean cattle. M. Baik, S. J. Park*, and N. Sang Weon, *Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Korea (The Republic of).*

Castration of bulls improves beef quality including intramuscular fat (IMF) content and tenderness. Studies have revealed that castration changes expression of many genes associated with beef quality and IMF deposition in longissimus muscle (LM). Limited information is available for global gene expression changes in the LM following castration. Objectives of this study were to understand global transcriptome changes following castration in the LM of beef cattle and to identify new genes associated with beef quality. By using RNA-sequencing (RNA-seq) technique, transcriptome profiles were compared in the LM between bulls and steer of Korean cattle. LM tissues samples of ten bulls and ten steers were prepared, and LM RNA samples from three bulls and three steers were used for the RNA-seq. Among total 18,027 genes identified by RNA-seq and subsequent read mapping analysis with TopHat software, total 1146 transcriptomes (521 upregulated and 625 downregulated genes following castration) were differentially expressed genes (DEGs) in the LM between bulls and steers with false discovery rate at < 0.05 and log fold change above 1.5. Pathway analysis with the 1146 DEGs showed significant ($P < 0.05$) changes in 9 KEGG pathways, including complement and coagulation cascade and peroxisome proliferator-activated receptor signaling. We conducted quantitative PCR (qPCR) with ten genes of the complement and coagulation cascades using LM tissue samples of ten bulls and ten steers. The qPCR data were analyzed using GLM of SAS. The qPCR analysis confirmed differential ($P < 0.05$) expression patterns of all genes including coagulation factor III and mannan-binding lectin serine peptidase 1. In conclusion, global transcriptome analysis using RNA-seq reveals for the first time that castration changes expression of many genes involved in complement and coagulation cascade pathway, which may be linked to beef quality.

Key Words: castration, complement and coagulation cascade, beef cattle

0339 Gene network regulated by microRNAs suggests modulation of fat deposition in cattle.
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Meat quality depends on many factors such as nutrition, management system and genetic. The mainly attributes of meat quality besides tenderness are juiciness and flavor, which are associated with intramuscular fat (IMF) content. In this study microRNAs expressed in Longissimus dorsi muscle from *Bos indicus* were identified to better understand the biological processes related to IMF deposition in skeletal muscle. MicroRNAs are small non-coding regulatory RNAs that play an important role in post-transcriptional gene regulation in many tissues and are associated with numerous biological processes. Total RNA was extracted from Longissimus dorsi muscle of 30 steers with extreme values of genomic estimated values (GEBV) for IMF content, classified into High (H) and Low (L) IMF content groups. MicroRNA libraries were constructed and sequenced using NGS technology (MiSeq-Illumina) generating 1 million reads/sample. MicroRNAs were filtered by FastX, annotated by miRDeep2 and, differentially expressed (DE) microRNAs were identified by DESeq2 package. A total of 463 known microRNAs were identified and six of them were DE (FDR < 0.1). MicroRNAs bta-let-7f, bta-let-7a-5p and bta-miR-423 were downregulated, while bta-miR-100, bta-miR-143 and bta-miR-146b were upregulated in the L group. MicroRNAs target genes were identified by Ingenuity Pathways Analysis (IPA®) MicroRNA Target Filter tool and filtered by muscle RNA-Seq data obtained in previous studies, creating a list with 2520 target genes. The metabolic pathways and gene networks were constructed and analyzed by IPA® software, to identify enriched biological processes and genes regulated by microRNAs that were associated with lipid metabolism. Important genes for fatty acid metabolism were related in three gene networks: "Gene Expression, Cell Cycle, Cancer," involving 32 target genes; "Drug Metabolism, Lipid Metabolism, Molecular Transport," with 32 target genes and "Lipid Metabolism, Small Molecule Biochemistry, Vitamin and Mineral Metabolism," with 30 target genes. This last network involved genes such as PPARGC1A, MYCN, ESR2 and ARL4D, targets of downregulated microRNAs; MED1, SMAD4, NEDD4 and MBOAT2, targets of upregulated microRNAs in the L group. These results indicate that gene regulation by microRNAs in this gene network influences lipid homeostasis, principally by PPARα signaling pathway activation and can modulate fat deposition in muscle.

Key Words: smallRNA, functional enrichment, lipid metabolism

0340 Differentially expressed miRNAs in skeletal muscle related to feed efficiency in Nellore cattle.
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Feed efficiency (FE), also referred as residual feed intake (RFI), is a production trait that can have a major impact on production costs, reduction of pasture area, and pollutants. Bovine transcriptomic studies have shown that the expression of many miRNAs are tissue specific and have potential roles in some biological mechanisms. In this study, Nellore steers genetically divergent for RFI (kg/d) were selected based on BLUP (Best Linear Unbiased Prediction) estimates and ranked to select the most extreme values for additive genetic merit. Sequencing of small RNA libraries from Longissimus dorsi (LD) muscle tissue of eight Nellore steers (N = 4 High RFI, N = 4 Low RFI) was conducted on a MiSeq using the Miseq Reagent Kit V3 150 cycles. After quality control, the miRDeep2 software was used to identify and quantify novel and known miRNAs using *Bos taurus* UMD3.1 as reference genome. Differentially expressed (DE) miRNAs (FDR = 10%) were identified by DESeq2 R package and potential regulatory target transcripts were predicted by TargetScan software. The bta-miR-486 (padj = 0.0072) was DE in LD muscle tissue. This miRNA was also identified as DE in a transcriptome analysis in skeletal muscle for differential RFI in pigs. The genes *PKHD1L1, ENAH, ATF3, GAS7, LIMK1, MPZ, C3* and *SLC26A2,* related to ion transport, glucose and pyruvate metabolic process and glycosylation, were identified as target genes of this DE miRNA. Supporting our findings, these genes were previously identified as DE in RNaseq study performed using liver and muscle tissues of this same set of samples. This study provides a better understanding of the role of miRNAs in biological mechanisms related to feed efficiency in Nellore beef cattle.

Key Words: *Bos indicus*, residual feed intake, gene regulation

0341 miRNAs related to fatty acids composition in Nellore cattle. P. S. N. Oliveira*[1], A. S. M. Cesar[2], G. B. Oliveira[2], P. C. Tizioto[1], M. D. Poleti[2], W. J. S. Diniz[3], A. O. D. Lima[3], J. M. Reecy[4], L. L. Coutinho[2], and L. C. A. Regitano[5], *[1]Embrapa Southeast Livestock, São Carlos, Brazil, [2]Animal Biotechnology Laboratory-ESALQ, University of São Paulo, Piracicaba, Brazil, [3]Federal University of São Carlos, Brazil, [4]Iowa State University, Ames, [5]Embrapa Southeast Livestock, São Carlos, Brazil.*

Fatty acid (FAs) content is an important trait that can influence the sensorial and nutritional value of meat and play a significant role in biological processes such as adipogenesis. In beef cattle, adipogenesis as well as several other biological processes have been reported that could be regulated by miRNAs. The goal of this study was identify differentially expressed (DE) miRNAs and biological processes associated with FA content between the groups Nellore steers that showed extreme genomic breeding values (GEBV) for oleic acid (OA) and conjugated linoleic acid cis9 trans11 (CLAc9t11). In this study, small RNA libraries from Longissimus dorsi (LD) muscle tissue from a group of 28 (top 14 animals with highest GEBV distribution (H) and bottom 14 with lowest GEBV distribution (L) for OA and CLAc9t11 content) were sequenced on a MiSeq using the Miseq Reagent Kit V3 150 cycles. After quality control, the miRDeep2 software was used to identify and quantify novel and known miRNAs using *Bos taurus* UMD3.1 as reference genome. Differentially expressed (FDR = 10%) miRNAs were identified by DESeq2 R package and potential regulatory target transcripts were predicted by TargetScan software. The bta-miR-126–5p (padj = 0.0987) and bta-miR-2419–5p (padj = 0.0041) were DE for OA and CLA, respectively. The genes *CDS2, FAR2, DIP2B, NAB1, EPT1, UBE2E3*, *PRKAG2* and *CAV3* were identified as target genes of these DE miRNAs, which were identified as DE in a previously RNaseq study. These genes are related to some biological process for fatty acids composition; like phospholipid and lipid metabolism, skeletal system development, proteolysis and insulin signaling pathway. This study helps to better understand of the biological mechanisms that control intramuscular fat deposition and composition, and could positively benefit beef production by supplying the product that the consumer wants.

Key Words: *Bos indicus*, adipogenesis, gene regulation

0342 Expression levels of the bovine SCD gene are significantly associated with fatty acid composition of cattle. H. Chung*, *National Institute of Animal Science, Wanju, Korea (The Republic of).*

The experiment shows that a long-term administration of low and high-energy diets may not functionally either increase or decrease SFA and UFA. The interesting finding was that variation for proportions of all FAC in the low-energy diet group were higher than that of the high-energy diet group except Linoleic acid (18:2n6) and PUFA. According to the variance analysis, the proportions of FAC in the low group tended to have an approximate normal distribution while the high group showed a skewed pattern. Expression analysis of stearoyl-CoA desaturase (SCD) revealed at least twofold high expression levels in the high-diet group, and especially, the SCD4 and SCD6 segments detected more than 10 folds high expressions, whereas none of the SCD segments had high expression values in the low-diet group. The results indicate that long-term feeding with high energy levels of diets lead high expression levels of the SCD gene. However, excessive proportions of nutritional materials limited metabolic availabilities or restricted functional systems for the ruminal bio hydrogenation between FA. Therefore, the present results deliver a critical issue to the public that manipulations of FAC with high nutritional levels in diets may be oriented toward increases of expression levels of SCD, but not activities of other genes that functional elongate and desaturase FA.

Key Words: expression, SCD, FAC

0343 Profiling microRNA expression in longissimus dorsi muscle of F2 pigs from the Michigan State University Duroc x Pietrain resource population. K. R. Perry*[1], J. P. Steibel[1,2], D. Velez-Irizarry[1], S. A. Funkhouser[3], N. E. Raney[1], R. O. Bates[1], and C. W. Ernst[1], *[1]Department of Animal Science, Michigan State University, East Lansing, [2]Department of Fisheries and Wildlife, Michigan State University, East Lansing, [3]Genetics Program, Michigan State University, East Lansing.*

MicroRNAs (miRNAs) are a class of small, non-coding RNAs shown to regulate gene expression post-transcriptionally through complementary binding with an approximately 7 nt "seed" sequence in the 3'UTR of target mRNAs. MiRNAs have been shown to regulate numerous complex biological processes across tissue types, including fetal and postnatal skeletal muscle in pigs. While miRNAs have been characterized for these developmental stages, a more comprehensive understanding of the effects of miRNA regulation in market-age pigs is needed. The objective of this study was to profile the expression of miRNAs in the Longissimus dorsi (LD) muscle of 174 F2 pigs (~5.5 mo of age) from the MSU Duroc x Pietrain Resource Population. Total RNA was extracted from LD samples using the QIAGEN miRNeasy Mini Kit, and library preparation for sequencing was conducted utilizing the Bioo Scientific NEXTflex Small RNA Sequencing Kit (v2) with one cDNA library prepared per sample. The 174 libraries were multiplexed and sequenced on an Illumina HiSeq 2500 platform in 1x50 bp format. Raw sequence reads (fastq format) were trimmed for adaptor sequences, size- and quality-filtered, and PCR duplicates were removed. After processing, 232,826,977

total reads (mean 1338,086 reads per library) were aligned to the *Sus scrofa* reference genome (10.2.79) using miRDeep2. In total, 74.8% of reads were successfully mapped to the reference genome (median = 76.4% of reads per library). The miRDeep2 software package was then utilized to quantify annotated *Sus scrofa* mature miRNAs from miRBase (Release 21). The mature miRNA expression profiles were then filtered for abundance across samples; miRNAs expressing less than 1 read count per million (cpm) in less than 44 samples were removed from the analysis. The remaining 295 profiles were normalized relative to quantified library size (cpm) utilizing the *cpm* function of the *edgeR* package of R. Among the expressed miRNAs ssc-miR-1, ssc-miR-133a-3p, ssc-miR-378, ssc-miR-206, and ssc-miR-10b were the most abundant, all of which have previously been shown to be expressed in pig skeletal muscle. The expression of these five miRNAs represented 47.85% of the total read cpm in the dataset. Further characterization of miRNA expression profiles in adult pig skeletal muscle tissue will help to elucidate the role of miRNA regulation on production efficiency-related phenotypes including skeletal muscle accretion and meat quality.

Key Words: microRNA, skeletal muscle, pig

0344 Scan for allele frequency differences from pooled samples in lines of pigs selected for components of litter size. B. A. Freking*, J. W. Keele, and G. A. Rohrer, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Direct single trait selection within two seasonal replicates for 11 generations resulted in a 1.6 pig advantage for uterine capacity (UC) and a 3.0 advantage for ovulation rate (OR) compared with an unselected control (CO) population. Our objective was to gain insight and identify genetic loci impacted by quantitative selection for these component traits. We utilized historical DNA samples from all three lines obtained five and six generations after selection had ceased. A total of 402 gilts contributed to pooled samples; 8 unique pools per line with an average of 16.6 gilts per pool with paternal-half-sibs kept in the same pool. These 24 DNA pools were applied to Neogen GGP Porcine HD BeadChips. Bead-level normalized X and Y values were analyzed rather than allele calls. Analyses to compare the populations were conducted on individual SNP frequency estimates using REML and also using a sliding 25-SNP window with Wright's fixation index (F_{ST}). Pedigree relationships of all gilts back to the common base population 18 generations prior were utilized to compare to the genomic relationships. The overall relationship between pedigree and genomic information was highly predictive (r^2 = 97.5%); however, OR and UC selected lines differed from CO line with above average genomic relationships observed for the same degree of pedigree relationship. This would be consistent with the idea that selection increased the average within line relationships beyond what was accounted for by drift. Sixteen SNPs had allele frequency differences that exceeded a modest false discovery rate ($P < 0.05$) with none exceeding a genome-wide level of significance. However, three SNP were closely linked on SSC 13 near 203 Mb, while two SNP each were identified on SSC 5 at 63–65 Mb and on SSC 14 at 22–24 Mb offering additional support to those locations. F_{ST}values marked similar chromosomal regions but, again, did not by themselves identify regions that exceeded genome-wide significance. In conclusion, the pooling strategy reduced the cost to initially scan the genome but estimates of allele frequency differences needed to be extreme to exceed differences expected from modeling genetic drift in these populations. Additional samples need to be added to supplement this initial scan.

Key Words: pigs, selection, pooling

0345 Construction and functional analysis of expression vector and miRNA interference vectors of Gsdma of Tibetan sheep. C. Li[1], L. Ren[1], Y. Wang[1], J. Zhong[2], L. Huang[1], Y. Lin[1], X. Zi[1], and Y. Zheng[*1], [1]*Southwest University for Nationalities, Chengdu, China,* [2]*Auburn University, Auburn, AL.*

Gsdm(*gsdermin*) is a newly reported gene family. The human *Gsdma* and mouse *Gsdma3* were demonstrated to regulate the formation and development of hair follicle through signaling pathways such as Wnt and TNF-α. However the functions of *Gsdm* family members from other animal species are poorly studied. The objective of this study was to explore possible functions of *Gsdma* of Tibetan sheep (*Ovis aries*) at cellular level. RNA were extracted from skin tissues of Tibetan sheep (n = 5), and the cDNA sequence of *Gsdma* was cloned by PCR. Tissue expression profile analysis and sequence alignments showed that Tibetan sheep *Gsdma* is skin-specific and shows 99.9% coding sequence similarity to that of predicted sheep *Gsdma* (XM_004012853.1). The deduced protein sequences of Tibetan sheep and human *Gsdma* have high similarity (approximately 90%). An eukaryotic expression vector (pCDsRed2-KG) containing skin-specific KAP6.1 promoter and four interference vectors (pcDNA6.2-GW/EmGFP-miR 1 to 4) for Tibetan sheep *Gsdma* were constructed. The pCDsRed2-KG vector was transfected into human hair inner root sheath cells in vitro, and the positive transfected cells were sorted by flow cytometry. Quantitative real time PCR using *GAPDH* and β-actin as reference genes proved that the expression vector was highly expressed in human hair inner root sheath cells after transfection. In addition, two of the four interference vectors exhibited significant silencing effect on pCDsRed2-KG expression (interference efficiency > 50%). Further analysis showed that the significantly increased *Gsdma* mRNA level was correlated with elevated caspase-3 mRNA level ($P < 0.05$) in the transfected human hair inner root sheath cells. However, the β-catenin showed no significant changes at both mRNA and protein levels. Since caspase-3 is involved in apoptotic pathway, our data suggest that

Gsdma gene may play an important role in regulating hair follicle development through this signaling mechanism.

Key Words: *Gsdma* gene, Tibetan sheep, hair follicle

0346 Genetic characteristics of semi-domesticated reindeer populations from different regions of Russia based on SNP analysis. V. R. Kharzinova*[1], A. V. Dotsev[1], I. M. Okhlopkov[2], K. A. Layshev[3], V. I. Fedorov[4], L. D. Shimit[5], G. Brem[1,6], K. Wimmers[7], H. Reyer[7], and N. A. Zinovieva[8], *[1]L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Science Institute of Biological Problems Cryolithozone, Yakutsk, Russian Federation, [3]North-West Center of Interdisciplinary Researches of Food Maintenance Problems, Federal Agency of Scientific Organizations, St. Petersburg, Russian Federation, [4]Federal Government Budget Scientific Institutions Yakut Scientific Research Institute of the Agriculture Federal Agency Scientific Institutions, Yakutsk, Russian Federation, [5]Tuva State University, Tyva Republic, Russian Federation, [6]Institute of Animal Breeding and Genetics, VMU, Vienna, Austria, [7]Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [8]L. K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation.*

Semi-domesticated reindeer are herded on the entire territory of Russian Far North and are represented by several populations which vary in exterior and morphological features. In the present work we considered the following populations: Nenets-NEN (the largest, with 800,000 individuals), Evenk-EVN (100.000 individuals) and Todzha-TOD (the smallest with around 1000 individuals). Genetic characteristics and structure of Russian reindeer populations are insufficiently studied and research in this field is undoubtedly necessary.

Our study aimed at evaluating genetic diversity and structure of NEN (n = 11), EVN (n = 29) and TOD (n = 11). Wild reindeer from Yakutia region (n = 14) were used as outgroup for cluster analysis. DNA was extracted from tissue samples using the Nexttec column (Nexttec Biotechnology GmbH, Germany) according to the manufacturer's recommendations and genotyped using the Bovine SNP50 v2 BeadChip. After quality control (MAF = 0.01) 544 polymorphic SNPs were selected for further analysis. Statistical analysis was performed with PLINK 1.07, Arlequin 3.5.2.2, HP-Rare 1.1, GENETIX 4.05 and STRUCTURE 2.3.4 software.

Greater values of unbiased expected heterozygosity were observed for NEN (0.214 ± 0.008) and EVN (0.211 ± 0.008) populations, while for TOD this was only 0.195 ± 0.008. Inbreeding coefficient (F_{is}) showed heterozygote deficiency in the TOD population (0.049) while NEN and EVN were in H-W equilibrium (0.003 and −0,004, respectively). Allelic richness was significantly higher for EVN (1.74 ± 0.02) and NEN (1.70 ± 0.02) in comparison with TOD (1.65 ± 0.02). AMOVA revealed that most of the variation was within populations (91.8%) and less (8.2%) among populations. The genetic differentiation (pairwise F_{ST}) among populations ranged from 0.05 between EVN and NEN to 0.11 between TOD and NEN. F_{ST}value between EVN and TOD was 0.10 ($p < 0.01$).

Since wild populations coexist with semi-domesticated populations and gene exchange may occur between them, the SNP profiles of wild reindeers were included in dataset for cluster analysis. At k = 4 all animals belonging to the EVN and NEN were distinctly differentiated, while admixture of wild reindeer was observed in three samples belonging to the TOD population.

The genome scan approach in reindeer used in our study revealed that every population was characterized by unique gene pool. Subsequent studies in this field will provide further information for investigating population structure along with a better understanding of biological features of reindeer. The study was supported by the Russian Science Foundation within Project no. 14–36–00039

Key Words: semi-domesticated reindeer, SNPs, genetic diversity, population structure

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0347 Candidate gene and marker for equine metabolic syndrome. S. Lewis*, H. Holl, M. T. Long, M. Mallicote, and S. Brooks*, University of Florida, Gainesville.*

Equine obesity gives rise to life-threatening secondary chronic conditions, similar to those in humans, livestock and other companion animal species, leading to loss of use or euthanasia. Elevated circulating insulin levels often characterize the primary disease associated with equine obesity, Equine Metabolic Syndrome (EMS). Due to clinical similarities with other conditions like Pituitary Pars Intermedia Dysfunction (PPID, formerly Equine Cushing's Disease) and hypothyroidism, conclusive diagnosis of EMS often proves challenging. Aside from changes in diet and exercise, few targeted treatments are available for EMS, emphasizing the need for genetic testing to identify at-risk individuals and implement preventative measures. A previous genome-wide association study, using horses with EMS and/or PPID and exhibiting severe laminitis, revealed statistically significant markers for the condition near a single candidate gene, *FAM174A*. A single study describing the function of this gene suggests it may play a role in cholesterol homeostasis. Sequencing of the *FAM174A* gene in EMS affected Arabian horses identified at least five polymorphic haplotypes. In this study, additional samples from a larger population of horses, consisting of 56 individuals, diagnosed with EMS disease were genotyped by Sanger sequencing for polymorphisms in the *FAM174A* gene and the results assessed for association with indicators of the EMS condition. Additionally, we genotyped the most significant intergenic marker

SNP from the previous GWAS, BIEC2–263524, by High Resolution Melt (HRM). An allele in a 3' untranslated region (UTR) of *FAM174A* correlated with both elevated insulin values ($p = 0.0082$) and BCS > 6.5 ($p = 0.0116$). The BIEC2–263524 marker SNP displayed similar associations to elevated insulin values ($p = 0.0060$) and BCS > 6.5 ($p = 0.0049$). The risk allele at both BIEC-263524 and the *FAM174A* 3'UTR correlated at a 95% frequency, indicating strong LD across this haplotype. Confirmation of the association between these markers and the EMS condition will enable genetic tests for the horse as a helpful tool in diagnosing and preventing EMS. In addition to improving our understanding of the etiology of this troubling condition in the horse, the *FAM174A* locus may prove an interesting candidate gene for human obesity.

Key Words: equine, obesity, metabolic

0348 The polymorphisms of Toll-like receptor 4 gene influences milk production traits in Chinese Holstein cows. X. Zhu, M. Wang, S. Xing, Z. Yang, and Y. Mao*, *College of Animal Science and Technology, Yangzhou, China.*

Toll-like receptor 4 (*TLR4*) is an important member of the Toll-like receptor gene family that is widely found in various organisms. *TLR4* can identify molecular patterns from various pathogenic microorganisms, and induce natural immunity and acquired immunity. Two single nucleotide polymorphisms (SNPs) of *TLR4* (c.-226 G > C and c.9788 C > T) were genotyped using Sequenom MassARRAY (Sequenom Inc., San Diego, CA) for Chinese Holstein cows ($n = 866$), and the EBV for each individual cow of milk production traits and somatic cell score (SCS) were analyzed by the multiple-traits multiple-lactation random regression test-day model, and then the associations between SNPs or haplotype and the EBV of milk production traits and SCS were analyzed by PLINK software. The c.-226 G > C and c.9788 C > T showed low linkage disequilibrium ($r^2 = 0.192$). There was no association between these two SNPs and SCS, but significant effects were found for SNP c.-226 G > C on fat content ($P < 0.025$), and SNP c.9788 C > T and haplotype CT on fat content and total solids ($P < 0.005$). The software MatInspector revealed that c.-226 G > C was located within several potential transcription factor binding sites, including transcription factor AP-2, and may alter gene expression, but further investigation will be required to elucidate the biological and practical relevance of these SNPs.

Key Words: milk production traits, SNP, Toll-like receptor 4

Table 0348.

Table Effects of SNPs of TLR4 genes on SCS and milk production traits

SNPs	Genotypes	DHI Records number	TDMY(kg)	FC(%)	Pers.	PC(%)	LC(%)	TS(%)	SCS	MUN
TLR4- -226	GG	4229	2.87±4.65	-12.63±4.23^{A}	0.36±0.13	-1.62±0.70	0.32±0.159	-8.34±4.71	-0.02±0.07	-0.85±0.39
	CG	10147	0.15±3.59	-0.14±3.422^{b}	0.47±0.12	-0.95±0.60	0.10±0.14	1.92±3.73	0.02±0.06	-0.15±0.28
	CC	6123	-3.96±6.30	2.914±5.89^{b}	0.14±0.14	0.04±0.99	-0.04±0.24	0.76±6.23	-0.01±0.01	0.27±0.49
	P value	20499	0.1804	0.0085*	0.2124	0.0836	0.08505	0.0875	0.44395	0.02607*
	a		3.416	-7.7735*	0.1095	-0.827	0.181	-4.549	-0.006	-0.5585
	d		0.691	4.7245	0.2185	-0.162	-0.047	5.702	0.022	0.1455
	a		3.4851	-7.3011*	0.1314	-0.8432	0.1763	-3.9788	-0.0038	-0.54395
TLR4-9788	CC	15414	0.48±3.05	-6.12±2.79^{Aa}	0.32±0.08	-1.25±0.47	0.18±0.11	-5.64±3.08^{Aa}	0.02±0.05	-0.39±0.24
	CT	4643	0.65±5.27	1.154±5.12^{B}	0.59±0.18	-0.48±0.88	0.12±0.12	7.57±5.37^{b}	-0.04±0.09	-0.13±0.42
	TT	442	-15.82±13.25	44.78±17.54^{Bb}	-0.11±0.37	3.87±3.47	-1.01±0.63	47.27±15.01^{Bb}	-0.03±0.31	2.05±1.41
	P value	20499	0.27345	0.0025**	0.2037	0.04228	0.1051	0.00054**	0.2322	0.0779
	a		8.1510	-25.4525**	0.2150	-2.5615	0.5945	-26.4515**	0.0265	-1.2185
	d		8.3200	-18.1755	0.4840	-1.7885	0.5335	-13.2405	-0.0365	-0.9585
	a		14.1414	-38.5389**	0.5635	-3.8492	0.9786	-35.9847**	0.00022	-1.90862

*significant association after Bonferroni correction for multiple testing at the significance level of 0.025; **significant association after Bonferroni correction for multiple testing at the significance level of 0.005. A,B within the same column with different superscripts indicate $P < 0.01$; a,b indicate $P < 0.05$.

TDMY: test-day milk yield; FC: fat content; PC: protein content; Pers.: Persistency; SCS: somatic cell score; LC: lactose content; TS: total solid; MUN: milk urea nitrogen.

0349 A polymorphism within the *PAPPA2* gene is associated with postpartum fertility traits in Holstein dairy cattle located in southern Sonora Mexico. P. Luna-Nevarez*[1], J. C. Leyva-Corona[1], M. A. Sanchez-Castro[1], R. Zamorano-Algandar[1], J. F. Medrano[2], G. Rincon[3], R. M. Enns[4], S. E. Speidel[4], and M. G. Thomas[4], *[1]Instituto Tecnologico de Sonora, Ciudad Obregon Sonora, Mexico, [2]University of California, Davis, [3]Zoetis Inc., Kalamazoo, MI, [4]Department of Animal Sciences, Colorado State University, Fort Collins.*

Postpartum fertility in Holstein cattle is challenging for dairy production systems in southern Sonora Mexico as lactating cows need to get pregnant early in spring to avoid the negative impacts of summer heat stress. The GH-IGF1 signaling

pathway is known as important mediator of physiological mechanisms that regulate fertility in dairy cattle. The PAPPA2 gene is one component of this pathway, which codes for a protease responsible to increase IGF1 bioavailability for reproduction. The objective was to study the associative relationship between a SNP polymorphism in the *PAPPA2* gene (rs109952914-A/T within intron 10) with fertility traits such as first-service pregnancy (FSP), services per conception (SPC), and days open (DO) in postpartum Holstein cows. This SNP had a minor allele frequency of 18% and did not deviate from Hardy-Weinberg equilibrium (X^2 = 1.00, P > 0.42) in 676 Holstein cows. Reproductive records were collected from these cows that were located in three dairy herds in southern Sonora. A blood sample from each cow was spotted on FTA cards and used to genotype a 179 tag SNP panel within 45 genes in the GH-IGF1 pathway. The associative analyses among SNP genotypes and reproductive phenotypes were performed using a mixed effects model for categorical traits (i.e., FSP) and continuous traits (i.e., SPC and DO). The model included phenotype as the response variable, genotype and herd as fixed terms, sire as a random term, and days in milk as a covariate. Frequencies of FSP among genotypes AA, AT, and TT were 38.8 ± 2.6, 54.1 ± 1.9, and 66.7 ± 1.8%, respectively. Least square means among genotypes AA, AT, and TT were 2.3 ± 0.12, 2.0 ± 0.08, and 1.9 ± 0.06 services for SPC, and 159.8 ± 6.4, 153.9 ± 5.9, and 131.2 ± 3.9 d for DO, respectively. The most favorable allele from the SNP was the T allele (P < 0.001) as it increased FSP (12.6 ± 1.3%), and reduced SPC (−0.16 ± 0.05) and DO (−19.5 ± 5.6 d). In conclusion, a SNP within the *PAPPA2* gene appears to be a predictor of postpartum fertility, as it was positively associated to FSP, SPC and DO in postpartum dairy cows. These results provide evidence to propose the *PAPPA2* gene as candidate gene associated with fertility traits in postpartum Holstein cows and that it could be useful in DNA-based genetic selection tools.

Key Words: fertility, Holstein, *PAPPA2*, polymorphism.

0350 Using LD structure of several populations to optimize an SNP panel for conservation and selection. C. Díaz*[1], L. Varona[2], M. J. Carabaño[1], E. Nicolazzi[3], M. Bichard[4], J. Baro[5], A. Molina[6], J. Piedrafita[7], A. Rossoni[8], H. Schwarzenbacher[9], F. Seyfried[10], T. R. Solberg[11], D. Vicario[12], J. Altarriba[2], and K. J. Abraham[13], *[1]INIA, Madrid, Spain, [2]Universidad de Zaragoza, Spain, [3]Fondazione Parco Tecnologico Padano, Lodi, Italy, [4]English Guernsey Cattle Society, Launceston, UK, [5]Universidad de Valladolid, Palencia, Spain, [6]Universidad de Córdoba, Spain, [7]Universitat Autònoma de Barcelona, Bellaterra (Barcelona), Spain, [8]ANARB, Italian Brown Cattle Breeders' Association, Bussolengo (VR), Italy, [9]ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria, [10]Qualitas AG, Zug, Switzerland, [11]Geno Breeding and A.I. Association, Hamar, Norway, [12]National Simmental Cattle Breeders Association, ANAPRI, Udine, Italy, [13]Estacio-Uniseb, Ribeirão Preto, Brazil.*

The success of conservation of genetic variability and/or prediction of breeding values by genomic selection is based on the existence of LD between SNP markers and the QTVs. The existing LD is the result of several driving forces acting in each population along their history. Commercial SNP panels have been designed based on the genomic information of a reduced number of breeds. Within the Gen2Farm project framework, communalities and singularities of LD of 12 breeds from 8 countries were used to improve the design of existing SNP panels to fulfill the conservations and/or breeding needs in a breed and/or multibreed context. We analyzed the genomic information provided by the Illumina's BovineHD Beadchip of a total of 1534 individuals from: Asturiana de los Valles (AST, N = 75), Avileña-Negra Ibérica (ANI, N = 72), Brown Swiss (BS, N = 418), Bruna del Pirineus (BP, N = 75), Fleckvieh (Fl,N = 317), Guersey (GUE, N = 28), Morucha (Mo, N = 75), Norwegian Red (NR, N = 100), Pirenaica (Pi, N = 72), Retinta (Re, N = 72), Rubia Gallega (RG, N = 72) and Simmental (Si, N = 158). After editing, 604,551 phased SNP markers per animal were available for the analysis. LD matrices were obtained for each breed-chromosome (348 in total). TagSNPs defined in terms of independency and representativeness, were obtained by a graphical clustering algorithm. After setting aside singletons in each chromosome-breed, a minimum set of TagSNPs along the genome was obtained by maximizing the distance between TagSNPs and minimizing the distance between TagSNPs (centers of clusters) and markers of the same LD block. This was so provided some threshold values obtained from the empirical distribution of the LD values. Communalities and connectivity as a measure of the ratio of the number of tight links present to the maximum number possible were calculated. Connectivity varied between 0.00018 and 0.0013 for the first chromosome in

AST and the chromosome 21 in RE, respectively. All breeds shared a total of 17,720 TagSNPs, with values ranging from 421 TagSNPs in chromosome 25 to 1130 in chromosome 19. Moreover, there was also a high number of private TagSNPs present only in one breed, ranging from 1225 in chromosome 21 to 5827 in chromosome 1. Finally singletons were incorporated to the set of identified TagSNPs. Singletons represented more than 50% of TagSNPs in most cases. However, as the LD between singletons and QTVs is unknown, the maintenance of singletons in the SNP array may be considered as a choice to prevent loosing information.

Key Words: linkage disequilibrium, tags, selection, multibreed

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0351 Meiotic recombination differences in ruminant livestock species. K. M. Davenport* and B. M. Murdoch, *University of Idaho, Moscow.*

Homologous recombination or crossovers (CO) ensures proper chromosome segregation while contributing to genetic variation. It is clear from previous studies that at least one CO per chromosome arm is necessary to avoid mis-segregation. Furthermore, it has been well documented that the locations of CO are not random, with some genomic regions exhibiting preferences, called hotspots. Global meiotic recombination rates determined from offspring studies underestimates the total number of meiotic recombination events due to independent assortment. Despite the importance of meiotic recombination in the production of viable gametes and toward predicting or estimating genetic breeding values, we know very little about meiotic recombination rates in livestock species. In this study we have used a cytological approach to quantify the number of recombination events in male sheep and cattle. Characterizing recombination events using a cytological approach allows us to accurately identify all recombination events during meiosis without the need for a large number of offspring and independent of an accurate reference genome that does not exist. Testicular tissue samples were taken from mature rams and bulls, and spermatocytes were spread and fixed on slides. Immunofluorescent staining was used to identify the synaptonemal complexes (SYCP3) and CO events (MLH1) of pachytene stage prophase cells. The total number of CO per meiocyte was quantified for different livestock species. Interestingly, the average number of CO per meiocyte in sheep is approximately 20% higher than in cattle despite having a similar number of chromosome arms and genome size. More specifically, sheep have on average a greater number of recombination events per chromosome arm (~ 2.8 CO per arm) in comparison to cattle (~ 1.7 CO per arm). This research provides important information regarding differences in recombination rates in sheep and cattle spermatocytes, and has a direct impact on the genetic predictions in these species. Moreover, this research contributes valuable information toward a greater understanding of the factors that control meiotic recombination in different species to enhance reproduction, improve accuracy of genetic prediction, and advance selection strategies that support the sustainability of the livestock industry.

Key Words: meiosis, recombination, selection

0352 Genetics of heat stress in purebred and crossbred pigs from different states using BLUP or ssGBLUP. B. D. Fragomeni*[1], D. Lourenco[1], S. Tsuruta[1], K. A. Gray[2], Y. Huang[2], and I. Misztal[1], *[1]University of Georgia, Athens, [2]Smithfield Premium Genetics, Rose Hill.*

The objective of this study was to evaluate potential of regular and genomic selection to mitigate impacts of heat stress in swine populations. Phenotypes of body weight were available for purebred Duroc nucleus animals from farms in North Carolina (n = 151,336) and Texas (n = 55,897); and for commercial crossbred animals (Duroc x Landrace-Large White), hot carcass weight was available from North Carolina (n = 141,756) and Missouri (n = 86,435). Pedigree file combined the two populations and included 553,442 animals. Genotypic information was available for 8232 Duroc animals, for 60k SNP. Analyses were done with an animal model as either single- or two-trait model using phenotypes measured in different states as separate traits. Additionally, reaction norm models were fitted for one or two traits using heat load index as covariable. Heat load was calculated as temperature humidity index above 70 degrees (equivalent to 21°C and 100% relative humidity) and was averaged over 30 d before data collection. Variance components were estimated by AIREML and (genomic) estimated breeding values ((G)EBV) by BLUP or single-step GBLUP (ssGBLUP). Validation was assessed for 146 genotyped sires with progeny in last generation. Accuracy was calculated as correlation of (G)EBV from reduced data (all animals, except the last generation) and (G)EBV with complete data. Heritabilities for purebred animals were similar across states (varying from 0.23 to 0.26), and reaction norm models did not show evidence of heat stress effect. Genetic correlations between states and heat loads were always high (> 0.91). For crossbred animals, no difference in heritabilities were found in single- or two-trait analysis (from 0.17 to 0.18), and genetic correlations between states were moderate (0.43). In the reaction norm for crossbreds, heritabilities ranged from 0.15 to 0.30 and genetic correlation between heat loads were as low as 0.36. Accuracies with genomic information by ssGBLUP were on average 25% higher than by BLUP. Accuracies were higher in two-trait reaction norm models and at extreme heat load values. Impacts of seasonality are evident only for crossbred animals. Genomic information can help mitigating heat stress in swine by identifying superior sires more resistance to heat stress.

Key Words: genotype-by-environment interaction, heat stress, single-step GBLUP

0353 Genetic evaluation for heat tolerance in growing Angus cattle. H. L. Bradford[*1], B. D. Fragomeni[2], D. Lourenco[2], and I. Misztal[2], *[1]University of Georgia, Athens, [2]University of Georgia, Athens.*

The purpose was to investigate the existence of heat stress on preweaning growth in Angus cattle and to develop a genetic evaluation to improve heat tolerance. The American Angus Association provided weight data, and records from the southern United States (n = 82,669) were used because of the hot, humid summer months. Heat stress was measured using heat load, defined as the average degrees of temperature-humidity index greater than 24°C for 30 d before the weigh date. Forty-five percent of cattle experienced heat loads greater than 0. Heat load was used in a reaction norm to assess phenotypic plasticity, and the results were compared with a univariate analysis. For both models, random effects included direct genetic, maternal genetic, maternal permanent environment, and residual; and fixed effects included a linear age covariate, age of dam class, sex, herd, and year. Moderate differences in heat load resulted in strong direct genetic correlations (r > 0.80), but large heat load differences had weaker direct genetic correlations. The same pattern occurred for Spearman rank correlations for proven bulls (n = 1048) with r = 0.30 between no heat load and extreme heat load. Selection decisions should differ depending on heat load, and producers could benefit from environment-specific selection tools. As heat load increased, the maternal genetic effect remained consistent even though heat stress decreased milk production in dairy cows. To compensate for the expected reduction in dam milk production during heat stress, calves may have consumed creep feed or other forages to maintain growth. In addition to comparing results, accuracy was assessed by the ability to predict phenotypes for young animals. Predictivity did not improve when using the reaction norm (r = 0.31) instead of the univariate model (r = 0.30). Thus, the univariate analysis performed as well as the reaction norm and sufficiently evaluated genetic differences in growth despite heat stress. Additional research is needed on methods for assessing heat tolerance in national cattle evaluations. Researchers implemented heat load successfully in species raised in confinement including dairy and swine, but heat load was confounded with contemporary group, calving season, seasonal fluctuations in forage quality and quantity, and fescue toxicity for beef cattle. A more robust measure of heat load would aid in understanding the effect of heat stress on preweaning growth and creating selection tools for improving beef cattle heat tolerance.

Key Words: beef cattle, heat stress, weaning weight

0354 Angus cattle at high elevation: Comparison of models to estimate breeding values of yearling pulmonary arterial pressure. X. Zeng[*1], T. N. Holt[2], S. E. Speidel[1], R. M. Enns[1], and M. G. Thomas[1], *[1]Department of Animal Sciences, Colorado State University, Fort Collins, [2]College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins.*

As an indicator of pulmonary hypertension, pulmonary arterial pressure (PAP) is widely used in the selection of cattle to reduce the incidence of high altitude disease (HAD). In initial analyses of yearling PAP data, a violation of normal distribution of residuals (i.e., skewed right tail) was observed. To remedy, alterative expressions of yearling PAP were investigated in this study with a goal of determining the effect of alternative expressions on genetic evaluation outcomes. Yearling PAP records (42.46 ± 0.58mmHg) were collected from 5296 Angus cattle from 280 sires from Colorado State University Beef Improvement Center (2150m elevation). The alternative phenotypes included power-transformed (PT) PAP records, an ordinal three-category phenotype (CAT3), an ordinal two-category phenotype (CAT2) and the non-transformed PAP observations (RAW). The CAT3 observations were defined as low risk (PAP < 41mmHg), moderate risk (41mmHg ≤ PAP ≤ 49mmHg) and high risk (PAP > 49mmHg) for HAD. The CAT2 observations were constructed by combining low and moderate risk categories of CAT3. Univariate linear and threshold animal models were applied in analyses of RAW and PT; CAT3 and CAT2, respectively. The fixed effects for PAP phenotypes included sex, age of dam, date and age (covariate) of PAP measurement. All fixed effects were significantly (P < *0.05*) associated with each PAP phenotype. The estimated heritabilities were 0.24, 0.24, 0.26, and 0.31 for RAW, PT, CAT3 and CAT2, respectively. Sire EBV accuracies from univariate models of RAW, PT, CAT3 and CAT2 ranged from 0.03 to 0.67, 0.03 to 0.68, 0.01 to 0.65 and 0.01 to 0.58 with means of 0.31, 0.31, 0.28 and 0.21, respectively (pooled sd = 0.13). The Rank correlations between EBV from RAW and PT, CAT3 or CAT2 were 0.92, 0.84 and 0.77, respectively. The lowest Rank correlation (0.69) was identified between PT and CAT2, while Rank correlation of 0.91 was obtained between PT and CAT3. All phenotypes resulted in decreasing genetic trends. Results suggested similar heritability, accuracy and rank of animals based on EBV from RAW and PT, yet losses in EBV accuracy and some re-ranking of sires was observed in ordinal categorical phenotypes compared with continuous PAP scores. In conclusion, violation of normality had limited influences on the genetic evaluation of yearling PAP measurements. Ordinal categorical phenotypes can be alternative dependent variables in studying susceptibility of HAD, however, they would cause some re-ranking of sires relative

to non-transformed PAP scores.

Key Words: cattle, pulmonary arterial pressure, genetic evaluation

0355 The effect of heterosis on pulmonary arterial pressure on beef cattle. M. M. Culbertson[*1], M. G. Thomas[2], L. L. Leachman[3], R. M. Enns[2], and S. E. Speidel[2], *[1]Colorado State University, Department of Animal Sciences, Fort Collins, [2]Department of Animal Sciences, Colorado State University, Fort Collins, [3]Leachman Cattle of Colorado, Fort Collins.*

Pulmonary hypertension can develop due to hypoxia-induced pulmonary vascular remodeling leading to right ventricular hypertrophy and edema, a condition known as brisket or high altitude disease (HAD). Pulmonary arterial pressure (PAP) is used at high altitude regions (> 1500 m) as an indicator of an animal's susceptibility to pulmonary hypertension and HAD. Cattle located at altitudes greater than 1500 m with PAP measurements between 31 and 43 mm Hg are considered to have a low risk of developing HAD at most elevations. To date, there has been no reported research for the effects of heterosis on PAP and therefore, the objective of this study were to examine the effect of heterosis on PAP measurements. Classically, heterosis is most beneficial for survival and fertility related traits; therefore, we hypothesized that increased heterozygosity would decrease an animal's PAP phenotype. Data collected from 2009 to 2015, was obtained from a multibreed seedstock database with an average PAP measurement of 44.56 ± 11.58, and a minimum and maximum of 32 and 149 mm Hg. Data included PAP records (n = 2001), PAP testing date, yearling management code, date of birth, sex and breed. A mixed animal model was used to estimate the effect of heterosis on PAP with the model containing degree of outcross and PAP age as covariates; and contemporary group (i.e., combination of PAP date and yearling management code) and sex as categorical fixed effects. Animal was included as a random effect. A 3-generational pedigree consisting of 9353 animals was used to estimate genetic parameters for PAP (h^2 = 0.29 ± 0.07). Breed effects were included as covariates of breed percentages for Angus, Red Angus, Charolais, South Devon, Gelbvieh, Simmental and "Other" breeds. The effect of breed on PAP had a range of 8.75 mm Hg. The estimated regression coefficient for PAP on heterosis was −0.02 ± 1.31 mm Hg/percent outcross ($P < 0.155$). These results indicate that heterozygosity has no effect on PAP measurements, although other multibreed populations should be examined. As a result we would reject our hypothesis that an increase in heterosis would decrease PAP.

Key Words: pulmonary arterial pressure, heterosis, regression

0356 Genetic and phenotypic analysis of Israeli Holstein milk, fat, and protein production as determined by the Afilab real-time milk analyzer. J. I. Weller[*1] and E. Ezra[2], *[1]ARO, The Volcani Center, Bet Dagan, Israel, [2]Israel Cattle Breeders Association, Caesaria, Israel.*

Given the day-to-day variation in milk components, especially fat, the standard DHIA procedure of measuring milk components in just 1 milking per month, may not be very representative of total production. The combination of much more frequently, but less accurately analyzed milk components, may be more representative of a cow's longer-term milk composition. The AfiLab system (Afimilk, Kibbutz Afikim, Israel) is a real-time individual cow milk analyzer that uses near-infrared spectroscopy for on-line milk analysis. AfiLab records for milk production and fat and protein concentration collected from January 2014 through January 2016 from 47 large Kibbutz (communal) herds distributed throughout Israel with a total of 37,486 Israeli Holstein cows were compared with the same statistics derived from monthly test day records derived by Bentley and Foss milk analyzers at the central laboratory of the Israel Cattle Breeders Association (ICBA). The SD for first and second parity daily records scored by the ICBA and AfiLab system were very similar for all traits, except for fat percentage. The SD for complete lactation production were slightly lower for the AfiLab results for all traits, except protein production. The lactation means for all traits were quite similar by the two methods in both parities, except for fat production, which was higher for the ICBA records. This corresponds to the fat lactation curves, which show that the ICBA results were higher with low DIM, but nearly equal to the AfiLab results after 125 DIM. AfiLab overestimated protein percentage before 150 DIM, and underestimated protein percentage in the second half of the lactation. First parity heritabilities (see table) were higher for AfiLab lactations for all traits, except for protein percentage. For AfiLab records, coefficients of determination to predict future lactation production from truncated lactations were greatest and root mean squared errors were smallest if the mean production from the last 2 wk before the truncation date were used to estimate future production. AfiLab first parity partial lactations with < 150 DIM predicted future lactation more accurately than the corresponding ICBA partial lactations. With only 30 DIM, genetic correlations between predicated and actual lactations ranged from 0.73 to 0.79 for the 3 traits. Further study is required to compare results of individual cows on multiple lactations, and to determine the optimum interval between calibrations for AfiLab meters.

Key Words: dairy cattle breeding, genetic evaluation, milk analysis

Table 0356.

Heritabilites (in **bold type**), genetic (above the diagonal) and environmental (below the diagonal) correlations among 7,866 first parity 305 d milk, fat and protein production records and fat and protein percentage computed from the ICBA and AfiLab records.

		Milk		Fat		Protein		% fat		% protein	
Trait	Method	ICBA	AfiLab	ICBA	AfiLab	ICBA	AfiLab	ICBA	AfiLab	ICBA	AfiLab
Milk	ICBA	**0.334**	0.996	0.267	0.529	0.848	0.902	-0.707	-0.519	-0.640	-0.420
	AfiLab	0.963	**0.351**	0.258	0.515	0.847	0.911	-0.709	-0.534	-0.633	-0.407
Fat	ICBA	0.548	0.509	**0.229**	0.590	0.333	0.263	0.492	0.312	-0.023	-0.046
	AfiLab	0.682	0.712	0.703	**0.309**	0.632	0.444	-0.042	0.449	-0.070	-0.263
Protein	ICBA	0.909	0.863	0.639	0.731	**0.271**	0.858	-0.526	-0.267	-0.137	-0.154
	AfiLab	0.894	0.932	0.535	0.668	0.869	**0.321**	-0.621	-0.510	-0.441	0.004
% fat	ICBA	-0.479	-0.481	0.464	0.015	-0.288	-0.384	**0.479**	0.698	0.556	0.345
	AfiLab	-0.367	-0.375	0.256	0.378	-0.171	-0.344	0.661	**0.565**	0.585	0.171
% protein	ICBA	-0.506	-0.515	0.010	-0.120	-0.106	-0.343	0.552	0.526	**0.545**	0.564
	AfiLab	-0.294	-0.299	0.006	-0.200	-0.057	0.066	0.319	0.133	0.524	**0.460**

0357 ADSA®-EAAP speaker exchange presentation: Genetic analysis of multivariate indices of detailed fatty acid profile determined by gas chromatography in bovine milk.

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The genetic improvement of fatty acid (FA) composition is a crucial point for enhancing milk dietary and nutritive properties. However the development of an appropriate breeding goal for this trait is hampered by the large number of FA and the complex correlation pattern among them. Multivariate factor analysis (MFA) is able to derive synthetic variables that can describe efficiently a multivariate system with a complex covariance structure. This study was aimed at: (1) elucidating the structure of relationships between milk yield, composition and detailed FA composition by using the MFA, and (2) estimating genetic parameters for the new-derived synthetic variables. Individual milk samples were collected from 1158 Brown Swisscows and gas chromatography was used to obtain detailed milk FA compositions. MFA was performed on 53 variables (i.e., 47FA and 6 milk production and composition traits). A total of 12 factors were extracted, able to explain about the 75% of the total variance. Factor scores were then used as new phenotypes for estimating (co)variance components using a Bayesian linear animal model via Gibbs Sampling. The model accounted for the effect of days in milk, parity, herd and animal additive genetic effect. Factor scores exhibited a clear structure in term of relationship with the original variables and they were classified, from a biological point of view, as: 'de novo FA,' 'milk yield-branched FA,' 'biohydrogenation,' 'long chain FA,' 'short chain FA,' 'milk-fat-protein,' 'odd FA,' 'conjugated linoleic acid,' 'linoleic,' 'udder health,' and 'vaccelenic,' respectively. Marginal posterior means (SD) of heritabilitiesfor the aforementioned factor scores ranged from 0.048(0.02) for 'vaccelenic' to 0.310(0.09) for 'desaturation.' Moderate heritability estimates were observed for 'milk yield-branched FA' (0.214 ± 0.07), 'linoleic' (0.201 ± 0.08), 'biohydrogenation' (0.193 ± 0.08), and 'short chain FA' (0.157 ± 0.07), respectively. Results highlight the existence of important and exploitable genetic variation in these derived phenotypes. In particular factors strongly associated with variables related to mammary neo-synthesis and desaturation, may offer interesting perspectives for improving

milkfat nutritional properties by selective breeding.

Key Words: fatty acid profile, multivariate factor analysis, heritability

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0358 Effectiveness of genomic prediction of boar taint components in Pietrain sired breeding populations. C. Große-Brinkhaus[*1], E. Heuß[1], J. Trautmann[2], D. Mörlein[2,3], K. Schellander[1], C. Looft[1], J. Dodenhoff[4], K. U. Götz[4], and E. Tholen[1], *[1]Institute of Animal Science, University of Bonn, Germany, [2]Department of Animal Science, University of Göttingen, Germany, [3]Isi GmbH & Co. KG, Rosdorf, Germany, [4]Bavarian State Research Centre for Agriculture, Institute of Animal Breeding, Poing, Germany.*

Systematic concern for animal welfare with regard to piglet castration without anesthesia is one challenge in European pig production. For instance, in 2013 the German Federal Council passed the law that non-anesthetized surgical castration will be prohibited by 2019. One alternative is the fattening of entire boars which is controversially discussed, because the risk of tainted meat has to be minimized. One possibility is to include selection for a low incidence of boar taint in breeding programs.

In this study, beside androstenone (And) and skatole (Ska), boar taint perception was recorded by a 10-member trained sensory panel (SENS) established by Mörlein and colleagues. Compiling data from four research projects, in total 4,000 records for And and Ska, and 1,016 records for SENS were available.

Genetic marker effects of 45,645 SNPs on And, Ska and SENS scores were estimated for 1,240 crossbred boars and 976 purebred Pietrain boars. These crosses and purebred boars reflect the heterogeneous population-structure of the Pietrain breed in Germany. Genomic BLUP was used to estimate genomic breeding values for animals in calibration and validation sets. Reliability of genomic prediction was assessed as correlation between genomic breeding value and conventional breeding values. Several scenarios were investigated to evaluate the effectiveness of genomic prediction.

Heritabilities for And, Ska and SENS were 0.64, 0.48 and 0.36, respectively. In a first scenario genomic prediction was evaluated using a five-fold cross validation within all crossbred animals and showed reliabilities ranging from 0.33 to 0.49. Based on a forward prediction, using crossbred boars as calibration set and Pietrain boars as validation set, reliabilities between 0.15 and 0.50 for all boar taint traits were observed.

Our analysis showed that genomic selection against boar taint is promising. It was possible to reach adequately high reliabilities, even in small populations.

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Key Words: swine, boar taint, genomic selection

0359 Understanding the genetic archticture of Hays Converter Cattle. M. K. Abo-Ismail[*1,2], R. Khorshidi[1], E. C. Akanno[1], J. Crowley[1,3], S. P. Miller[4,5,6], A. Fleming[7], J. Basarab[1,8], C. Li[1,9], P. Stothard[1], and G. Plastow[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Animal and Poultry Production, Damanhour University, Egypt, [3]Canadian Beef Breeds Council, Calgary, AB, [4]AgResearch Limited, Mosgiel, New Zealand, [5]Centre for Genetic Improvement of Livestock, University of Guelph, ON, Canada, [6]University of Queensland, Centre for Animal Science, QAAFI, St. Lucia, Australia, [7]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [8]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, Canada, [9]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Edmonton, AB, Canada.*

The Hays Converter (HC) was the first Canadian breed to be recognized in terms of the Canadian Livestock Pedigree Act and combines the genetics of the Hereford, Holstein and Brown Swiss breeds. Although, the improvement program has continued there is now a risk to its sustainability. The objective of this study is to utilize genomic tools to assess genetic diversity and inbreeding within the HC population. Historical samples for 265, 238, and 208 animals born between 1973 and 2015 have been genotyped for 19K (19,792 SNPs,), 6K (6829 SNPs) and Illumina BovineSNP50 (50K, 49,100 SNPs), respectively. A total of 49,100 SNPs across 29 autosomes that passed all quality control criteria were considered for imputation of the target populations with 19k (7496 SNPs) and with 6k (6253 SNPs) using FImpute. The actual and imputed genotypes were filtered for 702 animals and 41,734 SNPs across 29 autosomes passed quality control. Using only actual 50K genotypes of 208 animals, the genetic structure of the HC population was assessed in conjunction with individuals genotyped for Illumina BovineSNP50 from Angus (AN, $n = 486$), Hereford (HE, $n = 591$) and Holstein (HO, $n = 32$) breeds using principal component analysis (PCA). The genomic inbreeding coefficients for individuals within HC were estimated using pedigree information and 4 genomic methods. The genetic distances between animals within each population were calculated based on their genomic profile using Prevosti Distance. Although, the PCA indicated that the HC breed is genetically divergent from Holstein, Hereford and Angus, it was more closely related to Holstein cattle than the other breeds. Genomic inbreeding coefficients using imputed or actual genotypes indicated that the HC is inbred over years,

particularly from 1993 till 2005. Thus, this indicates a smaller effective population size for the HC population at that time. The result from genetic distance and phylogeny of the HC population indicated existence of sub populations within the HC. In conclusion, the study showed an increase of inbreeding within HC breeds so that managing inbreeding and maximizing diversity is required to avoid inbreeding depression. The observed diversity will influence HC design for future mate allocation using genomic information.

Key Words: genetic structure, Inbreeding, Illumina BovineSNP50 chip, Hays Converter beef cattle

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0360 Genetic parameters and trends for length of productive life and lifetime production efficiency traits in Thai Landrace and Yorkshire sows.

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Data from a commercial swine population in Northern Thailand were used to estimate genetic parameters and trends for length of productive life (LPL), lifetime number of piglets born alive per year (LBAY), lifetime number of piglets weaned per year (LPWY), lifetime litter birth weight per year (LBWY), and lifetime litter weaning weight per year (LWWY). Phenotypic records were from 2259 Landrace and 826 Yorkshire sows that had their first farrowing between 1989 and 2013. An average information restricted maximum likelihood procedure was used to estimate variance and covariance components, heritabilities and correlations. The 5-trait animal model included first farrowing year-season, breed group, and age at first farrowing as fixed effects, and sow and residual as random effects. Heritability estimates were 0.17 ± 0.04 for LPL, 0.07 ± 0.03 for LBAY, 0.13 ± 0.03 for LPWY, 0.04 ± 0.02 for LBWY and 0.13 ± 0.03 for LWWY. Genetic correlations between LPL and all lifetime production efficiency traits (LBAY, LPWY, LBWY and LWWY) were all positive ranging from 0.66 ± 0.14 (LPL-LBAY) to 0.95 ± 0.02 (LPL-LBWY). Rank correlations between EBV for LPL and lifetime production efficiency traits were, on the average, higher for boars than for sows in the top 5% (0.51 vs. 0.19), 25% (0.68 vs. 0.42) and 50% (0.86 vs. 0.58). Sire genetic trends were negative for LPL (−2.41 ± 0.59 d/yr; $P < 0.001$) and LWWY (−0.14 ± 0.06 kg/yr; $P < 0.04$) and near zero for LBAY, LPWY, and LBWY. Conversely, dam genetic trends were positive for LPL (1.10 ± 0.39 d/yr; $P < 0.01$), LPWY (0.12 ± 0.01 piglets/yr; $P < 0.0001$), and LWWY (0.26 ± 0.04 kg/yr; $P < 0.0001$) and near zero for LBAY and LBWY. Sow genetic trends were near zero for all traits. Improvement for LPL and lifetime production efficiency traits in this commercial swine population will require these traits to be included in the selection indexes used to identify replacement boars and gilts.

Key Words: swine, length of productive life, lifetime production efficiency

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0361 Estimation of genetic parameters on carcass traits and body type measurements in Hanwoo.

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The objective of this study is to estimate genetic parameters on carcass traits and body type measurements in Hanwoo cows (Korean native cattle). The data for this study were obtained from local rearing farms in Jeonnam province, South Korea from 2003 to 2014. Two hundred seventy-seven head of reproductive cattle were measured for withers height, rump height, body length, chest depth, chest width, rump length, pelvic width, rump width, hipbone width, chest girth, and shank girth. Of the 277 head of cattle, 151 were randomly selected for investigation of carcass traits. Birth year, birth location, and sex were considered as fixed factors.

Genetic correlation coefficients of live weight with chest depth, chest width, rump width, and chest girth were 0.67, 1.00, 0.97, and 0.99, respectively. Genetic correlation coefficients of rump length with withers height, rump height, chest width, and pelvic width were 0.85, 0.92, 0.85, and 0.98, respectively.

Positive selection for chest girth, chest width, chest depth, and rump width resulted in increased live weight. Correlation coefficients of rump length with withers height and rump height were highly positive, which suggests that rump length and rump width are informative indicators for selection of body type measurements.

Heritabilities of body type measurement and carcass traits ranged from 0.19 to 0.83. Estimates of heritability on marbling score, body length, and rump height were 0.18, 0.19, and 0.24, respectively. Estimates of heritability on eye muscle area, shank girth, and withers height were 0.30, 0.36, and 0.48, respectively. Heritabilities of carcass weight, chest width, live weight, hipbone width, rump length, and chest depth were 0.51, 0.67, 0.68, 0.71, 0.76, and 0.77, respectively.

The genetic correlation between carcass weight and chest depth was a negative value of −0.98. The genetic correlation between carcass weight and chest width was 0.68. Genetic correlation coefficients of eye muscle area with rump length, chest depth, hipbone width, and shank girth were 0.67, 0.84, 0.66, and 0.94, respectively. Genetic correlation coefficients of marbling score with withers height, rump length, and hipbone width were −0.54, −0.74, and −0.83, respectively.

Improvement in both quality and quantity traits of Hanwoo cows is difficult due to the negative correlation between the two traits. To develop an optimal breeding scheme for Hanwoo cows, rearing farms need to establish breeding goals for Hanwoo cows individually and obtain informative data, including

pedigree information and reproductive records, from each cow.

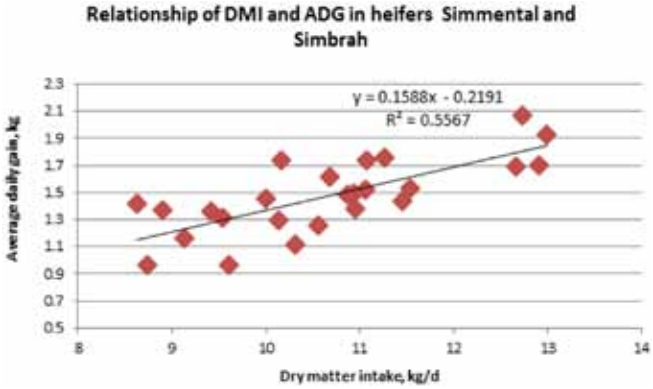
Key Words: Korean native cattle, genetic parameters, body measurement, genetic correlation

0362 Residual feed intake (RFI) for genetic selection of Simmental and Simbrah cattle. N. Manzanares-Miranda*[1], J. R. Kawas[2], H. Villalon-Mendoza[2], and G. Moreno-Degollado[2], *[1]Universidad Autonoma de Nuevo Leon, Posgrado Conjunto de las Facultades de Agronomia y Medicina Veterinaria y Zootecnia, San Nicolas de los Garza, Mexico, [2]Universidad Autonoma de Nuevo Leon, San Nicolas de los Garza, Mexico.*

Since two-thirds of the cost of cattle production is directly related to feed costs, strategies that improve the efficiency of feed utilization will increase the economic viability of livestock operations. An alternative measurement for feed efficiency is the residual feed intake (RFI). The objective of this study was to determine the possibility of using RFI as an indicator for genetic selection of males and females of Simmental and Simbrah cattle breeds. Thirty-one Simmental and 26 Simbrah, males (32) and females (25), were randomly assigned to a 2 × 2 factorial design (breeds and gender). Variables measured were dry matter intake (DMI), average daily gain (ADG) and RFI. There was no correlation between RFI, DMI and ADG. Individuals with negative RFI were detected in the test group among both breeds. ADG was greater ($P < 0.05$) for males (1.81 kg/d) than females (1.47 kg/d). A significant association ($P < 0.05$) between the different variables studied. No statistical differences in RFI were observed for breed ($p = 0.44$) or gender ($p = 0.52$). It was not possible to use RFI as an indicator for genetic selection for Simmental and Simbrah cattle.

Key Words: Simmental, Simbrah, residual feed intake

Table 0362.



0363 Multivariate analysis of reproductive and productive traits in Sindhi breed females (*Bos indicus*). R. R. C. Mello[1], L. D. P. Sinedino*[2], S. L. G. Sousa[1], and M. R. B. Mello[1], *[1]Federal Rural University of Rio de Janeiro, Seropedica, Brazil, [2]University of Florida, Gainesville.*

The aim of this study was to investigate the possibility to generate different productive groups in Sindhi breed through multivariate techniques, to give directions to genetic improvement programs in this breed. For this goal, performance data provided by the Brazilian Association of Zebu Breeders related to 560 Sindhi breed females from 28 different herds in Brazil, born in the period from 1987 to 2011, were used. The traits age at first calving, calving interval, reproductive efficiency, total milk yield and lactation period were analyzed, being submitted to the principal components and cluster analysis, with the GENES® statistical program. By the principal components analysis, these five components were estimated, and the first three explained 90.79% of the data's total variation. The traits considered most relevant to the discrimination of the data set, in decreasing order of importance, were: calving interval, lactation period, age at first calving, total milk yield, and reproductive efficiency. By cluster analysis, 12 different groups were generated from the pool of Sindhi herds analyzed, with a great homogeneity among females for the traits evaluated, and only few females generating separate groups. Four hundred twenty-nine females were clustered in one group, representing 76.60% of the genotypes. This indicates that, although there are genotypes with large genetic diversity, more than two thirds of the animals are similar to the traits evaluated, showing a high degree of relationship between them. The traits for total milk yield showed 71.92% of the total variation, and age at first calving contributed with 23.06% of the variation, being the two most important traits for the variability of the data. Thus, there is evidence of divergence between the groups regarding total milk yield, indicating that this trait stands out in the differentiation of groups, and these groups could be benchmarks for the use of genetic improvement programs whose focus is the increase in milk yield. In conclusion, the multivariate procedures were effective to summarize the evaluated information and to discriminate the most important traits, providing better identification of the most appropriate females to certain herds or milk production systems. The analysis of the relative contribution was effective in identifying total milk yield and age at first calving as the most relevant traits for the differentiation of groups, and they can be useful targets for genetic improvement programs that focus on milk yield and reproductive precocity.

Key Words: cluster analysis, reproductive efficiency, milk yield

0364 Repeatability of egg weight in Japanese quail. O. T. Abanikannda, O. N. Ottun*, and A. O. Leigh, *Lagos State University, Ojo-Lagos, Nigeria.*

Knowledge of genetic parameters is useful in designing efficient breeding systems, and accurate estimates of genetic parameters are essential for construction of applied breeding. Repeatability, the ability of individual animal to repeat its performance and maintain its ranking in a population in successive records is of immense benefit in predicting the expected rate of annual genetic gain in the trait. The objective of the study was to evaluate and assess changes in measurements of eggs by quail hens over a period of time and estimate its repeatability. The study was conducted at the Poultry Breeding Research Laboratory of the Lagos State University, Ojo-Lagos, lying at 06.48N and 003.20E in the humid tropics of Nigeria. The hens studied were brooded and raised from hatch to 6 wk before being separated and raised in individual compartments for ease of egg collection, identification and measurements. In all, 70 hens were studied over a period of 34 d, with each hen laying between 17 and 33 eggs during the study period. The eggs were picked as soon as it was laid and properly tagged to reflect the hen's identification and day of lay. Measurements taken include, hen weight (HenWt), feed consumed (FeedCon), egg weight (EggWt), egg length (EggLt) and egg width (EggWd). The statistical model describing each of the three (egg weight, egg length and egg width) variables studied is given as $Y_{ijklm} = D_i + H_j + C_k + F_l + e_{ijklm}$, where day of lay (D) and Hen (H) are fixed factors and HenWt (C) and FeedCon (F) are covariates to adjust for differences among hens, and it accounted for 62.67%, 49.40% and 71.94% of the total variation, respectively. With the exception of feed consumed which was not significant ($P > 0.05$) on any of the three responses and day of lay which was not significant ($P > 0.05$) on egg weight, all other factors/covariates were highly ($P < 0.01$) significant. Repeatability estimates for the three variables studied were estimated using the one way ANOVA of Hen effect on each of the three variables by $r = [(MS_b – MS_w)/n_0]/\{MS_w + [(MSb\text{-}MS_w)/n_0]\}$ and repeatability values obtained were 0.56, 0.15 and 0.12 respectively for egg weight, egg length and egg width. The repeatability estimate for egg weight, the most desirable trait in successful poultry business is moderate (0.56) and can be employed early in lay to select hens with potentials for bigger eggs.

Key Words: repeatability estimates, quail, Nigeria

365 Genetic parameters of cyclicity and other fertility indicators in dairy cattle. D. Gonzalez-Pena[*1], H. Jeong[2], P. J. Pinedo[3], J. E. P. Santos[4], G. M. Schuenemann[5], G. J. M. Rosa[6], R. O. Gilbert[7], R. C. Bicalho[7], R. Chebel[4], K. N. Galvão[8], C. M. Seabury[9], W. W. Thatcher[10], and S. L. Rodriguez Zas[2], *[1]Zoetis, Kalamazoo, MI, [2]University of Illinois, Urbana-Champaign, [3]Colorado State University, Fort Collins, [4]University of Florida, Gainesville, [5]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [6]University of Wisconsin, Madison, [7]Cornell University, Ithaca, NY, [8]Department of Large Animal Clinical Sciences, University of Florida, Gainesville, [9]Texas A&M University, College Station, [10]Department of Animal Sciences, University of Florida, Gainesville.*

Resumption of ovarian cyclicity after calving is crucial to achieving reproductive efficiency in cattle. Early onset of ovulation after calving can decrease veterinary costs and calving interval while augmenting the length of lactation, total milk yield, and genetic improvement of the herd. Four fertility indicators are frequently used: probability of cycling at 45 d post-calving (Pr_Cyc), probability of disease diagnosis at 45 d post-calving (Pr_Sck), probability of pregnancy after 2 AIs (Pr_Prg), and days open (DO). The goal of this study was to identify significant covariables that affect these fertility indicators and to estimate their genetic parameters in dairy cattle. Measurements from approximately 5000 cows from 4 U.S. states (CA, FL, MN, TX) across two calving years were analyzed and relevant covariables were identified by stepwise selection. The three indicator probabilities were described using a logistic model including the explanatory variables: dystocia, retained placenta, stillbirth, body condition score at 7 d and 35 d post-calving (BCS7 and BCS35, respectively), score of vaginal mucous (0 = no mucus to 5 = brownish fetid discharge) at 7 d, 12 d, and 35 d post-calving, and blood β-hydroxybutyrate (BHBA), an indicator of subclinical ketosis. A univariate sire model including the effects of contemporary group and lactation number was used to estimate the genetic parameters of four fertility indicators: Pr_Cyc, Pr_Sck, Pr_Prg, and DO. The percentage of cows cycling, diagnosed with a disease, and pregnant after 2 AIs were 75.5%, 16.6%, and 62.5%, respectively. The marginal probabilities of the significant covariables indicated that Pr_Cyc was 4.8%, 1.5%, and 1.2% lower per unit increase in BHBA, and mucus score at 7 d and 35 d post-calving, respectively. Also, Pr_Cyc was 7.0% higher per unit increase in BCS35. Similarly, the Pr_Prg was 3.2% and 3.0% lower per unit increase in BHBA and mucus score at 35 d post-calving, respectively. The Pr_Sck increased 33.8% per unit increase in BHBA and 2.3% with stillbirth. The heritability estimates for Pr_Cyc, Pr_Sck, Pr_Prg, and DO were 0.12, 0.03, 0.07, and 0.06, respectively. Our findings

corroborate that early resumption of cyclicity postpartum is an important indicator of cow reproduction performance and has substantial genetic variability that can be exploited in selection practices. Improved accuracy of pregnancy predictions is maybe one of the potential benefits of including this indicator in fertility indices. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: reproduction, cattle, pregnancy

0366 Genetic parameters of early lactation diseases in dairy cattle. D. Gonzalez-Pena[*1], T. M. Goncalves[2], P. J. Pinedo[3], J. E. P. Santos[4], G. M. Schuenemann[5], G. J. M. Rosa[6], R. O. Gilbert[7], R. C. Bicalho[7], R. Chebel[4], K. N. Galvão[8], C. M. Seabury[9], W. W. Thatcher[10], and S. L. Rodriguez Zas[2], *[1]Zoetis, Kalamazoo, MI, [2]University of Illinois, Champaign-Urbana, [3]Colorado State University, Fort Collins, [4]University of Florida, Gainesville, [5]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [6]University of Wisconsin, Madison, [7]Cornell University, Ithaca, NY, [8]Department of Large Animal Clinical Sciences, University of Florida, Gainesville, [9]Texas A&M University, College Station, [10]Department of Animal Sciences, University of Florida, Gainesville.*

Early lactation diseases impact herd profitability, compromise animal welfare, increase antibiotic use, and affect consumer preferences. Therefore, genetic improvement of disease resistance is becoming an increasingly important goal in dairy cattle breeding. The objectives of this study were to estimate the genetic parameters of major diseases and to identify variables that affect the incidence of these diseases. The probabilities of a cow to develop metritis (Pr_Met), clinical endometritis (Pr_End), ketosis (Pr_Sck), and clinical mastitis (Pr_Mas) were evaluated. Disease records from approximately 5000 cows across U.S. regions (West, Midwest, South, and Southwest) and two calving years were analyzed. Univariate logistic sire models including the effects of contemporary group and lactation number and additional covariates were used to estimate genetic parameters. Additional explanatory variables included: dystocia, retained placenta, stillbirth, body condition score at 7 d and 35 d post-calving (BCS7 and BCS35, respectively), vaginal mucous score at 7 d, 12 d, and 35 d post-calving (on scale of 0 = no mucus to 5 = brownish fetid discharge), and blood β-hydroxybutyrate (BHBA) as indicator of subclinical ketosis. Stepwise selection enabled the identification of the explanatory variables significantly associated with the probability of each disease. The percentage of cows with metritis, endometritis, ketosis, and mastitis were 28.8%, 22.4%, 16.6%, and 7.6%, respectively. Among the significant explanatory variables, Pr_Met increased 5.1% per unit increase in BHBA. Also, Pr_Met increased 35.9% and 7.6% in cows diagnosed with retained placenta and dystocia, respectively. On the other hand, Pr_Met decreased 6% per unit increase of BCS7. The heritability estimates (and standard errors) for Pr_Met, Pr_End, Pr_Sck, and Pr_Mas were 0.06 (0.01), 0.07 (0.02), 0.03 (0.02), and 0.02 (0.007), respectively. The association between explanatory variables and early postpartum disease probabilities and low heritability estimates identified in this study confirm that reliable prediction of disease incidence in dairy herds requires comprehensive accounting for health and management information. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: resistance, genetic parameters, indicators

0367 Genetic evaluation of mastitis, metritis, and ketosis in Holstein cattle using producer recorded data. G. C. Márquez*, Y. Zare, K. L. Stephan, and K. Olson, *ABS Global, DeForest, WI.*

The objective of this study was to develop a genetic evaluation of mastitis (MAST), metritis (MET), and ketosis (KET) from producer recorded data. The period from calving to 60 d postpartum is one of the most challenging times in a cow's lactation when up to 75% of diseases occur. Dairy producers routinely collect health data for management purposes, and these data are also valuable for genetic evaluation. Limited genetic evaluation of these traits exists. Data from on farm management systems was mined by finding keywords that would indicate that a cow had a case of one of the diseases. Only cases within the first 60 d of a cow's first lactation were used. A total of 3264,415, 2822,312, and 2035,174 observations from first lactation Holsteins coming from 776, 593, and 421 farms were used in the evaluations of MAST, MET, and KET, respectively. ASReml was used to fit a linear sire model with an eight-generation pedigree. For each trait a mean as well as herd-year-season of calving and age at first calving were fitted as fixed effects. The random genetic effect of sire was used for all traits. The mean first lactation disease incidence was 16%, 10%, and 3% for MAST, MET, and KET, respectively. The heritability of MAST, MET, and KET was 2%, 4%, and 3%, respectively. There was genetic variation between the best 10% and the worst 10% of sires by EBV. On average the disease incidences of the bottom 10% of sires was higher than the incidences of the top 10% of sires by 5%, 8%, 4% for MAST, MET, and KET, respectively. MAST, MET, and KET have a large economic impact on dairies, and selecting sires whose daughters have lower disease incidence is a cost effective way to make cumulative and permanent change in the population. Given the low heritability of these traits and the wide array of economically relevant traits in dairy, these should be incorporated into a selection index to achieve healthier transition cows.

Key Words: dairy cattle, genetic evaluation, transition period

0368 Genetic evaluation of dairy cow livability.

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Predicted transmitting abilities (PTA) for cow livability (LIV) were developed to measure a cow's ability to stay alive while on the farm, whereas PTA for productive life (PL) measures a cow's ability to avoid dying on the farm or being culled. About 20% of dairy cows died instead of being sold over the last decade, averaging 7% per lactation. LIV has been recorded since 1970. Records for 69,710,392 lactations of 25,514,760 cows were evaluated with an all-breed animal model, using edits similar to a 2008 study. The scale reports cow livability instead of mortality so that positive PTAs are favorable (0 = died; 100 = lived for each lactation) and reports PTA on lifetime instead of per lactation basis to express LIV differences as a percentage of all cows exiting the herd. The model used individual lactation records for culling as a correlated trait to increase reliability of LIV. Heritability was 1.3% on the observed scale for LIV per lactation vs. 3.0% for overall culling per lactation. The SD of true transmitting ability for LIV was 0.82% per lactation or 2.3% per lifetime using an average of 2.8 lactations per cow. For recent bulls with > 80% reliability, PTA LIV were correlated favorably to PTA for PL (0.70), daughter pregnancy rate (0.45), and somatic cell score (−0.25); correlations with PTA for yield traits were low. The 0.70 correlation with PL was sufficiently below 1 to add value from selecting for both LIV and PL in an index. Genomic PTA (GPTA) for young bulls computed from 4-yr truncated LIV data had squared correlations with future data about twice as high as parent averages (PA) for LIV. Genomic reliability was 56% compared with 30% for PA, but lower than 70% for GPTA PL. Economic values for LIV and PL were estimated assuming $1,200 less income for cows that die than for those sold for beef. Relative emphasis on LIV was 7% of total emphasis, but relative emphasis on PL declined to 14% from 19% currently used in net merit. Thus, total emphasis on PL and LIV could increase to 21% using 2 correlated traits instead of 19% with just 1 trait. The United States in 1994 was the first country to evaluate longevity, and can also become the first country to evaluate cow mortality or livability as a specific economic trait.

Key Words: mortality, productive life, economic value

0369 Genetic associations between milk production and growth traits in Guzerat breed.

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In Brazil, the Guzerat breed is used for beef, milk production or as dual purpose breed. Progeny tests of dairy bulls are available for the breed (Programa Nacional de Melhoramento Genético do Guzerá para Leite–National Breeding Program of Dairy Guzerat Cattle), in addition to genetic evaluations of growth traits performed by the Brazilian Association of Zebu Breeders (Associação Brasileira de Criadores de Zebu-ABCZ). For this reason, beef bulls are used in dual purpose herds. To identify differences in the growth and milk production patterns of bulls of this breed, two-trait analyses were performed between cumulative milk production at 305 d (P305) and weight at 120 d (W120), weaning weight (WW), yearling weight (YW), post-weaning weight (PWW), and weight at 24 mo of age (W24). The data files contained 97,394, 65,181, 50,443, 40,425, and 31,279 records, respectively, obtained from the database maintained by ABCZ. The model used included the fixed effects of contemporary group and age of cow at calving (linear and quadratic covariate), and direct additive genetic, permanent environmental (maternal for weights; direct for milk) and residual effects as random effects. The variance components were estimated by the restricted maximum likelihood method using the WOMBAT program. The heritabilities estimated in the two-trait analyses were 0.24 (0.003), 0.14 (0.009), 0.16 (0.0012), 0.18 (0.0014), 0.21 (0.0017) and 0.22 (0.020) for P305, W120, WW, YW, PWW and W24, respectively. The genetic correlations between weights at different ages and P305 were positive but low, ranging from 0.27 (0.111) to 0.38 (0.099), indicating a low association between the breeding values of the traits. Selection for P305 resulted in a low correlated response to increase weights at the ages studied. Based on the breeding values estimated, bulls with a high milk production potential and bulls with a high beef production potential were identified by cluster analysis. The separation of bulls for each selection objective will potentiate the result of genetic selection of the breed.

Key Words: production traits, selection criteria, dual purpose, genetic parameters, Zebu

0370 Production, reproduction, and health of Holstein, Jersey, and crossbred cattle in a seasonal calving pasture-based dairy.
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Crossbreeding of dairy cattle has received increasing interest among researchers and farmers over the past several years. In a seasonal calving herd, crossbreeding could improve reproductive performance to ensure that more cows become pregnant during the relatively short breeding season. In the current study, we examined data from 14 yr of Holstein–Jersey crossbreeding in a seasonal calving, pasture-based dairy herd in Goldsboro, NC. Approximately 125 calves were produced each year, maintaining populations of pure Holsteins (HH, n = 286), pure Jerseys (JJ, n = 335), reciprocal F1 crosses (HJ, n = 182; JH, n = 233); F1 crosses were backcrossed to either H or J sires on alternate years, and crosses that were > 50% of one breed were always mated to the other breed (HX, n = 571; JX, n = 501). HJ, HX, JH, and HH cows had greater milk, fat, and protein yields per lactation than JX and JJ cows ($P <$ 0.05), whereas JJ and JX cows had greater fat and protein percentage in their milk than HH and HX cows. Milk production and fat percentage for the various breed crosses were 8042 ± 121 kg and 4.15 ± 0.06% for HH, 7828 ± 86 kg and 4.70 ± 0.04% for HX, 8063 ± 144 kg and 4.77 ± 0.07% for HJ, 7439 ± 124 kg and 4.85 ± 0.06% for JH, 6776 ± 94 kg and 4.91 ± 0.04% for JX, and 6180 ± 108 kg and 4.64 ± 0.05% for JJ. Crossbreds had some reproduction advantages, including younger age at first service, age at conception, fewer days to first service, and a greater percentage of cows pregnant during the breeding season. Holstein heifers were less likely than other breed groups to survive to 26 mo of age, but those that survived had reproductive success similar to Jerseys and crosses for subsequent lactations. HH were significantly more likely than JJ to have mastitis (16.4 ± 3.0% vs. 9.3 ± 1.9%, $P < 0.05$). Incidences of retained placenta, metritis, cystic ovaries, udder edema, lameness, milk fever, and the need for hormonal intervention for reproduction were no different among breed groups. Within a seasonal calving pasture-based system, Holstein-Jersey crossbred cattle have some production and reproduction advantages over their purebred contemporaries.

Key Words: dairy crossbreeding, pasture system, lifetime performance

0371 Between and within-lactation repeatabilities for hoof lesions in Canadian Holsteins.
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This study aimed to estimate genetic parameters and between and within-lactation repeatabilities for hoof lesions, considering the hoof lesions as binary traits or as categorical traits, using a severity score. Hoof lesions were recorded by 23 hoof trimmers during the routine trimming activity in 365 herds located in Alberta, British Columbia, and Ontario from 2009 to 2012. The hoof trimmers were trained to use a rugged touchscreen computerized lesion recording system. The lesions included in the analysis were: digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion. Hoof lesions were coded as binary traits (0; 1), where 1 was assigned to the presence of a lesion in any claw or leg or as categorical traits, using a severity score from 0 to 3, where 0 was assigned to the absence of a lesion, 1 to less severe lesions, 2 to moderately severe lesions, and 3 to more severe lesions. The edited dataset contained 107,933 observations from 53,654 animals. The final pedigree file contained 196,899 animals and included 7 past generations. Hoof lesions were analyzed with univariate animal models using the average information-restricted maximum likelihood procedure in the DMU package. Two different permanent environmental effects were included to separate between-lactation permanent environmental effects from within-lactation permanent environmental effects when multiple lactations per cow occurred. For most lesions, affected cows showed higher proportion of moderate severe cases. Sole hemorrhage and white line diseases had very similar proportion of less severe and moderate severe cases (45.8% and 41.1%; 43.4% and 40.7%, respectively). Most of the cows affected by interdigital dermatitis showed less severe lesions (75.6%), and only 1.2% of affected cows showed more severe cases of interdigital dermatitis. Heritabilities ranged from 0.005 (for toe ulcer) to 0.07 (for digital dermatitis). Heritabilities estimated considering the presence or absence of the lesion, or using a severity scale, were very similar. Repeatabilities were low to moderate, both between and within-lactation. However, they were 3- to 90-fold larger than the heritabilities. The most repeatable lesion was toe ulcer, which showed a within-lactation repeatability coefficient of 0.45, and a between-lactation repeatability coefficient of 0.36. Sole hemorrhage showed the lowest coefficients (0.10, for both within and between-lactation repeatabilities). Results suggested that all the repeated observations might be valuable

for increasing accuracy of estimated breeding values.

Key Words: hoof lesions, repeatability, severity

0372 Sexed-semen usage for Holstein AI in the United States. J. L. Hutchison*[1] and D. M. Bickhart[2], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The dairy industry has used sexed-semen to increase the number of heifer calves born on the farm for over a decade. While the efficacy of sexed-semen has been determined experimentally, we sought to tabulate statistics on the generalized use of the technology in the U.S. dairy herd and determine its effectiveness in the field. Sexed-semen breeding status was determined by a National Association of Animal Breeders' 500-series marketing code or by individual breeding information in a cow or heifer reproduction record from a dairy records processing center. Only breedings from 2007 through 2015 with confirmed outcomes (pregnant or not pregnant) were included: 5,963,876 heifer breedings (1,323,721 to sexed semen) and 42,232,502 cow breedings (253,586 to sexed semen). Sexed-semen breedings resulted in 87 and 89% female offspring, for cows and heifers, respectively. This was a notable improvement over conventional Artificial Insemination (AI), which results in 48% female births, on average. Usage of sexed-semen in heifers has increased from 9% in 2007 to 31% in 2015. Furthermore, mean conception rates for heifer sexed-semen breedings has recently increased due to improved technology (42% in 2007 compared with 49% in 2015). Comparable conception rates for heifer conventional breedings were 56, and 59% for 2007, and 2015, respectively. Smaller increases were seen in sexed-semen breedings to cows where 0.2% of all breedings used sexed semen in 2007, and 1% in 2015. Conception rates for sexed-semen breedings to cows were 26% in 2007, and 30% in 2015 compared with 30, and 32% for conventional breedings during the same years, respectively. Usage of sexed-semen for both heifers and cows has increased, with a bigger increase seen in heifers. Mean conception rates for sexed-semen breedings have also increased for both heifers and cows.

Key Words: sexed semen, conception rate, breeding

0373 Effect of semen type (cooled-fresh vs. frozen-thawed) on fertility of lactating dairy cows. A. H. Souza*[1], H. J. Bessoff[2], and E. Danzeisen[3], *[1]Ceva Animal Health, Libourne, France, [2]Dairy Management Solutions, Tulare, CA, [3]Global AG Alliance, Tulare, CA.*

The objective of this retrospective data analysis was to compare pregnancy per AI (P/AI) in dairy cows inseminated with cooled-fresh semen or frozen-thawed semen. Lactating Holstein cows from 11 confined dairies in CA were detected in estrus or synchronized with a Ovsynch-like timed AI protocol and received an AI with a single dose of either fresh (15 to 40 x 10^6 sptz/straw) or frozen semen (15 x 10^6 sptz/straw) once/day in the mornings. Both types of semen from multiple service-sires were used within all herds throughout a period of 10 mo (Jan 2015 to October 2015). Transcervical AI procedure was performed regularly with deposition of semen in the body of the uterus with the assistance of an AI applicator. Fresh semen was delivered to all farms on a daily basis and kept at 2° to 7°C until AI, which was performed within 24 h after fresh semen delivery to the farm. Pregnancy diagnosis was performed at 30 to 40 d post AI across all participating herds. The final database comprised 37,281 breeding records with confirmed AI outcomes (Fresh = 18,042 and Frozen 19,239). Statistical analysis was performed with the proc GLIMMIX of SAS (version 9.3), considering main effects and meaningful one-way interactions with service-sire and cow included in the model as random effects. At 30–40 d after AI, P/AI was greater for cows bred with fresh semen compared with frozen-thawed semen [Fresh = 36.6% (6603/18,042) vs. Frozen = 30.8% (5926/19,239); $P = 0.02$]. In addition, the amount of sperm cells in the fresh semen straw did not influence P/AI ($P > 0.10$). Interestingly, there were no significant interactions ($P > 0.10$) between type of semen (fresh vs. frozen) and month-of-AI, herd, cow parity, days in milk at AI, or even AI breeding-code (natural estrus vs. synchronization programs), suggesting that positive effects of fresh semen in relation to frozen semen was independent from the above mentioned variables. We conclude that the use of cooled-fresh semen improved P/AI in lactating dairy cows compared with the standard AI utilizing frozen-thawed semen.

Key Words: fresh semen, dairy cow, fertility

0374 Subclinical ketosis in the oocyte donors of Holstein × Gir cows. R. C. de Souza*[1], R. C. Souza[1], B. C. M. V. Reginaldo[1], G. C. M. V. da Silva[1], C. A. G. Pellegrino[2], M. I. V. Melo[1], J. P. Lustosa[1], and A. B. D. Pereira[3], *[1]Pontificia Universidade Catolica de Minas Gerais, Betim, Brazil, [2]Faculdade Alis de Bom Despacho, Brazil, [3]University of New Hampshire, Durham.*

In Brazil, the prevalence of subclinical ketosis in F1 *Holstein* × *Gir* oocyte donors has never been assessed in published literature. The aim of this study was to evaluate the prevalence of subclinical ketosis (SK) in F1 Holstein × Gir embryo donors and the effects of this syndrome on reproductive and economic efficiency. Data was collected from several farms in Minas Gerais, Brazil, from May to August 2015. Twenty-eight lactating F1 Holstein × Gir cows were used as oocyte donors. The dosage of ketone bodies was performed using the handset Ketovet (Ketovet Brazil, TaiDoc technology, Taiwan). Cows with blood β-hydroxybutyrate (BHBA) above 1.2 mmol/dL in

the blood were considered as with SK. Donor cows were aspirated for follicules, which were then taken to the laboratory and classified into viable, non-viable and irregular, according to the methodology recommended by the International Embryo Transfer Society (IETS, 2010). Economic analysis was performed considering the following: average price of one follicular aspiration ($75.00), in vitro production of one embryo ($17.75) and cost of each embryo transfer ($12.75). The experiment was analyzed as a complete randomized block design, and means were compared by the Tukey test with significance declared as $P < 0.05$. Results show that each cow produced an average of 20 oocytes, with only 6 oocytes converted into embryos with a final ratio of 3.5: 1 (oocytes:embryos). Two embryos were required to result in 1 pregnancy. Of the 28 donors evaluated, 17 were healthy and 11 had SK, resulting in a disease prevalence of 39.3%. Specifically, the prevalence of SK was higher in primiparous cows (71.4%) compared with multiparous cows (28.6%, $P < 0.05$). Cows with SK produced less total oocytes (11.5 vs. 26.1; $P = 0.014$); less non-viable oocytes (2.09 vs. 10.65; $P = 0.004$), less viable oocytes (6.45 vs. 15.41; $P = 0.005$) and fewer embryos (1.82 vs. 5.41; $P = 0.038$) when compared with healthy cows. The total cost of pregnancy in cows with SK was $142.41, whereas, for healthy cows, was $87.25. In summary, oocyte donors with SK were less efficient as embryo donors. High prevalence of SK observed in this study had a negative effect in the economic efficiency of embryo transfer, causing this technology to be 60% more costly when compared with the same technology used in healthy cows.

Key Words: subclinical ketosis, economic efficiency, embryo transfer

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0375 Clinical signs associated with bovine respiratory disease diagnosis and high heritability in beef and dairy cattle.

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Bovine respiratory disease (BRD) is an infectious multifactorial disease in cattle. To facilitate industry selection of cattle that are less susceptible to BRD, a uniform diagnosis of the disease that maximizes heritability (h^2) estimates, and is easy to measure is needed. Therefore, the objective of this study was to evaluate the effect of different clinical signs used to diagnose BRD on heritability estimates of BRD in dairy and beef cattle. This study was conducted on two pre-weaned dairy calf populations (California-CA, $n = 2000$; New Mexico-NM, $n = 798$) and two beef feedlot populations (Colorado-CO, $n = 1000$; Washington-WA, $n = 1000$). Cattle within each population were initially diagnosed with BRD using the McGuirk scoring system, which evaluates five clinical signs (CS): cough, temperature, nasal discharge and either eye discharge or ear droop (McGuirk, 2008). Heritability was calculated using EMMAX in each population for 15 different CS combinations, including the original combination used by the McGuirk scoring system. The CS that explained the most h^2 varied by population. In dairy cattle, the h^2 in the different CS combinations ranged from 0.12–0.24 for CA and 0.07–0.2 for NM and in beef cattle ranged from 0.04–0.24 in CO to 0.2–0.25 in WA. Identification of cattle using cough alone as the CS resulted in the highest h^2 estimates in CA ($h^2 = 0.23$) and CO ($h^2 = 0.22$), whereas eye or ear CS resulted in the highest h^2 estimates in NM ($h^2 = 0.17$) and WA ($h^2 = 0.19$). Two CS explained the most h^2 (mean $h^2 = 0.17$) across all populations: temperature, cough and nasal and the McGuirk scoring system. In each population, the CS explaining the least h^2 also differed (CA = nasal, NM = cough, CO = temperature, WA = nasal) although collectively, the nasal CS was ranked lowest (mean $h^2 = 0.14$). Multiple factors (age, pathogens and location) contributed to the differences in importance of CS between the different populations. These results determined that diagnosing BRD based on temperature, cough and nasal CS would facilitate a uniform diagnosis of BRD that could be used for development of breeding values to select beef and dairy cattle that are less susceptible to BRD. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: BRD, cattle, heritability

0376 Estimating enteric methane and carbon dioxide emission from lactating dairy cows using GreenFeed system.

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Enteric methane (CH_4) and carbon dioxide (CO_2) emissions from lactating dairy cows vary over time depending on various factors that include feed intake, feeding strategy, diet composition, and the time of day. GreenFeed system (C-Lock Inc., Rapid City, SD) is an on-farm "bait station" that captures the breath of cattle when they visit and quantitatively analyzes

the emitted gasses for CH_4 and CO_2 flux. The objective of this study was to determine the correlation between measurements of CH_4 and CO_2 at 2 selected time points of the day vs. 8 equally spaced time points over the 24 h in the diurnal cycle. A GreenFeed system was placed at the University of Alberta-Dairy Research and Technology Center in an open area and cows were moved from their stalls to the unit during measurement time. Individual average daily CH_4 and CO_2 emissions were estimated from lactating dairy cows (N = 29) varying from 32–76 average days in milk (DIM). Individual daily CH_4 and CO_2 emissions were estimated 2 times a day (09:00–12:00; 18:00–20:30 h) for 14 consecutive days and then emissions were measured on the same cows at 8 equally spaced time points (0200, 0500, 0800, 1100, 1400, 1700, 2000, and 2300 h) in the diurnal cycle within 2–3 d. The two time points during the day included the higher and the lower peaks in the diurnal pattern of CH_4 and CO_2 emissions. The number of visits during the 2 times a day and over 24 h measurement ranged from 11–31 and 2–8, respectively. Daily individual CH_4 and CO_2 emissions were estimated by averaging visit fluxes and extrapolating over a day. The result showed a strong correlation of dry matter intake (r = 0.73; P < 0.001), CH_4 g/d (r = 0.74; P < 0.001) and CO_2 g/d (r = 0.72; P < 0.001) production between 2 times vs. 8 time-point measurements. The Pearson correlation coefficient for CH_4 yield (g/kg of DMI) also showed moderate correlation (r = 0.41; P < 0.05) between the two measurements. Taken together, daily CH_4 and CO_2 emissions can be estimated with lower frequency of sampling per day as long as the minimum and maximum emission points in the diurnal cycle are included with an adequate number of visits.

Key Words: methane, carbon dioxide, GreenFeed

0377 Evaluation of factors affecting NaCl content the evolution in ewes milk and of its effect on technological properties.

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The work was aimed at investigating factors affecting variation of NaCl content in sheep milk and at evaluating its relationships with (MCP) and cheese yield. A total of 2778 individual milk samples were collected from 607 Sarda dairy ewes farmed in 34 flocks. MCP (rennet coagulation time = RCT, curd firming time = k20, curd firmness = a30) were measured by Formagraph. Individual laboratory cheese yield (ILCY) were determined by micro-manufacturing experiments. NaCl content (mg NaCl/100 mL milk) was measured by MilkoScanTM. NaCl content was analyzed with a mixed linear model that included the fixed effects of parity, season of lambing, birth type, altitude, and the random effects of flock-test-date and of the animal. Moreover effects of NaCl on MCP were investigated with a similar model, that included also the fixed effect of NaCl class. Four classes were considered according to the 25th, 50th, 75th and 100th percentiles of the NaCl distribution: A = 57–113.3, B = 113.4–132.9, C = 133–157.8 and D = 157.9–259.6. The average content of NaCl was 137.55 ± 34.44 mg/100 mL, ranging from 57.60 to 259.60. NaCl content increased with days in milk, and it was lowest in secondiparous ewes compared with older parities. The season of lambing influenced NaCl concentration, which was higher in milk of ewes lambing in late winter and early spring (from February to April) compared with ewes lambed in early winter (October and November), with values for December and January being intermediate. Birth type at lambing and altitude of location of flocks did show significant effects on NaCl content. MCP were affected by NaCl concentration. In particular, RCT and k20 tended to increase moving from A to D NaCl classes, whereas a30 exhibited the opposite pattern. ILCY showed the highest value for in the class of the highest content of NaCl. Results of the present study highlight the influence of factors related to the physiological status of the animal on the NaCl variation. The results on milk coagulation properties found in this work seems to suggest a relationship between NaCl and cheese making attitude of sheep milk.

Key Words: NaCl, milk coagulation properties, sheep milk

0378 A survey on breeding strategies and selection objectives for increased feed efficiency and decreased methane emission.

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The combined effects of world population growth, rising incomes and dietary changes have resulted in an increasing

international demand for dairy and meat products. However, livestock can have negative impacts on the environment and the greater awareness of climate change has placed pressure on the dairy industry to reduce its environmental impact. Enteric methane from cattle has been recognized as one of the major contributor to greenhouse gas emissions. In addition, methane resulting from digestive processes in ruminants represents important dietary energy losses. Therefore, reducing methane emissions (ME) will not only improve the environmental impact of livestock but also increase cows feed efficiency (FE). Collecting phenotypes for FE and ME is difficult and expensive. The increased use of genomic data in dairy cattle breeding programs has provided an opportunity to investigate the selection of more complex traits requiring fewer phenotypic observations. However, a sizeable genotyped and phenotyped reference population is required to accurately predict genomic breeding values. Combining international data sets will help to achieve the overall goal of producing genomic predictions for FE and ME to be used for breeding application in the dairy cattle industry. However, this could be quite challenging, as different traits that describe FA and Me have been proposed, and different methods are used for measuring the same trait. The International Committee for Animal Recording (ICAR) recently approved the creation of a Feed & Gas working group. This group aims to provide an overview of the current data available, to facilitate the standardization of recording dry matter intake and methane output in cattle around the world, and to enhance international collaboration by providing technical and methodological tools for data sharing and merging. A survey to collect information about current and future measurements of FA and ME has been developed. The survey will be sent to research centers and to industry organizations in member countries of ICAR and it contains some specific questions regarding the breeding strategies for these two novel traits. Results of the survey will allow assessment of a better understanding of the breeding strategies planned in different country once routine genomic evaluations will be available for the two novel traits.

Key Words: feed efficiency, methane emission, survey

0379 Genetic analysis of superovulation and embryo transfer traits in Holstein cattle. K. L. Parker Gaddis*[1], S. Dikmen[2], J. B. Cole[3], and P. J. Hansen[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Uludag University, Faculty of Veterinary Medicine, Department of Animal Science, Bursa, Turkey, [3]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

The objectives of this study were to estimate variance components and investigate genomic regions of interest associated with superovulation and embryo transfer in dairy cattle. Superovulation and embryo transfer are methods commonly used by dairy producers to increase the rate of genetic gain achievable from superior females. A limiting factor of these reproductive technologies remains the variability of animal response to treatment. If some of this variability is attributable to genetics, selection for traits related to superovulation and embryo transfer may allow for further improvement. Data were collected from a Holstein dairy operation in Florida from 2008 through 2015, including 926 superovulation records (total number of structures recovered, total number of good embryos), 628 in vitro fertilization records (number of ooctyes recovered, number of cleaved embryos, number of high- and low-quality embryos, number of transferred embryos), and 12,399 embryo transfer records (pregnancy success). Two transformations of count data were compared: Anscombe and logarithmic. Univariate repeatability animal models were fitted for each trait of interest, with the exception of pregnancy success, for which a threshold liability model was used. For traits where a significant genetic component was estimated (total structures collected and number of good embryos), single-step genomic BLUP analyses were conducted using AIREMLF90 (version 1.116). PostGSf90 (version 1.35) was used to calculate SNP effects and 10-SNP window variances. The two transformation methods produced very similar results. Significant genetic components were estimated for total number of structures recovered and number of good embryos in the superovulation dataset, with heritabilities of 0.31 ± 0.07 and 0.21 ± 0.06, respectively. Genetic components estimated from the in vitro fertilization dataset were not significantly different from zero. Heritability of recipient pregnancy success after embryo transfer was estimated to be 0.024 (SD = 0.01). The region explaining the largest proportion of variance for total structures collected in the superovulation data was located on chromosome 8, at 55,663,248 basepairs with additional peaks located on chromosomes 5, 13, 14, and 21. Similar regions were identified for total number of good embryos, with the largest proportion of variance explained by a region on chromosome 14 at 26,713,734 basepairs. Results indicate that these traits have a genetic component. Significant genomic regions can be further investigated for genes putatively associated with these traits.

Key Words: embryo transfer, genetic analysis, superovulation

0380 Genetic correlations of hoof lesions and trimming status with feet and leg conformation traits in Canadian Holsteins.

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The objectives of this study were to estimate genetic correlations between hoof lesions and feet and legs conformation traits and to evaluate the association between those latter traits and the pre-selection process that leads a cow to be presented or not to the hoof trimmer. Hoof lesions were recorded by 23 hoof trimmers in 365 Canadian herds from 2009 to 2012. Hoof lesions included in the analysis were digital dermatitis, interdigital dermatitis, interdigital hyperplasia, sole hemorrhage, sole ulcer, toe ulcer, and white line lesion. Hoof lesions recorded during the first parity and hoof lesions recorded in second or later parities were considered as different traits. Conformation traits considered were bone quality (BQ), foot angle (FA), heel depth, rear leg side view, rear leg rear view (RLRV), locomotion (LOC) and the overall score for feet and legs (FL). In total, 37,158 cows that had a trim record in first and/or later parities also had conformation traits records. A second series of analyses considered all cows that were in a given herd during the trimming period, including cows that did not have any hoof data during the lactation. An additional trait, the trimming status, was defined as follows; a value of 1 was assigned to cows that had been visited at least once by the trimmer during the lactation, and a value of 0 to cows that did not have a hoof trim recorded during the lactation but were in the herd during the trimming session. Approximately 30% of cows were not presented to the trimmers during the lactation. Digital dermatitis, interdigital dermatitis and interdigital hyperplasia detected in first and later parities were negatively correlated to RLRV, FL, and LOC, with genetic correlations ranging from -0.24 ± 0.11 to -0.62 ± 0.15. With the exception of white line lesions, all of the horn lesions recorded in parities ≥ 2 showed moderate positive correlations with FA (from 0.29 ± 0.12 to 0.55 ± 0.20). White line lesions detected in parity 1 showed moderate genetic correlation with RLRV (0.65 ± 0.19), FL (0.53 ± 0.18), and LOC (0.44 ± 0.21), and those detected in parities ≥ 2 were correlated to BQ (-0.27 ± 0.10) and LOC (0.37 ± 0.16). The trimming status had moderate negative correlations with LOC and FL, suggesting that the pre-selection process for which cows are presented to the hoof trimmer is not random, but rather is associated with mobility and the conformation of the cow.

Key Words: hoof lesions, conformation traits, trimming status

0381 Genetic parameters for number of embryos produced by superovulated donors as heifers or cows using an in vivo or in vitro technique.

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Genetic gain in a population can be improved by using multiple ovulation and embryo transfer (MOET) in elite females. Multiple embryos can be produced using two different techniques, either using superovulation and producing the embryos in vivo or using ovum pickup (OPU) and in vitro production (IVP) of the embryos. Moreover, embryos can be produced by donor cows or virgin heifers as young as 7 mo of age. The objectives of this study were to assess the genetic parameters for the number of embryos produced by Holstein donors superovulated either in vivo or in vitro and for the number of embryos produced by donors either as a cow or a heifer at embryo recovery. Data was provided by Holstein Canada and contained the number of viable embryos from every successful flushing performed across Canada. After editing, 137,446 records of superovulation performed on 54,463 donors between 1992 and 2014 provided information about the type of technique used, and 130,252 records from 51,323 donors provided information about the status of the donor (heifer or cow) at embryo recovery. Bivariate repeatability animal model analyses were performed. Heritability estimates for the donor were between 0.135 (0.007) and 0.155 (0.038), whereas estimates for the service sire were close to zero (from 0.004 ± 0.002 to 0.019 ± 0.010), indicating that the number of embryos produced is influenced by the genetic potential of the donor and not by the service sire. Moreover, moderate repeatability estimates indicated that the number of embryos produced should be somewhat consistent within a donor. Genetic correlations found for the number of embryos produced using either type of technique was strong (0.834 ± 0.094) for the donor, but not significant for the service sire (-0.202 ± 0.234). For the number of embryos produced by either a heifer or a cow, the genetic correlations were 0.702 (0.058) for the donor and 0.699 (0.206) for the service sire. Overall, our results suggest that the number of embryos produced by a superovulated donor should be similar regardless of the technique (in vivo or in vitro) used or the status (heifer or cow) of a donor at embryo recovery. On the other hand, using the same service sire will not increase similarity between the two techniques, but could influence the number of embryos produced by a donor as a heifer or as a cow in a similar way.

Key Words: superovulation, Holstein, genetic parameter

0382 Estimation of genetic progress and profitability of dairy herds using varying proportions of in-vitro produced sexed embryos. K. Kaniyamattam[1], J. Block[2], P. J. Hansen[1], and A. De Vries[*1], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*OvaTech LLC, Gainesville, FL.*

The objective of the study was to estimate the genetic and economic performance of a dairy herd in which varying proportions of animals were impregnated with in-vitro produced sexed embryos (IVP-ET) obtained from the genetically best heifers. A daily dynamic stochastic model that includes the 12 genetic traits in the lifetime Net Merit index (NM$) was used. Phenotypic performance depended on genetic values. A herd of 1000 milking dairy cows, heifers and embryos were simulated over time. Genetic progress came from selecting superior donors and external sires. Eleven scenarios were evaluated, from 0% IVP-ET conceptions to 100% IVP-ET conceptions, with increments of 10% points. Each scenario was run 20 times. Animals with the greatest Estimated Breeding Value (EBV) for NM$ were selected as donors. Recipients were selected from heifers first, and from cows with the greatest EBV for fertility traits second. Sexed semen was used on the genetically better heifers for 2 inseminations. All other non-recipients were inseminated with conventional semen. To maintain a 33% annual cow cull rate, surplus heifer calves were sold based on the lowest EBV of NM$ and received a premium price based on their EBV of NM$. Results were measured by the true breeding values (TBV) of NM$ of all cows and profit per cow per year in yr 15 after the start of the IVP-ET program, and cumulative profit in the 15 yr after the start of the program. The mean ± SE of TBV of NM$ of all cows was $608 ± 7 greater for 100% IVP-ET compared with 0% IVP-ET in yr 15. The maximum increase in profit per cow per year (and optimum IVP-ET program) in yr 15 when embryo costs were $120 and $160 was $125 (100% IVP-ET) and $75 (42% IVP-ET), respectively, compared with a 0% IVP-ET program. Because return on investment in an IVP-ET program is not immediate, the 15-yr cumulative discounted profits per cow in comparison with the 0% IVP-ET program at embryo costs of $80, $120, and $160 were obtained at 72% IVP-ET, 21% IVP-ET, and 0% IVP-ET, respectively. The optimal proportions of IVP-ET depended greatly on the costs of embryos and the sale price of surplus calves. In conclusion, the use of IVP-ET at current prices was profitable but the optimal amount of IVP-ET was sensitive to realistic variations in prices of embryos and surplus heifer calves.

Key Words: in-vitro production, embryo, profit

0383 Single-step genomic prediction accuracies for lactation and reproduction traits in Yorkshire sows. D. M. Thekkoot[*1], R. A. Kemp[2], N. J. Boddicker[2], and G. Plastow[3], [1]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada,* [2]*Genesus Inc., Lethbridge, AB, Canada,* [3]*Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Most economically important traits associated with lactation and reproduction in pigs are either less heritable, sex-limited, expressed later in life, or difficult to measure on a routine basis. Genomic predictions using single-step BLUP (SSBLUP) methodologies, which utilizes information on phenotypes, pedigree and markers from genotyped and non-genotyped animals simultaneously, is an alternative to phenotype and pedigree based (BLUP) methods. The objective of this study was to estimate and compare prediction accuracies for lactation and reproduction traits using SSBLUP and BLUP methods. Data from 2481 litters from 1431 Yorkshire sows farrowed between August 2011 and August 2015 were used in this study. Of these 1161 sows were genotyped using Illumina's Porcine SNP60 Bead Chip. The sows were weighed and scanned for back fat and loin depth before farrowing and at weaning. Piglets were weighed at birth, weaning and death. Feed consumption of each sow during lactation was measured using the Gestal feed recording system. Reproductive traits studied were total number born, number born dead, number alive at 24 h and number weaned. Lactation traits analyzed were average daily feed intake of sow during lactation, sow body weight, back fat and loin depth at farrowing, body weight, back fat and loin depth loss during lactation, and litter weight gain from birth to weaning. The training data included sows born before April 1, 2013, and validation data included sows (n = 242) born on or after April first 2013. BLUP breeding values for animals in the validation data were computed using all information from the test data plus pedigree information for animals in the validation data. Both SSBLUP and BLUP evaluations were computed using MiX99 software. Accuracies for animals in the validation data were estimated as the correlation between their estimated breeding values and phenotypes, corrected for fixed effects, divided by the square root of heritability of the trait. For all traits studied, prediction accuracies using SSBLUP were higher (0.23 to 0.84) than those from BLUP (0.18 to 0.72). On average the SSBLUP accuracies were 39% and 33% higher, respectively for reproductive and lactation traits. The results indicate that the SSBLUP methodology produces more accurate estimated breeding values for lactation and reproduction traits in pigs.

Key Words: single-step genomic prediction, pig, reproduction, lactation

0384 WS Influence of first calving date on stayability in *Bos indicus* crossbred cows. B. N. Engle*, C. A. Gill, J. O. Sanders, D. G. Riley, J. E. Sawyer, and A. D. Herring, *Department of Animal Science, Texas A&M University, College Station.*

Longevity is one of the most important, complex, and difficult to improve traits sought by cow-calf producers. Consequently, a measurement or tool that could be utilized early in a cow's life to predict her future reproductive performance would be advantageous to producers and researchers alike. In this study, we sought to determine the effect of first calving season period on stayability in Nellore-crossbred females through 5 yr, 6 yr, and 7 yr of age. Stayability through each age was scored as a binary trait, with 1 indicating the cow remained in the herd and 0 indicating she was culled, given either a perfect calving or weaning record. Each female was assigned a value of 1, 2, 3, or 4 corresponding to the respective 21-d period of her first calving season (for first, second, or third 21-d period, or > 63 d, respectively). Cow stayability models were evaluated through mixed model procedures (PROC MIXED in SAS). Of the cows with perfect calving records, more ($P < 0.05$) females that calved in the first 21-d period remained in the herd than those that calved in the second 21-d period through 5 yr (66.9% vs. 53.6%), 6 yr (60.0% vs. 45.9%), and 7 yr of age (56.7% vs. 39.3%). They also differed ($P < 0.005$) from females whose first calf was born 63 d or later into the calving season through ages 5 (66.9% vs. 36.0%), 6 (60.0% vs. 29.5%), and 7 (56.7% vs. 27.2%). Of the cows with a perfect weaning record, more ($P < 0.05$) of the females that calved in the first 21-d period of the calving season remained in the herd through 5 yr (56.1% vs. 31.0%) and 6 yr of age (48.3% vs. 26.0%) than heifers whose calf was born at the end of the calving season. These results document that regardless of the culling criteria, *Bos indicus* crossbred heifers that calve early in their first calving season are more likely to maintain a perfect calving or weaning record later in life than females that calve late in the first calving season. Consequently, there is potential that the heifer's first calving season period may be used as valuation or culling criteria when selecting for stayability and longevity, or when merchandizing beef replacements.

Key Words: beef cows, calving season, stayability

0385 Use of a threshold animal model to estimate calving ease and stillbirth (co)variance components for U.S. Holsteins. J. B. Cole*[1], D. J. Null[1], and S. Tsuruta[2], [1]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD,* [2]*University of Georgia, Athens.*

(Co)variance components for calving ease and stillbirth in U.S. Holsteins were estimated using a single-trait threshold animal model and two different sets of data edits. Six sets of approximately 250,000 records each were created by randomly selecting herd codes without replacement from the data used for the December 2015 national evaluations, and from a second extract using more stringent edits than the official run. The stricter edits required that records have a valid dam ID in addition to a known sire, cows have corresponding lactation records, and animals have a breed composition of at least 93.75% of the breed of evaluation. Calving ease was recorded on a five-point scale ranging from no assistance needed (most common) to extreme difficulty (least common). Stillbirth was coded as a binomial trait indicating whether or not the calf was alive 48 h postpartum. Gibbs sampling was used to estimate (co)variance components from each sample; 100,000 samples were drawn, the first 10,000 rounds were discarded as burn-in, and every fifth sample was retained. The model included fixed parity (1 through 5) and sex-of-calf effects, and random herd-year-season, animal (direct), maternal, maternal permanent environment, and residual error effects. (Co)variance components and heritabilities were averaged over the six replicates of each scenario for each trait and are shown (with standard errors). Direct animal effects in the animal model are comparable to sire calving ease and sire stillbirth in the sire-maternal grandsire (S-MGS) model, and heritabilities were similar for the S-MGS and animal models. Maternal heritabilties were slightly lower in the animal model. Heritability estimates were very similar between scenarios within traits, although maternal heritabilities were slightly higher using the new edits. These differences may be due in part to larger estimates of direct-maternal covariances than reported in previous studies, as well as stricter requirements for known parent IDs in the new edits. The implementation of an animal model for calving traits will provide direct estimates of genetic merit for all animals, not only males, and the adoption of stricter

Table 0385.

	Calving Ease		Stillbirth	
Component of variance	Official	New edits	Official	New edits
Herd-year-season	0.6312 (0.07)	0.7294 (0.14)	0.1064 (0.007)	0.0873 (0.005)
Direct genetic	0.2679 (0.02)	0.3233 (0.07)	0.0546 (0.002)	0.0370 (0.004)
Maternal genetic	0.0997 (0.02)	0.1118 (0.02)	0.0467 (0.002)	0.0572 (0.006)
Direct-maternal covariance	0.0387 (0.02)	0.0489 (0.04)	0.0083 (0.002)	0.0164 (0.002)
Maternal permanent environment	0.1604 (0.02)	0.2364 (0.06)	0.0731 (0.003)	0.0373 (0.007)
Residual	1.8558 (0.21)	2.0667 (0.32)	1.0000 (0.000)	1.0000 (0.000)
Direct heritability	0.09 (0.01)	0.09 (0.02)	0.03 (0.002)	0.03 (0.003)
Maternal heritability	0.03 (0.01)	0.04 (0.01)	0.04 (0.001)	0.05 (0.005)

edits will improve data quality without having large effects on the (co)variances used in the evaluation. It also is anticipated that such a change will increase correlations of U.S. evaluations with other Interbull participants for calving traits.

Key Words: animal model, calving traits, (co)variance components

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0386 Genetic parameters for production traits and heifer pregnancy in Red Angus cattle.

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Heifer pregnancy (HPG) is a prediction of the probability that a female will conceive during her first breeding season, typically at a year of age. An inherent issue in the genetic prediction of HPG is that phenotypes can only be collected on females, which limits the amount of information available. To overcome this, inclusion of correlated traits that can be recorded on both sexes, or fertility traits recorded on males could be used to improve accuracy of HPG predictions. Therefore, the objective of this study was to estimate genetic parameters for HPG, 205-d weight (WW), 160-d post weaning gain (PWG), 365-d weight (YW), and scrotal circumference (SC). The project included records on 142,146 animals from the Red Angus Association of America. (Co)Variance parameters were estimated using multiple, two trait animal models and a REML procedure. Heritability and genetic correlations between HPG and production traits were then calculated. Contemporary group was included as a fixed effect for all analyses, additionally, sex and age of dam were included for BW, WW, PWG, and YW analyses, and the linear effect of age was fit for HPG. The random effect of animal was used to estimate additive genetic effects for all analyses, the random effect of dam was fit for the WW and YW analyses to estimate maternal effects, and a random, maternal permanent environment effect was included for WW. Heritability estimates were 0.58 ± 0.01, 0.27 ± 0.01, 0.22 ± 0.01, 0.29 ± 0.01, 0.45 ± 0.02, and 0.12 for BW, WW, PWG, YW, SC, and HPG (averaged across all analyses on the underlying scale), respectively. Genetic correlations between HPG and BW (−0.06 ± 0.05), SC (−0.08 ± 0.09), WW maternal (−0.02 ± 0.09), PWG (0.06 ± 0.07), YW maternal (0.00 ± 0.11), had confidence intervals that included or were near zero, suggesting minimal genetic relationship between the traits. Correlations were highest between HPG and WW direct (0.29 ± 0.08) and YW direct (0.21 ± 0.07). These results suggest that Red Angus females with high genetic potential for weight at 205 d and 365 d have an increased probability of becoming pregnant during their first breeding season. Additionally, the traits WW or YW could be used to help improve accuracy of HPG genetic predictions.

Key Words: beef cattle, genetic correlation, growth, heifer pregnancy

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0387 Daily rumination time in Italian Holstein cows: Heritability and correlation with milk production.

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The aim of the study was to investigate the genetic variation of daily rumination time (min) and its correlation with test-day milk production (kg). Data for the analysis consisted of 91,589 records for rumination time and milk yield from 398 cows (age: 43.21 ± 16.11 mo), collected from September 2014 to October 2015 in two Italian Holstein herds (TAD and MIL). There were 493 calvings, and data distribution across parities was 46.4%, 26.7% and 26.7% for first, second and later parities, respectively. DIM classes were defined as one class for every 30 d, resulting in 11 classes, and there were a total of 378 herd-test-day contemporary groups. The average rumination time was 513.51 ± 115.84 min, and the average milk yield was 33.59 ± 9.18 kg.

Pedigree information was available for 11,634 animals. A Repeatability Animal Model was fitted using the AIREMLF90 software. Herd, yr/mo of calving, and DIM classes within parity were treated as fixed effects, while herd-test-day, permanent environmental, and the additive genetic cow effects were treated as random. Rumination time was longer in pluriparous than in primiparous cows and showed a decreasing trend across DIM. On average, at the beginning of the lactation, pluriparous cows ruminated 75 min longer than primiparous. As expected, pluriparous cows had a higher production levels across DIM than primiparous, with a peak around DIM class 2 and 3 (i.e., 60–90 d). The herd with the highest daily rumination time had the lowest milk production yield: the fixed effects solutions were 569.5 min and 25.8 kg (Herd TAD; rumination time and milk yield, respectively) and 446.4 min and 31.9 kg (Herd MIL; rumination time and milk yield, respectively). The heritabilities for test-day milk yield and daily rumination time were 0.13 (SE = 0.06) and 0.32 (SE = 0.09), respectively. Although the negative phenotypic correlation observed, genetic correlation between the two traits was 0.38 (SE = 0.47); this high standard error is possibly the consequence of the dataset dimension. So far, rumination time has been used as a key monitor of dairy cow health at farm level. Investigating its genetics aspect and the relationship with other important yields and health traits may turn this management tool in a new informative selection criterion for

the dairy cattle breeding strategies.

Key Words: rumination time, milk production, genetic variation

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0388 Relationship between linear type and fertility traits in Nguni cows. T. J. Zindove*[1], K. A. Nephawe[2], S. P. Ndou[3], and M. Chimonyo[1], *[1]University of KwaZulu-Natal, Pietermaritzburg, South Africa, [2]Tshwane University of Technology, Pretoria, South Africa, [3]University of Manitoba, Winnipeg, Canada.*

The objective of the study was to assess the dimensionality of seven linear traits (body condition score, body stature, body length, heart girth, navel height, body depth and flank circumference) in Nguni cows using factor analysis and indicate the relationship between the extracted latent variables and calving interval and age at first calving. The traits were measured between December 2012 and November 2013 on 1559 Nguni cows kept under thornveld, succulent karoo, grassland and bushveld vegetation types. Low partial correlations (−0.04 to 0.51), high Kaiser statistic for sampling adequacy (MSA) scores and significance of the Bartlett sphericity test ($p < 0.01$) showed that there were significant phenotypic correlations between the linear traits and the data were suitable for factor analysis. Two factors had eigenvalues greater than 1. Factor 1 included body condition score, body depth, flank circumference and heart girth and represented body capacity of cows. Factor 2 included body length, body stature and navel height and represented frame size of cows. Calving interval and age at first calving decreased linearly with increase of factor 1. There was a quadratic increase in age at first calving as factor 2 increased ($P < 0.05$). It was concluded that the linear type traits under study can be grouped into two distinct factors, one linked to body capacity and the other to the frame size of the cows. Small-framed cows with large body capacities have shorter CI and AFC.

Key Words: Nguni cows, body depth, calving interval, flank circumference, heart girth

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0389 Estimation of genetic parameters for birth to weaning traits in meat goats. K. M. Andries*, F. Bebe, A. McKay, A. Bodrick, and A. Hartell, *Kentucky State University, Frankfort.*

Meat goat production in American grew repeatability in the early 2000s and has started to slow in growth over the past several years. Different reasons have been given for this decline, including limited improvement in animal performance and production. There has been a limited amount of research into the genetic parameters for goat growth and repeatability of dam production. A project was conducted at Kentucky State University to evaluate heritability and genetic correlations of birth and weaning weights in meat goat kids and to evaluate the heritability and repeatability of number of kids born and weaned by meat goat does in a multi-breed herd of meat goat. Records of birth to weaning performance and dam reproduction were collected between 2005 and 2015 in the meat goat research herd at Kentucky State University. The data set included 886 kidding records. The data included birth type, number reared, birth and weaning weights and daily gain between birth and weaning. The data was analyzed using ASReml with maternal effects in an animal model. The results of this study found that direct heritability of birth weight was 0.27% ± 0.081 and maternal heritability of 0.14 ± 0.035. For weaning weight heritability estimates were 0.33 ± 0.078 and 0.25 ± 0.042 for direct and maternal, respectively. Genetic correlation between these two traits was 0.39 ± 0.102 and the maternal correlation was 0.56 ± 0.074. Reproduction is one of the most economically important traits in livestock production. Number of kids born and weaned is critical for success of the meat goat industry. We used a repeated measures model in ASReml on the dam performance data set that contained 886 kidding records. We found that the heritability for number of kids born was 0.07 ± 0.068 with a repeatability of 0.14 ± 0.044 and for number of kids weaned was 0.18 ± 0.092 and 0.25 ± 0.046 for heritability and repeatability, respectively. Based on this research birth and weaning weights in meat goats are highly heritable and maternal effects on weaning weight are high. While heritability of number of kids born was low, the repeatability was significantly and number of kids weaned had a moderate heritability. Repeatability of both traits was lower than expected.

Key Words: meat goat, heritability, repeatability

0390 Economic selection index coefficients for terminal traits in Beefmaster cattle. K. P. Ochsner*[1], R. M. Lewis[1], M. D. MacNeil[2], and M. L. Spangler[3], *[1]University of Nebraska, Lincoln, [2]Delta G, Miles City, MT, [3]University of Nebraska, Lincoln.*

In the design of an economic selection index, the relative importance of traits in the breeding goal is reflected by their economic weighting in the index. The objective of this study was to develop an economic selection index for Beefmaster cattle for a terminal production system where bulls will be mated to mature cows with all resulting progeny harvested. Selection criteria were chosen from expected progeny differences (EPD) currently reported by Beefmaster Breeders United (BBU), and included yearling weight (YW), ultrasound rib-eye area (UREA), ultrasound rib fat (UFAT), and ultrasound intramuscular fat percentage (UIMF). Goal traits, which directly influence profitability in a terminal system, included hot carcass weight (HCW), marbling score (MS), rib-eye area (REA), 12th–rib fat (FAT), and feed intake (FI). Phenotypic and genetic parameter values among the selection criteria and goal traits were obtained from literature. National averages of feed prices, veterinary costs, and carcass premiums/discounts from 2010 to 2014 were used to establish income and expenses associated with a terminal system. Economic values

were determined from a simulation of 100,000 animals using SAS 9.4. Values were obtained by approximating the partial derivatives of the profit function by perturbing traits one at a time, by one unit, while holding the other traits constant at their respective means. In the simulation, the means (SD) for HCW, MS, REA, FAT and FI were based on literature values, and were 320 (38.8) kg, 5.4 (0.9) marbling score units, 76.5 (9.3) cm^2, 1.2 (0.32) cm, and 8.59 (1.09) kg, respectively. Relative economic values for HCW, MS, REA, FAT and FI were found to be 91.29, 17.01, 8.38, −7.07, and −29.66, respectively. By using phenotypic (co)variances among the selection criteria in the derivation, index coefficients may be applied to phenotypic measures. Index coefficients for phenotypic measures of YW, UREA, UFAT and UIMF were 0.74, 0.08, −31.04, and 13.32, respectively. By using genetic (co)variances among the selection criteria in the derivation, index coefficients may be applied directly to EPD. Index coefficients for EPD of YW, UREA, UFAT and UIMF were 1.72, 0.81, −36.60, and 12.37, respectively. The application of this index would aide Beefmaster breeders in their sire selection decisions, facilitating genetic improvement for a terminal breeding objective.

Key Words: beef cattle, economic weight, selection index

0391 Genomic regions associated with residual feed intake of divergently selected lines of Yorkshire pigs when fed a low-energy, high-fiber diet.

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Feed intake and efficiency remain key targets for improvement in the pork industry, as feed is the number one source of production costs. To better understand feed efficiency, divergent selection for residual feed intake (RFI) was performed in purebred Yorkshire pigs for 10 generations at Iowa State University. Phenotypes for RFI (n = 2623) and component traits were recorded across generations and lines (High RFI and Low RFI). A corn and soybean-meal based diet that was higher in energy and lower in fiber content (HELF) was fed during selection. To explore the effect of diet on RFI, a lower-energy, higher-fiber (LEHF) diet was fed to a subset of pigs from generations 8, 9, and 10 (n = 314). The LEHF diet had 18% less net energy and 175% more neutral detergent fiber, yet lysine to metabolizable energy ratios were similar between diets. Pigs were genotyped using the Illumina Porcine SNP60 BeadChip. (Serão et al., 2016) reported genomic regions on *Sus scrofa*chromosome (SSC) 2 and 6 associated with RFI of pigs fed the HELF diet (n = 1692). The objective of this study was to identify genomic regions associated with RFI when pigs were fed a LEHF diet. Using bivariate models for RFI between diets, heritability of RFI was estimated to be 0.24 ± 0.05 for the HELF diet and 0.35 ± 0.17 for the LEHF diet, while the genetic correlation of RFI between diets was 0.82 ± 0.28. Pigs (n = 310) fed the LEHF diet with phenotypes and genotypes for 46,467 SNP, after quality control, were used for a genome wide associate study. GenSel4 was used to fit BayesB and C models with $\pi = 0.9933$. Results from BayesC found no significant genomic associations for RFI. BayesB identified associations for RFI on SSC 6 and 14 that each explained ~0.75% of the genetic variance and on SSC 1, 5, and 16 that each explained ~0.50% of the genetic variance. None of these regions overlapped with those reported by Serão et al. (2016). In conclusion, RFI is a polygenic trait with many QTL across the genome with small effects and those effects may depend on the diet fed. This work was supported by AFRI-NIFA Grant no. 2011–68004–30336.

Key Words: genomic regions, RFI, swine

0392 Genetic architecture of feed efficiency in mid-lactation Holstein dairy cows.

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The objective of this study was to explore the genetic architecture and biological basis of feed efficiency in lactating Holstein cows. In total, 4918 cows with actual or imputed genotypes for 60,671 SNP had individual feed intake, milk yield, milk composition, and body weight records. Cows were from research herds located in the United States, Canada, the Netherlands, and Scotland. Feed efficiency defined as residual feed intake (RFI) was calculated as the residual of the regression of DMI on milk energy (MilkE), metabolic body weight (MBW), and body weight change along with systematic effects of parity class by days in milk fitted as a fifth order Legendre polynomial (fixed), diet within experiment within location (random) and test week (random). Adjusted phenotypes for DMI, MilkE, and MBW were calculated as the sum of the animal and residual components from the regression of each trait on the same systematic effects used for RFI. Animal

relationships were represented with a genomic relationship matrix. Genome-wide association studies were performed for RFI, DMI, MilkE, and MBW using the Bayes B method in GenSel version 4.4 with 1% of SNP assumed to have a non-zero effect. One megabase windows with the greatest percent of the total genetic variation explained by the markers (TGVM) were identified, and within windows explaining more than 0.5% of the TGVM, the SNP with the highest posterior probability of a non-zero effect was tested for significant additive and dominance effects. Marker-based heritabilities were estimated for RFI (0.10), DMI (0.25), MilkE (0.20), and MBW (0.44). Tentative results for RFI identified regions explaining the greatest percent of the TGVM on chromosomes X, 9, and 14, and all tested SNP had significant additive effects ($p < 0.05$). Four of the 10 regions with the greatest effect on DMI also were included in the 10 regions with greatest effects on RFI, but not in the top 10 regions for MilkE or MBW, suggesting a genetic basis for intake that is unrelated to energy consumption required for milk production or maintenance. Candidate genes found within windows explaining the greatest percent of the TGVM for RFI include solute carrier family 25 member 14 and leptin. In conclusion, feed efficiency is a polygenic trait exhibiting genetic variation distinct from that underlying maintenance requirements and milk energy output.

Key Words: residual feed intake, genome-wide association study, feed efficiency

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0393 Analysis of genetic residual feed intake in Danish Holstein cows by covariance functions using random regression models. C. Pfeiffer*, B. Li, P. Lovendahl, and J. Lassen, *Department of Molecular Biology and Genetics, AU Foulum/ Aarhus University, Tjele, Denmark.*

Feed efficiency is of major concern due to economic reasons and environmental impacts but also because of limited feed resources. So far, feed efficiency cannot be defined unambiguously. One trait to select for can be residual feed intake (RFI), which is primarily determined by dry-matter intake (DMI), production traits and body weight. The aim of this study was to derive variance-covariance components of RFI over the first 44 lactation wk in primiparous Danish Holstein cows by a covariance function from a tri-variate random regression analysis to describe genetic and permanent environmental effects of average DMI, average metabolic body weight (mBW) and average kg milk (Mkg) over the whole lactation. Commonly, RFI is derived from phenotypic regression and subsequently genetically analyzed. In total, 22,375 records of 648 primiparous Holstein cows from the Danish Cattle Research Centre were used. Phenotypic information was collected between 2003 and 2015 over the entire standard-lactations. The random regressions were fitted using DMU 6.5.2. The pedigree was traced back as far as possible resulting in 16,339 animals. After estimating variance-covariance components of DMI, mBW and Mkg, the covariance function was applied to directly derive RFI due to the assumption that RFI is defined as a depended genetic variance of DMI, body weight and milk yield. The approach gave reliable results for RFI. Heritabilities for RFI ranged from 0.05 to 0.15. The highest heritability for RFI was observed in the first wk of lactation, the lowest in lactation wk 22. Heritabilities for the traits DMI, mBW and Mkg ranged from 0.30 to 0.46, 0.53 to 0.61 and 0.25 to 0.55, respectively. The genetic variance of RFI was on average 9.5% (ranging from 4.3% in lactation wk 23 to 28.7% in lactation wk 1) of the genetic variance of DMI. Heritabilities of RFI, DMI, mBW and Mkg were in accordance with previous studies. The genetic variance of RFI in DMI has to be considered as low to moderate. Results imply that a genetic improvement of DMI, independent of production, is limited, except for the first 4 wk of lactation where the genetic variance of RFI was > 20% of the genetic variance of DMI.

Key Words: dairy cow, random regression model and residual feed intake

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0394 Greenhouse gas emission related traits differ in RFI divergent lactating dairy cows. D. Hailemariam*[1], G. Manafiazar[1], J. Basarab[1,2], F. Miglior[3,4], G. Plastow[1], Z. Wang[1], *[1]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Lacombe Research Centre, Alberta Agriculture and Forestry, Lacombe, AB, Canada, [3]Canadian Dairy Network, Guelph, ON, Canada, [4]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada.*

In dairy cattle, the magnitude of dry matter intake (DMI), methane (CH_4) and carbon dioxide (CO_2) reduction in feed efficient (-RFI) lactating cows is not well documented. The objective of this study was to quantify the comparative advantage of -RFI lactating dairy cows managed in an intensive tie-stall system with regard to DMI, CH_4 and CO_2 emission. RFI was predicted for 43 lactating dairy cows with components of metabolic body weight (MBW), empty body weight change (EBWC), and milk production energy requirements (MPER) over 255 d in milk (DIM) using a random regression technique, and correspondingly, DMI, CH_4, CO_2 and other traits were measured. CH_4 and CO_2 emissions were measured from lactating dairy cows using a GreenFeed system (C-Lock Inc., Rapid City, SD). The measurement was performed in three batches (15 cows in each) twice a day (0900–1200; 1800–2030 h) for 14 consecutive test days. Before each test period cows were allowed to visit the unit twice a day (4–7 d) for adaptation purpose. The RFI prediction revealed 19 cows with–RFI (efficient) and 24 cows with +RFI (inefficient). The mean dry matter intake (DMI), CH_4 production (g/day), CH_4

yield (g/kg of DMI), CH_4 g/kg of milk, milk yield (kg/d) and CO_2 g/d were calculated for both-RFI (N = 19) and +RFI (N = 24) groups. Data was analyzed using t test for each trait and the result indicated that -RFI cows have significantly (P < 0.05) decreased DMI (20 ± 3 vs. 23 ± 3), CH_4 g/d (334 ± 71 vs. 392 ± 70), and CO_2 g/d (12,070 ± 1348 vs. 12,895 ± 1704) and CH_4 g/kg of milk (9 ± 2 vs. 10 ± 2) compared with their +RFI counterparts. As expected, body weight, milk yield and CH_4 (g/kg DMI), were not statistically significant (P > 0.05), between -RFI and +RFI groups. Taken together, feed efficient lactating dairy cows compared with the inefficient cows consumed less feed, emitted less daily CH_4 (g/d), CH_4 (g/kg of milk) and CO_2 (g/d) by 13.0, 14.8, 10, and 6.4% respectively, without differing in milk production.

Key Words: RFI, methane, carbon dioxide

0395 Genetic relationship between methane emissions and conformation traits in Danish Holstein cattle. L. Zetouni[*1], M. Kargo[1,2], J. Lassen[1], *[1]Aarhus University, Tjele, Denmark, [2]SEGES, Aarhus N, Denmark.*

Conformation traits have been widely explored in dairy cattle evaluation, being a part of the total merit index for Holstein cows in different countries. They have been used as a way to access the cow's condition in general, based on its body features. Lots of studies have analyzed the relationship between conformation traits and other traits of interest in dairy cattle, such as fertility, longevity and feed efficiency, but little is known about how methane emissions correlate with conformation traits. Therefore, our goal was to evaluate the genetic correlations between methane and six conformation traits in Holstein cows: height (H), body depth (BD), chest width (CW), dairy character (DC) and body condition score (BCS). Data was collected on 1114 Holstein cows from 11 commercial herds in Denmark. Methane emission was measured during milking in milking robots, and then quantified using information on milk production, weight and days carried calf to predict carbon dioxide production and multiplied by the ratio between methane and carbon dioxide. Bivariate linear models were used in the analysis to estimate the correlations between methane and each one of the traits analyzed. Heritabilities estimates were moderate, ranking around 0.3 for methane and between 0.11 (for CW) and 0.5 (for H) for the other traits. The estimated genetic correlations were mainly positive, implying that the bigger the cow, the more methane it produces. Our results could be partially explained by the fact that, in general, broader, deeper cows eat more, and it is a known fact methane production is associated with higher feed intake in ruminants. Due to high standard errors of the estimates further analyses are being conducted to more deeply evaluate and understand how conformation traits relate to methane emissions.

Key Words: methane, conformation traits, genetic correlations

0396 Genetic variation of predicted milk fatty acids groups in Canadian Holsteins. S. G. Narayana[*1], F. S. Schenkel[1], A. Fleming[1], A. Koeck[1], F. Malchiodi[1], J. Jamrozik[1,2], M. Sargolzaei[1,3], M. Corredig[4,5], B. Mallard[1,6], A. Ali[7], and F. Miglior[1,2], *[1]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [2]Canadian Dairy Network, Guelph, ON, Canada, [3]Semex Alliance, Guelph, ON, Canada, [4]University of Guelph, ON, Canada, [5]Gay Lea Foods, Guelph, ON, Canada, [6]Department of Pathobiology, OVC, University of Guelph, ON, Canada, [7]Department of Mathematics and Statistics, University of Guelph, ON, Canada.*

The objective of this study was to investigate genetic variability of mid infrared predicted fatty acids groups in Canadian Holstein cows. Milk samples were collected by CanWest DHI (Guelph, ON, Canada) and Valacta (Ste.-Anne-de-Bellevue, QC, Canada) during routine milk recordings. Milk samples were analyzed using MilkoScan FT6000 spectrometers (Foss, Hillerød, Denmark). Milk mid infra-red spectra generated from January 2013 to July 2015 were standardized and then predicted for five groups of fatty acids: short-chain (C_4–C_{10}), medium-chain (C_{12}–C_{16}), long-chain (C_{17}–C_{22}), saturated (no double bond), and unsaturated (one or more double bonds) fatty acids. The predicted fatty acid values were log transformed to improve normality. The data set included 49,127 test-day records from 10,029 first lactation Holstein cows in

Table 0395.

Table 1. Heritabilities and correlations between methane and conformation traits

		Methane			
	h^2	r_g	SE	r_e	SE
BCS	0.4	-0.009	0.2	-0.14	0.08
BD	0.14	0.45	0.24	-0.12	0.07
CW	0.11	0.3	0.3	-0.13	0.06
H	0.5	-0.12	0.2	0.0963	0.0931
DC	0.12	0.12	0.2	0.05	0.07
Methane	0.3	-	-	-	-

BCS = body condition score; BD = body depth; CW = chest width; H = height; DC = dairy character
r_g = genetic correlations; r_e = residual correlations

810 herds. The total number of animals in the pedigree was 76,074. The random regression animal test-day model included: days in milk, herd test day, and season-age of calving (polynomial regression) as fixed effects, and herd-year of calving, animal and permanent environment effects as random polynomial regressions, and random residual effect. The significance of fixed effects and the best degree of the fixed Legendre polynomial regressions for season-age effect (third degree) were determined using AI-REML. Bayesian methods with Gibbs sampling were then used for fitting models with different degree of random regressions, assuming the best degree for fixed regressions, and the same increasing degree for all random effects (from intercept only to 4thdegree). Fourth degree random regressions yielded the best fitting based on the Deviance Information Criterion (DIC). No polynomials with degree higher than 4 were fit due to low number of cows with more than 5 fatty acid measurements and the cubic shape of the phenotypic distribution of the fatty acid groups. The estimate of average daily heritability over the lactation for medium-chain fatty acid (0.37) was higher than for short-chain (0.30) and long-chain (0.24). The average daily heritability for saturated fatty acid (0.38) was larger than for unsaturated fatty acid group (0.23). These results provide evidence for the existence of genetic variation in fatty acids groups, and thus indicate possibility of altering milk fatty acid composition through genetic selection.

Key Words: milk fatty acids, mid-infrared, random regression model

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0397 Genetic correlations between predicted milk fatty acids and milk production traits in Canadian Holsteins.

A. Fleming*[1], F. S. Schenkel[1], A. Koeck[1], F. Malchiodi[1], A. Ali[2], B. Mallard[3], M. Corredig[4], and F. Miglior[1,5], *[1]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [2]Department of Mathematics and Statistics, University of Guelph, ON, Canada, [3]Department of Pathobiology, OVC, University of Guelph, Guelph, ON, Canada, [4]University of Guelph, ON, Canada, [5]Canadian Dairy Network, Guelph, ON, Canada.*

The fatty acid profile of milk is of importance due to its implications on human health and nutrition, and technological attributes. Any consideration of selection for fatty acids requires knowledge of their genetic relationship with other milk production traits. The objective of this study was to investigate the genetic correlations between mid-infrared predicted milk fatty acids and recorded production traits and somatic cell score (SCS) in Canadian Holsteins. Test-day records for milk yield, fat and protein percentage, fat:protein ratio, and SCS, along with predicted quantities of short (4 to 10 carbon length), medium (12 to 16 carbon length), and long-chain (17 to 22 carbon length) fatty acid groups were analyzed. First lactation Holstein cows between the ages of 19 and 43 mo with at least 3 test-day fatty acid records were considered in the analysis. A total of 109,249 records from 29,542 Holstein cows and 2198 herds acquired between January 2013 and April 2015 were used. Genetic analysis was performed using bivariate sire random regression models fitted using the Average Information-Restricted Maximum Likelihood (AI-REML) procedure in the DMU package with Legendre polynomials used to describe the regression curves. Daily genetic correlations were averaged across the lactation. Strong genetic correlations of 0.90, 0.96, and 0.88 were found between fat percentage and short, medium, and long-chain fatty acids, respectively. Ranges of genetic correlations for fatty acid groups and milk yield (−0.48 to −0.50), protein percentage (0.69 to 0.80), and fat protein ratio (0.51 to 0.63) were similar to those found between the production traits and milk fat percentage. Weak, negative genetic correlations were observed between SCS and short and medium-chain fatty acids (−0.14 for both), while a weak, positive correlation was found between SCS and long-chain fatty acids (0.17). Milk fatty acids had moderate to strong genetic correlations with production traits, but weak genetic correlation with SCS. However, disentangling the high correlation of fatty acids with fat percentage may be challenging for selection purposes.

Key Words: fatty acid, milk production, genetic correlation

0398 Genetic associations between milk β-hydroxybutyrate and fatty acids in early first lactation of Canadian Holsteins.

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Hyperketonemia (or ketosis) is one of the most frequent diseases in dairy cattle. As clinical ketosis is not widely recorded, the level of milk β-hydroxybutyrate is used as its indicator. Milk fatty acid profile is considered to be related to the energy balance of cows in early lactation. The objective of this study was, therefore, to investigate the genetic associations between milk β-hydroxybutyrate and milk fatty acids in early first lactation of Canadian Holstein cows. Test-day data were available on milk β-hydroxybutyrate and five fatty acid groups: short-chain (C_4–C_{10}), medium-chain (C_{12}–C_{16}), long-chain (C_{17}–C_{22}),

saturated (no double bond) and unsaturated (one or more double bonds). Only the first cow's test-day record between 5 and 40 DIM was considered for all traits, because most of the metabolic changes occur over this time period. The data set consisted of 23,345 cow records from 1541 sires and 2510 herds. Data were analyzed with a 6-variate linear sire model using the Average Information-Restricted Maximum Likelihood (AI-REML) procedure in the DMU package. Heritability of 0.13 was found for milk β-hydroxybutyrate. Heritability estimates for fatty acids ranged from 0.10 to 0.29. Genetic correlations between milk β-hydroxybutyrate and short chain, medium chain and saturated fatty acids were low and not significantly different from zero. Genetic correlations between milk β-hydroxybutyrate and long chain and unsaturated fatty acids were 0.51 and 0.48, respectively. These results confirm the known relationship between milk β-hydroxybutyrate and energy balance status in early lactation, explained by the release of long chain fatty acids from the mobilization of body fat reserves.

Key Words: milk β-hydroxybutyrate, fatty acid, genetic correlation

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0399 Relevance of mid-infrared spectroscopy predictions of milk fine composition and technological properties for selective breeding.

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To evaluate the potential use of novel milk infrared predictions as indicator traits in selective breeding, genetic variation in 92 traits, describing the fine composition and technological properties of milk, and their predictions was assessed in the Italian Simmental (IS) population. The genetic relationship between measured traits (MT) and infrared predictions (IP) was investigated. Fatty acid and protein composition, lactoferrin and mineral contents were available for 1040, 3337, 558, and 689 individual milk samples, respectively. Measures of pH and milk coagulation properties were available for 3438, and 3266 samples, respectively. Curd yield and curd composition were obtained by laboratory micro-cheese making techniques for 1177 samples. Infrared calibration models were developed for all traits and IP were obtained for 143,198 spectra of 17,619 IS cows. (Co)variance components for MT and IP were estimated in a set of bivariate analyses, each including one MT and its IP. There was a positive relationship between the R^2 in cross-validation (R^2_{CV}) of calibration models and the decrease in both the phenotypic variance ($r = 0.78$; $P < 0.01$) and the additive genetic variance ($r = 0.61$; $P < 0.01$) of IP compared with the estimates for MT. For the 92 traits, the average decrease in total variance of IP compared with the variance of MT was approximately 35%. The decrease in genetic variance was on average 64%. As a consequence, 88 traits exhibited lower h^2 estimates for IP than for MT. The R^2_{CV} exhibited a positive relationship ($r = 0.57$; $P < 0.01$) with the estimated genetic correlation (r_a) between MT and IP. For calibration models having $R^2_{CV} > 0.75$, r_a between IP and MT was greater than 0.9. The variability in the estimated r_a values increased when R^2_{CV} decreased and, for calibration models having moderate predictive ability, estimates of r_a ranged from 0.2 to 1.

Calibration equations showing high predictive accuracy would lead to a faster genetic progress compared with calibration models having moderate or low prediction accuracy. Nevertheless, the estimated r_a between IP and MT was generally very high, even when calibration models had moderate R^2_{CV}. Hence, even calibrations showing low predictive accuracy may be successfully used in selective breeding, particularly when multiple predictions per animal are available from the routine application of calibration models.

Key Words: infrared spectroscopy, animal breeding, fine milk composition

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0400 Markers associated with metabolome, and microbiome measures in a grain and sugar challenge in dairy heifers.

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The aim of this preliminary study was to identify associations between the bovine genome, metabolome, and microbiome in cattle subjected to a grain and sugar challenge. The objective was to identify markers for ruminal acidosis. Genome wide association was performed on Holstein heifers ($n = 34$ samples with quality DNA out of 40) that were allocated to 5 feed additive groups. Heifers were fed twice daily a 62% forage:38% concentrate total mixed ration at 1.25% of bodyweight (BW) dry matter (DM)/d for a 20-d adaptation period with their additive(s). Fructose (0.1% of BW/d) was added to the ration for the last 10 d of adaptation. On d-21 heifers were challenged with a ration consisting of 1% of BW DM wheat and 0.2% of BW fructose plus their additive(s). Stomach tube rumen samples were collected weekly and at 5 time points over 3.6 h after consumption of the challenge ration on d-21 and analyzed for pH, and ammonia, D- and L-lactate, and volatile fatty acids (VFA) concentrations and relative abundance of total bacteria and archaea using an Illumina MiSeq platform. All rumen fermentation measures were normalized and combined to produce an eigenvector to indicate the risk of ruminal acidosis. Bovine DNA was sequenced using the Geneseek® Genomic Profiler Bovine 150K Illumina SNPchip. Genome wide association was completed using an additive model and linear regression with PCA population stratification and a Bonferroni correction for multiple comparisons. There were few genome associations found with rumen pH,

acetate, propionate, total VFA, or ammonia concentration or the relative abundance of the Firmicutes and Bacteroidetes phyla ($P < 0.5$). A number of associations occurred for D-lactate, L-lactate, and total lactate concentration and the acidosis eigenvectors at all time points before d 21 ($P < 0.05$). Ten associations were found at one time-point only for butyrate and valerate concentrations ($P < 0.05$). A number of associations were found with the Actinobacteria, Chloroflexi, Euryarchaeota, Fibrobacteres, Proteobacteria, and Tenericutes phyla at one or more time points ($P < 0.05$). Gene-wide associations with the metabolome and microbiome were present despite the small population size and suggest the presence of markers for ruminal acidosis. Qualitative trait loci and candidate gene analysis is being conducted.

Key Words: genome wide association, lactic acid, ruminal acidosis

BREEDING AND GENETICS SYMPOSIUM: RESILIENCE OF LIVESTOCK TO CHANGING ENVIRONMENTS

0401 Production, biological, and genetic responses to heat stress in ruminants and pigs.

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Heat stress (HS) compromised efficient animal production and reduced livestock output during the summer was traditionally thought to result from decreased nutrient intake. Our data from ruminants and monogastrics challenge this dogma and indicate that heat-stressed animals utilize homeorhetic strategies to modify metabolic and fuel selection priorities independently of feed intake. Systemic shifts in bioenergetics are characterized by increased basal and stimulated circulating insulin. Hepatocytes and myocytes also show clear differences in glucose production and metabolic flexibility, respectively, during HS. Intriguingly, HS animals do not mobilize adipose tissue despite being in both a negative energy balance and catabolic state. The origin of the aforementioned metabolic changes may lay at the gastrointestinal tract. For a variety of reasons, HS compromises intestinal integrity. Increased permeability to luminal contents results in local and systemic inflammatory responses. Consequently, heat-stressed animals are simultaneously confronted with life-threatening hyperthermia and endotoxemia. Determining how these systems are homeostatically and homeorhetically coordinated to prioritize acclimation and survival vs. agriculturally productive purposes would presumably reveal mechanisms amenable to manipulation. Interestingly, thermoregulatory and production responses to HS are only marginally related. In other words, increases in body temperature indices poorly predict the decrease in both milk yield and growth. Further, HS-induced decreased feed intake is also an inaccurate predictor of milk yield or growth during HS. This suggests that traits associated with production and thermoregulation during HS may be governed by separate genomic loci and potentially interdependent biological mechanisms. Thus, selecting animals with a "tolerant" phenotype based solely or separately on thermoregulatory capacity or production may not ultimately increase HS resilience. Therefore, the variation of multiple phenotypes and genotypes needs to be accounted for to generate a more comprehensive heat tolerant animal. In summary, HS is one of the primary hurdles to efficient animal production. Defining the physiological mechanisms through which HS and other environmental factors influence complex, multifactorial traits, is critical for developing approaches to ameliorate current production issues and is a prerequisite for generating future strategies (genetic, managerial, nutritional, and pharmaceutical) to maximize livestock efficiency.

Key Words: heat stress, genetics, insulin, tolerance

0402 Breeding for resilience to heat stress effects: A comparison across dairy ruminant species.

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Dairy animals are more susceptible to heat stress (HS), because milk production results in a large metabolic heat strain. As a consequence, selection for increased milk production will tend to decrease animals' tolerance to increasing heat loads. A comprehensive approach to characterize HS effects on dairy production and to develop breeding tools to select for heat tolerance (HT) was followed by making use of available milk recording information, climatological data and genomic information on three dairy ruminant populations, Holstein cattle and local breeds Manchega sheep and Florida goats raised in the warm southern regions of Spain. Heat stress thresholds were around 55/63 (15/18) and 63/65 (19/20) for average daily values of THI (°C temperature) for fat/protein yields in Holstein and Manchega, respectively. For goats, HS thresholds could not be clearly identified. Sufficient genetic variability was observed in productive response to heat to consider this trait for selection in the three populations. Genetic antagonism between milk production and HT (ability to maintain milk production under high heat loads) was found for the three populations but stronger for cattle and goats. Several selection criteria including eigen-components of the response variability (looking for tolerance criteria independent of production level) were compared and slopes of the genetic response curves in the HS region were recommended. Estimated genetic correlations between production

under cold and comfort or heat conditions was different from unity in all species (down to 0.3 in cattle), indicating the different genetic mechanisms involved in heat and cold tolerance. Genome-wide association studies using slopes of polynomial curves of response as pseudo-phenotypes have been performed. Beside genomic regions related to fat metabolism (e.g., ACSL3), regions highlighting the effect of HS on the regulatory activity of transcription factors (TBL1XR1, DCHAU1), a number of genes involved in basic processes related to proteins transport and intracellular signal transduction (CNIH3 and CNIH4 ubiquitines and chaperones such as NVL from the chaperone-like AAA-ATPase family) showed signinficant signals. Although the use of milk recording and weather data has been proven useful to identify HT animals, the use of finer phenotypes together with genomic information are deemed important to succeed in selecting HT animals while maintaining productivity.

Key Words: heat tolerance, selection, dairy ruminants

0403 Climate change and selective breeding in aquaculture. P. Sae-Lim*, *Nofima, Ås, Norway.*

Aquaculture is an important sector that strengthens food security. Based on FAO, aquaculture production has to increase up to 42.9% to meet the global population demand in 2020. According to the reports by IPCC and FAO, climate change may result in global warming, sea-level rise, changes of ocean productivity, water shortage, and more frequent extreme climate events. Climate change may affect aquaculture directly and indirectly, depending on climatic zones, aquaculture activities, and farmed species. Climate change may introduce opportunities—rise of temperature may increase growth and open up new farming opportunities due to aquatic species migration—as well as several challenges to aquaculture. First, genotype-by-environment interactions (GxE) may increase because aquatic animals may expose to more fluctuating rearing environments. Rainbow trout (*Oncorhynchus mykiss*), the most popular farmed salmonid worldwide, has a very narrow range of optimal temperature to grow. The magnitudes of GxE, i.e., average genetic correlation (r_g), from 1964–2013 were reviewed across 38 species. The review revealed strong re-ranking for growth of rainbow trout in different temperatures (r_g = 0.36), indicating lower-than-expected production in suboptimal rearing temperature when selecting for growth based only on optimal rearing temperature. Second, it can be hypothesized that climate change may increase environmental variance in sensitive genotypes. Third, climate change may facilitate an outbreak of (new) pathogens or parasites, increasing mortality and hence reducing production. Fourth, 20% reduction of ocean productivity worldwide has been predicted, implying a decline of fishmeal and fish oil supplies and hence the replacement of the raw materials may become more important in the future. Finally, reduction in biodiversity may threaten genetic variation and the ecosystems of wild stocks. Furthermore, this may imply a lack of founder populations for breeding in the future. To ensure the food security, the impacts of climate change have to be addressed through resource management, reduction of environmental impacts, and selective breeding strategies. Breeding goals may change toward "resilience," i.e., stability of performance under fluctuating rearing environments or toward new trait mean. The breeding goals may include disease resistance or tolerance for emerging pathogens and parasites. Anyhow, more research is needed to better understand the opportunities of selective breeding for resilient animals in aquaculture under climate change. To avoid any loss of biodiversity in wild stocks, an international gene bank of the wild stocks may store genetic resources of founder populations for future breeding programs.

Key Words: climate change, genotype-by-environment interaction, selective breeding

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0404 Introgression of genes conveying resistance to heat stress into cattle populations using the "Slick" genetic variant as a model. S. R. Davis*, R. J. Spelman, and M. J. Littlejohn, *Livestock Improvement Corp., Hamilton, New Zealand.*

There are ~270 million dairy cows globally and over 75% of these are found in hot climates and most of these have not undergone intensive, genetic selection. The ability to integrate genetically-improved cows into tropical cattle populations will underpin improvement of production performance.

The main impediment to the introduction of genetically-improved, high producing dairy cattle, typically from temperate countries, into tropical climates is the relatively poor heat tolerance and low tick resistance of the cattle breeds common in temperate climes. The concept of using gene introgression to improve heat tolerance and tick resistance was given momentum more than 15 yr ago following the identification of "slick," a major, dominant, gene for heat tolerance (and likely, tick resistance), segregating in the Senepol beef breed.

Our discovery, in 2013, of the "slick" causal mutation, a truncation of the prolactin receptor, provided the impetus to embark on crossbreeding of NZ dairy cattle with Senepol to enhance dairy performance in the tropics. A further advantage of the Senepol is that it is a *Bos taurus* breed, avoiding the potential disadvantages of *Bos indicus* crossbreds, which includes poor milk let down and late age at first calving.

The "slick" mutation is an enabling genetic variation which provides the necessary physiological traits (notably sweating ability) to improve animal welfare and performance in hot climates. The characteristics of NZ dairy breeds provide fertility, grazing ability and lactation performance on high roughage diets.

The primary objective of the breeding program is to produce homozygous "slick" bulls that have 75% NZ dairy genetics. The (5 yr) breeding program requires crossbreeding to produce 50% dairy F1 daughters; using these animals as egg

donors through JIVET to produce 75% dairy F2 offspring and then inter-crossing the lines to generate homozygous sires. Gene editing of the "slick" mutation directly into dairy sires is not a practical option in NZ at the current time.

Further improvements in tropical dairy cow development are possible if more genetic variations associated with heat tolerance are found, although introgression of additional variations (for example, coat color) will be challenging in a breeding program such as that outlined here.

Key Words: Senepol, thermoregulation, dairy

0405 Genetic solutions to infertility caused by heat stress. P. J. Hansen*[1], S. Dikmen[2], J. B. Cole[3], M. S. Ortega[1], and G. E. Dahl[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Uludag University, Faculty of Veterinary Medicine, Department of Animal Science, Bursa, Turkey, [3]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD.*

Reproductive function in mammals is very susceptible to disruption by heat stress. In lactating dairy cows, for example, pregnancy rates per insemination can be as low as 10–15% in the summer vs. 25–40% in cool weather. Reduced fertility is caused by a combination of (1) the negative consequences of the physiological adjustments engaged to minimize hyperthermia during heat stress and (2) direct deleterious effects of elevated body temperature on the gamete and embryo (i.e., heat shock). There is genetic variation body temperature regulation during heat stress as well as in cellular resistance to elevated temperature. Thus, opportunities exist for improving reproduction during heat stress by modifying livestock genetically to improve body temperature regulation and cellular resistance to heat shock. Genetic improvement can be achieved by identifying genetically superior animals within a breed (heritability for rectal temperature during heat stress is 0.17) as well as by transferring genes from thermotolerant breeds to thermosensitive ones. A successful example of gene transfer is for a mutation in *PRLR* causing the slick hair phenotype. Holstein cattle inheriting this mutation have increased ability to regulate body temperature during heat stress and are less likely to experience a decrease in milk yield during summer than other Holsteins. Among the genes conferring cellular resistance to heat shock is a mutation in the promoter of *HSPA1L* identified in cattle. Selection for the beneficial allele of this gene, as well as other genes controlling cellular resistance to heat shock, might reduce the damage to the oocyte and embryo caused by elevated body temperature.

Key Words: heat stress, infertility, reproduction, body temperature

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0406 Resilience and lessons from studies in genetics of heat stress. I. Misztal*, *University of Georgia, Athens.*

Production environments are expected to change, mostly to hotter climates but also possibly more extreme and drier. This raises a question whether the current generation of farm animals can cope with the changes or should they be specifically selected for changing conditions. In general, genetic selection produces animals with smaller environmental footprint but also with smaller environmental flexibility. Some answers are coming from heat stress research across species, with heat tolerance partly understood as a greater environmental flexibility. Specific studies in various species show complexities of defining and selecting for heat tolerance. In Holsteins, the genetic component of heat stress on production approximately doubles in second and quadruples in third parity. Best production under heat stress is by cows with elevated body temperature, probably at a risk of increased mortality. In hot but less intensive environments, the effect of heat stress on production is minimal although the negative effect on fertility remains. Mortality peaks under heat stress and increases with parity. In Angus, the effect of heat stress is stronger only in selected regions, probably due to adaptation of calving seasons to local conditions and crossbreeding. Genetically, while the direct effect shows variability due to heat stress, the maternal does not, probably due to dams shielding calves from environmental challenges. In pigs, the effect of heat stress is strong in commercial but almost none in nucleus farms. This is partly due to lower pig density and better heat abatement in nucleus farms. Under intensive management, heat stress is less evident in drier environments because of more efficient cooling. A genetic component of heat stress exists but it is partly masked by improving management and selection based on data from elite farms. Genetic selection may provide superior identification of heat-tolerant animals but a few cycles may be needed for clear results. Also simple traits exist that are strongly related to heat stress, e.g., slick hair in dairy and shedding intensity in Angus. Defining resilience/robustness may be difficult especially when masked by improving environment. Under climate change, the current selection may be adequate if it (1) is accompanied by constantly improving management, (2) uses commercial data and (3) includes traits important under climate change such as mortality.

Key Words: G x E interaction, animal stress, robustness

0407 Genomic selection for methane emission.

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Climate change is a growing area of international concern, and it is well established that the release of greenhouse gases (GHG) is a contributing factor. Of the various GHG produced by ruminants, enteric methane (CH_4) is the most important contributor. One mitigation strategy is to reduce methane emission through genetic selection. Our first attempt used beef cattle and a GWAS to identify genes associated with several CH_4 traits in Angus beef cattle. The Angus population consisted of 1020 animals with phenotypes on methane production (MeP), dry matter intake (DMI), and weight (WT). Additionally, two new methane traits: residual genetic methane (RGM) and residual phenotypic methane (RPM) were calculated by adjusting CH_4 for DMI and WT. Animals were genotyped using the 800k Illumina Bovine HD Array. Estimated heritabilities were 0.30, 0.19 and 0.15 for MeP, RGM and RPM respectively, and estimated genetic correlations of MeP with DMI and WT were 0.83 and 0.80, respectively. Strong associations with MeP were found on chromosomes 4, 12, 14, 19, and 30. We have recently tried another approach in dairy cattle, where we aimed to enlarge the reference population for genomic selection by combining data on methane emissions in dairy cattle using data from 5 countries (Australia, Denmark, Ireland, the Netherlands and UK). The total dataset consists of 3060 dairy cows, of which most were genotyped, but with various kinds of SNP chips. We ended up with a uniform set of SNPs for each cow. Even though three different types of measurement equipment (laser, sniffer and SF_6) and protocols (measuring for 3 d, 1 wk, multiple weeks) were used, these data will be analyzed jointly to establish genetic and genomic parameters for enteric methane. The average methane production was 448 g/d in Australia (354 cows); 554 g/d in Denmark (1769 cows); 381 g/d in IRL (260 cows); 549 g/d in NL (457 cows); and 325 g/d in UK (216 cows). This clearly shows that the populations and diets are different in addition to the equipment and protocol. Therefore, a multi-trait approach will be used in the analysis. Following the experiences of a similar project (gDMI), it is expected that each country will benefit for contributing to an international reference set with increased accuracies of the estimates.

Key Words: esnteric methane, genomic selection, international collaboration

0408 How is genomics changing cattle breeding?

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Genomic selection offers considerable flexibility to increase genetic trends in dairy cattle breeding, through a decrease in generation interval, an increase in selection intensity, and an increase in reliability for females and for low heritability traits. It is also an opportunity for more sustainable breeding, in terms of breeding goal and genetic variability. With a shorter generation interval, there is a big risk of increasing inbreeding if semen dissemination policy of elite bulls is not changed. However, using a large number of young bulls both as service bulls and bull sires is a simple solution for both maximizing genetic trend while reducing inbreeding trend. Female genotyping is a key challenge for within herd selection and, simultaneously, for replacing current reference populations based on progeny tested bulls, assembling new ones in breeds of more limited size, and for selection of newly recorded traits. At a reasonable price and coupled with use of sexed semen, female genotyping is profitable for the farmers and is becoming a routine practice in an increasing number of herds. New applications are generated, such as renovated mating plans, efficient management of genetic defects, prediction of cows' future career and optimization of culling policy. With more diverse bulls on the market and with female genotyping, genomic selection also opens new avenues for more customized breeding across herds or production systems. A big challenge is to reduce the dependency of genomic predictions on relationship between candidates and the reference population. A strong effort is presently dedicated to integrating genome sequence information into predictions, to improve their accuracy and persistency. To increase the accuracy, within and especially across breeds, causal variants or very close proxies should be identified and included in the predictions, while discarding or limiting the weight of many other variants generating noise. In the longer term, further customization of selection will be possible by accounting for GxE interactions. Important developments are also necessary to decrease loss of favorable alleles through genetic drift.

Key Words: dairy cattle, genomic selection

0409 Genomic prediction using imputed sequence data in dairy and dual purpose breeds. M. Erbe[*1,2], M. Frischknecht[3,4], H. Pausch[5], R. Emmerling[1], T. H. Meuwissen[6], B. Gredler[3], B. Bapst[3], I. Consortium[7], K. U. Götz[1], and H. Simianer[2], *[1]Bavarian State Research Centre for Agriculture, Institute for Animal Breeding, Grub, Germany, [2]Georg-August-University, Department of Animal Sciences, Animal Breeding and Genetics Group, Göttingen, Germany, [3]Qualitas AG, Zug, Switzerland, [4]Bern University of Applied Sciences, School of Agricultural, Forest and Food Sciences HAFL, Zollikofen, Switzerland, [5]Technische Universität Müchen, Chair of Animal Breeding, Freising, Germany, [6]Norwegian University of Life Sciences, Department of Animal and Aquacultural Sciences, Ås, Norway, [7]Interbull Centre, Uppsala, Sweden.*

Technical progress has made it possible to re-sequence individuals within a reasonable time frame and at acceptable costs. However, as sequencing all individuals of a breeding population is still too expensive, only key individuals of a population contributing most to the genetic variation usually are chosen to be sequenced. All other individuals genotyped with common single nucleotide polymorphism (SNP) arrays are then imputed up to all known SNPs and possibly biallelic short insertions or deletions (indels) at sequence level. Different simulation studies have shown that using sequence data for genomic prediction can have a positive effect on the accuracy and the stability of marker effect estimates especially when using variable selection methods. We thus tested these hypotheses with two different data sets: one with over 6000 Fleckvieh bulls genotyped with 50k or 777k and one with over 2000 Brown Swiss dairy cattle genotyped with 30k, 50k or 777k, both imputed to sequence level with a reference set of 150 and 123 sequenced individuals, respectively. With the Fleckvieh data set, no or only very slightly higher prediction accuracies were found with imputed sequence data than with SNP array data for six different traits studied. This was true for different genomic BLUP models as well as for GBCPP, a fast EM-based variable selection method similar to Bayes Cπ. Attempts to reduce noise by modeling only specific subsets of SNPs (e.g., very accurately imputed SNPs, SNPs from genic regions) generally improved prediction compared with modeling all imputed SNPs. Sequence-based predictions did not appear to be more stable as prediction ability decreased similarly for both 50k and sequence data when sires and/or grandsires of candidates were removed from the calibration set. For Brown Swiss, a slight increase in prediction accuracy was found for non-return rate after 56 d in heifers when modeling all imputed SNPs with GBCPP compared with modeling only SNPs from the 50k array. Using prior biological information by modeling only the 50k most significant SNPs obtained from a genome-wide association study did not improve prediction accuracy, but outperformed prediction based on the 50k array. Possible explanations for the limited success of genomic prediction with sequence data are inaccuracies in imputed genotypes, especially for variants with small minor allele frequencies, lack of proper models to account for the underlying genetic architecture, and incompleteness of genome maps and structural annotation.

Key Words: genomic prediction, sequence data

0410 Multi-breed genomic evaluations for 1 million beef cattle in Ireland. A. Cromie[*1], R. Evans[2], F. Kearney[2], D. Berry[3], M. C. McClure[1], and J. McCarthy[4], *[1]Irish Cattle Breeding Federation, Bandon, Ireland, [2]Irish Cattle Breeding Federation, Bandon, Co. Cork, Ireland, [3]Teagasc, Moorepark Research Centre, Fermoy, Cork, Ireland, [4]Irish Cattle Breeding Federation, Cork, Ireland.*

Key stakeholders in Ireland (Irish Cattle Breeding Federation, Teagasc and the Department of Agriculture and Marine) are currently developing multi-breed genomic evaluations for some 1 million beef cattle. The project is co-funded through the EU's Rural Development Program, with the overall objective of increasing rates of genetic gain for key traits related to profitability and environmental sustainability within the Irish suckler beef herd. A total of $338 million has been allocated to the project over the 6-yr period (2015–2020), of which some 15% will be allocated toward the cost of genotyping and related genomic evaluations.

Phase 1 of the project is underway, with 300k beef animals genotyped in 2015. This is in addition to a further 100k animal's which were genotyped in 2013 and 2014, as part of an initial Irish government and industry funded initiative to help establish the required infra-structure (phenotypes and genotypes) for large scale multi-breed genomic evaluations. All animals have been genotyped on the International Dairy and Beef chip (IDB), with the latest version (the IDBv3) being a customised 54k chip developed in conjunction with Teagasc and Illumina Inc. It is anticipated that a further 300k animals/year will be genotyped in 2016 and 2017, resulting in a total of 1 million beef animals required for routine genomic evaluations by end 2017. Phase 2 of the project, will result in a further 1 million animals being genotyped in 2018–2020, bringing the total requirement for routine genomic evaluations to in excess of 2 million animals.

Analysis to-date has been based on a subsample of some 100k sires and cows with reliable evaluations for key profit traits. Single-step genomic evaluations using Mix99 software have been applied to the dataset, with an almost doubling of reliability from the current 20% to almost 40% for individual traits and the relevant economic indexes. Initial feedback from industry has been very positive, with an expectation that the evaluations will become official from August 2016, after which we anticipate running routine evaluations, based on the

increasing genotype and phenotype data every 2–3 mo.

Key Words: genomics, beef cattle, multibreed

FUNCTIONAL ANNOTATION OF ANIMAL GENOMES (FAANG) ASAS-ISAG JOINT SYMPOSIUM

0411 Important lessons from complex genomes.

T. R. Gingeras*, *Cold Spring Harbor Laboratory, Functional Genomics, NY.*

The approximately three billion base pairs of the human DNA represent a storage devise encoding information for hundreds of thousands of processes that can go on within and outside of a human cell. This information is revealed in the RNAs that are composed of 12 billion nucleotides considering the strandedness and the allelic content each of the diploid copies of the genome. Results stemming from the efforts to catalog and analyze the RNA products made by cells in the human (ENCODE), fly-worm (modENCODE) and mouse ENCODE projects have shed light on both the functional content and how this information is organized by various genomes. In human cells, a total of ~161,000 transcripts present within ~50,000 genic regions represent our previously best manually-curated annotation (based on v 7 Gencode) of the transcriptome. The results from the ENCODE project point to considerable supplementation of these data. Analyses of these transcriptome data sets have resulted in important and under appreciated lessons such as: (1) pervasive genome-wide transcription prompts a need to redefine the definition of a gene, (2) expression ranges follow transcript types and subcellular localization, (3) expression of isoforms of a gene by a cell do not follow a minimalistic strategy, and (4) genomic characteristics of potential *trans*-acting enhancer regions are distinguishable from other types of *cis*-acting regulatory regions. These and other lessons drawn from the landscape of both coding and non-coding RNAs present in eukaryotic cells have been used to assist in understanding and organizing what is often seen as dauntingly complex genomes.

Key Words: annotation, ENCODE, transcriptome

0412 Causal inference of molecular networks integrating multi-omics data.

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Recent developments of massively parallel technologies allow assaying different biological molecules at very high throughput rates, including sequencing and genotyping of DNA, quantifying whole-genome gene expression, including measuring mRNA and microRNA abundance, identifying genome-wide epigenetic modifications, such as DNA methylation, and measuring different proteins and cellular metabolites. These advancements provide unprecedented opportunities to uncover the genetic architecture underlying phenotypic variation. In this context, the main challenge is to decipher the flow of biological information that lies between the genotypes and the phenotypes under study; in other words, the new challenge is to integrate multiple sources of molecular information, i.e., multiple layers of omics data, to reveal the causal biological networks that underlie complex traits. It is important to note that knowledge regarding causal relationships among genes and phenotypes can be used to predict the behavior of complex systems, as well as to optimize management practices and selection strategies. Here, we describe a multistep procedure for inferring causal gene-phenotype networks underlying complex phenotypes integrating multi-omics data. We initially assess marginal associations between genotypes and either intermediate phenotypes (such as gene expression) and endpoint phenotypes (such as carcass fat deposition and muscularity), and then, in those genomic regions where multiple significant hits co-localize, we attempt to reconstruct molecular networks using causal structural learning algorithms. These algorithms attempt to infer networks assuming that the pattern of conditional independencies observed in the joint probability distribution of these set of correlated variables are compatible with the unknown causal model. As a proof of principle of the significance of this integrative approach, we show the construction of causal molecular networks underlying economically relevant meat quality traits in pigs using multi-omics data obtained from an F2 Duroc x Pietrain resource population. Interestingly, our findings shed light on the mechanisms underlying some known antagonist relationships between important phenotypes, for instance, carcass fat deposition and meat lean content. More generally, the proposed methodology allows further learning regarding phenotypic and molecular causal structures underlying complex traits in farm species.

Key Words: causal inference, graphical models, systems biology

0413 Genotypes to phenotypes: Lessons from functional variation in the human genome and transcriptome.

B. E. Stranger*, *Section of Genetic Medicine, Department of Medicine, Institute of Genomics and Systems Biology, Center for Data Intensive Sciences, University of Chicago, IL.*

Complex trait association mapping in humans has successfully identified genetic loci influencing trait variation for hundreds of different phenotypes, including disease. The vast majority of associated loci localize to non-coding regions of the genome, suggesting possible effects on gene regulatory mechanisms. Without a clear understanding of the regulatory code of the human genome, deep characterization of the molecular function(s) of genetic variants in the human genome has become increasingly important for defining that code and for understanding genetic associations to complex traits. Studies of the human

transcriptome, its complexity, and its relation to genetic variation in a variety of contexts have proven highly informative for understanding genome function and for suggesting testable hypotheses involving candidate genes for complex traits and the functional mechanisms though which they may act. These approaches are increasingly leading to successful functional characterization of trait-associated variants, in some cases, suggesting possible targets for trait manipulation. Finally, these characterizations are being used to build models predicting variant function, further extending possible applications.

Key Words: genome function, non-coding variants, regulatory mechanisms

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0414 Recurrent chimeric transcripts in human and mouse.

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The formation of chimeric transcripts (chimeras) has been widely reported. Some of them reflect underlying chromosomal rearrangements, or are the results of the propensity of reverse transcriptase to engage in template switching, however, a proportion of cases genuinely appear to correspond to *trans*-splicing of RNAs, as has previously been described.

Here we use ENCODE and mouse ENCODE deeply sequenced and bio-replicated RNaseq data from 18 human and 30 mouse samples, and the ChimPipe program, to identify chimeras occurring in multiple biological samples (recurrent), and between the same pairs of genes in human and mouse, since they are more likely to be transcriptionally induced and functional.

Recurrent common chimeras tend to connect gene pairs located on the same chromosome and relatively near to each other (< 100kb), therefore pointing to polymerase read-through, however interchromosomal chimeras are also observed, pointing to *trans*-splicing. Importantly, these recurrent chimeras tend to maintain an open reading frame, and could therefore generate chimeric proteins. We also observe that not only the gene-to-gene connection is conserved, but strikingly so are specific junction sites. The genes connected in common chimeras tend to be involved in morphogenesis and body plan formation, and consistently tend to be detected in cell lines of embryonic origin.

Validation of human chimeras by RT-PCR yielded a success rate of 50%, and subsequent cloning and sequencing revealed novel transcript structures, of which some preserve the domains from the two parent genes. Applying this method to multiple animal species and breeds will help us understanding chimera evolution as well as reveal some links between genotype and phenotype.

Key Words: chimeras, transcripts, *trans*-splicing

0415 Improving genomic selection across breeds and across generations with functional annotation.

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Identification of causal mutations which affect complex traits in livestock (including production, health and fertility) could accelerate genetic gains for these traits by improving the accuracy of genomic estimated breeding values, particularly across breeds and with greater persistency of accuracy across time. Identification of these causal mutations could also reveal facets of the biology underlying such traits. A significant proportion of the genomic variation in cattle, for *Bos taurus* breeds at least, has been identified. The 1000 bull genomes project now includes whole genome sequences from 1682 cattle of 55 breeds, from which 67.3 million variants (64.8 million SNP, 2.5 million indel) have been identified. The challenge is now to determine which subset of these variants affect complex traits. This challenge is magnified by the fact that the size of effects of the causal mutations are likely to be small, given the large number of mutations typically affecting complex traits. We propose that an approach that includes (1) a multi-breed reference population (necessary to break down the extensive linkage disequilibrium that exists within many livestock breeds), (2) intermediate phenotypes, such as gene expression and protein abundance, where mutation effect is much larger than on the complex trait phenotype, (3) genome annotation information, to identify which classes of variants are more likely to affect complex traits, and (4) a genomic prediction algorithm that uses all this information simultaneously, will lead to identification of causal mutations on a genome-wide scale. Several examples identifying potential causal mutations affecting milk composition from dairy cattle are given. The results highlight the need for better annotation of the bovine genome—many of the most significant mutations are in poorly annotated genomic regions, likely regions regulating gene expression. The functional annotation of animal genomes (FAANG) consortium will greatly improve this situation.

Key Words: genomic selection, functional annotation

0416 Integrating dynamic omics responses for universal personalized medicine. G. I. Mias*, *Michigan State University, East Lansing.*

The advent of readily available omics technologies, and the recent Precision Medicine Initiative announced by the White House and National Institutes of Health are guiding our efforts to make advances in the implementation of personalized medicine. High quality genomes are now complemented with other dynamic omics data (e.g., transcriptomes, proteomes, metabolomes), that may be used to profile temporal patterns of thousands of molecular components in individuals. We are pursuing the profiling of multiple such omics in parallel $n = 1$ studies that extend the pilot integrative Personal Omics Profiling (iPOP) approach to diseases affecting the immune system. In particular, we will describe our investigations that follow longitudinally healthy and asthmatic individuals, and the integration of multiple omics obtained from peripheral blood cells, that we believe may provide novel medical insights. Concurrently, we are developing the necessary statistical and computational methodology for integrating the different omics platforms toward a medical interpretation, including our MathIOmica framework. Our approach enables us to query RNA sequencing, mass spectrometry (proteomics/metabolomics) and any longitudinal omics data, starting from lab samples to raw data, and including downstream quantitation methods for each analysis. We will present a clinically relevant classification scheme of longitudinal patterns, integration that accounts for missing data and uneven time sampling, and ultimately a biological interpretation and dynamic visualization of an integrated profile. Additionally, we are developing the necessary experiments and data sets for future iPOP investigations, with dense profiling of cell-drug treatment responses utilizing Rituximab and other interventions. Our combined transcriptome-proteome profiles enable us to reconstruct dynamic pathways of Rituximab's action on B-cells on a global scale. In summary, our clinical, laboratory and computational investigations are providing the next steps in the development of omics data generation and integration, toward a universal personalized medicine implementation.

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Key Words: disease, personal omics profiling, transcriptome-proteome profiles

0417 A review of sequencing and assembly methods that enhance computational use. W. C. Warren*, *McDonnell Genome Institute, Washington University School of Medicine, St Louis, MO.*

In essence high quality genome references are proven to be a necessity to enable research on so many levels of biological investigation including disease etiology, small molecule drug screening and interactions, canonical disease pathway manifestation, and so many others. To date very few genomes can be classified as near finished, defined as only missing small regions that are recalcitrant to known molecular biology methods. Ultimately our goal is to produce contiguous chromosomes for genomes de novo at the lowest cost. So far most published de novo genome assemblies are derived from deep coverage Illumina only sequencing, most often utilizing two popular but independent assembly algorithms, yet all are documented to be inadequate for numerous types of genetic investigation. During this surge of short reads genome assembly new long read sequencing technology arrived, albeit at considerable cost, ~6-fold higher than pure Illumina de novo assembly approaches. However, long reads, now averaging ~14 kb in length, have transformed our ability to capture most chromosomes that compel us to fund these approaches to obtain higher quality. Our lab and others now routinely assemble human genomes with N50 contig lengths of 10 Mb and up to 53 Mb size contigs, contigs defined as uninterrupted consensus sequence. In our studies we have seen how an incomplete genome sequence was hindering studies designed to detect signatures of selection in the poultry industry, such as missing microchromosome sequence assignments and partial or completely missing gene models in the chicken. In the chicken, despite the use of older long read sequencing technology (average read length of 8 kb), we observed an increase of ~180 Mb in assembled size, added 1920 new gene models and reduced gaps by sevenfold among ordered chromosomes. Given the intense interest in better genome reference models, I will review the generally compartmentalized phases for producing high quality genome references and provide examples of analysis outcome.

Key Words: assembly, genome reference, long reads

COMPANION ANIMAL

0418 *Ehrlichia canis* in canines from Culiacan, Sinaloa, Mexico. I. Enríquez Verdugo*, B. E. Lopez Gallegos, C. Barraza Tizoc, N. Castro del Campo, D. Solis Carrasco, S. M. Gaxiola Camacho, J. Gaxiola Montoya, and M. C. Rubio Robles, *FMVZ-Universidad Autonoma de Sinaloa, Culiacan, Mexico.*

Ehrlichia canis is a Gram-negative obligate intracellular bacteria and is recognized as the causative agent of Canine Monocytic Ehrlichiosis (CME). CME is transmitted by the bite of previously infected ticks, and the main vector includes *Rhipichepalus sanguineus*. In the last decade, this tick has been considered a potential zoonotic pathogen, particularly in the area of veterinary medicine. Clinical diagnosis is based on history, clinical signs, hematological studies, cytology, serology and isolation methods. The aim of this study was detection of *Ehrlichia canis* in dogs from Culiacan, Sinaloa, Mexico by ELISA technique. The study was done in the laboratory of parasitology from the FMVZ-UAS. Blood from 81 dogs, with or without clinical signs or presence of ticks, was collected in sterile EDTA tubes from each dog using the cephalic vein. The bacteria was detected by blood smear and each sample was stained with Wright's solution and observed under light microscopy (100x) using a double blind approach. The serological study was performed using ELISA techniques (IDEXX® 4Dx). Detection of *E. canis* was performed using light microscopy, resulting in 11 positive samples and a frequency of 13.5%. Serological tests resulted in 14 samples reacting to the presence of specific antibodies against the bacteria, and a frequency of 17.2%. In conclusion, the presence of *Erhlichia canis* in dogs from Culiacan, Sinaloa, Mexico, indicates a risk to public health due to the close contact with pet dogs and the vector *Rhipichepalus sanguineus*, causing dogs to be a factor for the dissemination of this zoonotic pathogen.

Key Words: *Ehrlichia canis,* canine, blood, ELISA

419 Effect of dietary composition over food preferences of dogs. J. Figueroa, S. A. Guzmán-Pino, S. Morales*, and C. Muñoz, *Universidad de Chile, Santiago.*

The feeding behavior of dogs has been studied during several years by food preference tests that allow formulating new and specifics diets satisfying animals' needs and increasing animals' pleasure. Nevertheless, besides the sensorial characteristics of diets (smell, taste, viscosity, etc.), nutrient composition (energy, protein, dry matter, etc.) may influence dogs' food preferences. The aim of this study was to analyze the relationship between the nutritional compositions of dog's diets and their associated preferences. A database of preference test from 10 yr (2003–2013) was obtained from the Research Center of Pet Feeding Behavior (Facultad de Ciencias Veterinarias y Pecuarias, Universidad de Chile). Preference tests performed during those years consisted on the placement of two simultaneous feeders in the front of dogs' cannels during 10 consecutive minutes. Food was weighted at the beginning and end of each test to calculate animals' food intake. In each preference test, the nutritional composition of both diets was analyzed, and the difference between the nutrient components of the most preferred diet (A) and the other diet (B) was used for the statistical analysis. To evaluate how nutritional components or group of components may explain food preferences, data was analyzed by doing a principal component (PC) analysis using the princomp procedure of the statistical software SAS. A linear regression was performed between each principal component obtained and dogs' preferences. Later, a Spearman correlation was performed with the nutritional components that represented the greatest variability within the main component that showed a significant linear regression. The first tree principal components presented eigenvalues close to 1 that explained the 74% of the data variability (37.4, 25.1 and 12.5%, respectively). After the linear regression between each principal component and dogs' food preferences (diet A) it was observed that only the third component (dry matter, nitrogen-free extract and metabolizable energy) presented a relation ($P = 0.040$). Dry matter and nitrogen-free extract showed negative correlations with preferences ($r = -0.239$; $P = 0.008$ and $r = -0.188$; $P = 0.039$), respectively. These results show that some nutritional components may affect the food preferences of domestic dogs. Diets humidity, followed by carbohydrate fractions, seems to have the highest repercussion on dogs' behavior during a food choice test.

Key Words: domestic dog, food preferences, nutrient composition

0420 Hind limb kinematics of the Weimaraner at the trot. L. Carlisle[1], M. C. Nicodemus*[1], and K. Slater[2], *[1]Mississippi State University, Starkville, [2]Banfield Pet Hospital, Magnolia, TX.*

Large dog breeds are plagued with hip dysplasia, and yet, some larger breeds such as the Weimaraner have been reported to have a lower percentage rate of hip dysplasia within the general population. Temporal variables of the trotting Weimaraner have been reported as being unique from other large breeds. Understanding the uniqueness of the gait mechanics of the Weimaraner may assist in early clinical diagnosis of hip dysplasia and help in the understanding of why this particular breed has a lower rate of dysplasia. Therefore, study objectives were to measure the trotting hind limb kinematics of the Weimaraner. Six American Kennel Club registered Weimaraner dogs were filmed at 60 Hz being led on even, natural footing at the trot (velocity: 1.9–2.3 m/s). Reflective markers

attached to palpation points on the proximal and distal aspects of the lateral side of the hind limb were tracked and analyzed using APAS (Ariel Dynamics Inc., Trabuco Canyon, CA). Ten strides per dog were used to determine means + SD of measured kinematic variables. Selection of strides was based on soundness, gait correctness, consistency, and noticeable foot placement and lift-off. During the trot the dogs stayed fairly level across the hindquarters demonstrating minimal horizontal displacement of the pelvis (2.8+0.7 cm) throughout the stride cycle. This may be due to the relatively minimal horizontal displacement of the trotting hind paw (9.7+2.1 cm) suggesting despite the presence of suspension during the stride the hind limbs stay fairly low to the ground at the trot similar to that seen in the German shepherd. When comparing the joint data collected for the Weimaraner to other large dog breeds (Labrador, Rottweiler), joint angular displacements were comparable in the hip joint (29.8+1.0°), but slightly less range of motion than the other breeds in the tarsal (36.1+3.7°) and stifle (46.8+5.6°) joints. This could be related to breed differences or could be attributed to weight differences as the other breeds were heavier made breeds in which obese dogs were found to increase range of motion with increased weight to assist in absorbing the extra concussion. Furthermore, the slightly less angular displacements of the tarsus and stifle would also explain the minimal pelvic horizontal displacement in which this reduced lifting and dropping of the hindquarters will assist in minimizing concussive forces. These kinematic variables demonstrate uniqueness within the breed and suggest further kinematic research of other large dog breeds.

Key Words: Weimaraner, kinematics, trot

0421 The effect of source and drying process on amino acid composition and protein quality of dried poultry used in high-quality pet diets and select human foods.

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Information regarding composition, functionality, acceptability, and nutrient utilization of new protein sources used in pet foods can be relatively scarce. The objective of this experiment was to evaluate nutrient composition and protein efficiency ratio (PER) of various poultry proteins used in processed pet and some human foods. The experimental protein sources were analyzed for proximate and amino acid composition. Experimental protein sources from spray dried egg (SDEG), chicken by-product meal (CPBM), chicken meal (CKML), 6 fluid-bed-dried chicken samples (FBC 1–6), fluid bed dried turkey (FBDT), 4 spray-dried chicken samples (SDC 1–4), and a spray-dried high fat chicken (SDHF) were added to a N-Free basal ration in exchange for an equal portion of the corn starch and dextrose to provide 10% CP. Day old male broiler chicks (Cobb X Cobb) were acclimated to battery pens for 7 d with ad libitum access to starter diet (23% CP) and water. Chicks were fasted overnight then allotted to pen by weight. Pen (5 chicks ea) was the experimental unit with four pens per treatment randomly assigned to battery (block). Chicks were fed treatment diets for 10 d then weighed and feed intake recorded. The PER was computed as chick gain per unit protein intake and analyzed for differences using the GLIMMIX procedure of SAS (v9.4). The CP ranged from 50.1% for SDEG, to 67.4% and 67.7% for the CBPM and CKML, to an average of 71.7% for the FBC1–6, 73.3% for FBDT, average 74.6% for the SDC1–4 and 45.6% for the SDC5. The CBPM, CKML, and FBC6 had the highest hydroxyproline levels, the EAA:NEAA were high (> 0.95) for all samples except CBPM, CKML, and FBC6 (0.70, 0.70 and 0.80, respectively) and availability of lysine exceeded 95% for all samples. The PER for SDEG was 4.84. When PER was expressed as % of egg PER (EGGPER) the CBPM and CKML were lower ($P < 0.05$; 71% and 62%) than egg PER. FBC1–5 and FBDT did not differ from EGGPER, but the FBC6 was lower ($P < 0.05$; 88.2% of EGGPER) The SDC1–5 had a lower ($P < 0.05$) EGGPER (average of 85.6%) than fluid bed dried chicken. These data suggest that gently drying poultry via fluid-bed retained protein quality similar to SDEG and may differ slightly relative to spray-drying. However, whether this was because of process or ingredient composition differences was not fully elucidated by this study.

Key Words: pet food, protein ingredients, chick PER

0422 The amino acid composition and protein quality of various poultry and vegetable proteins commonly used in the production of dog and cat diets.

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Novel protein ingredients support the growth of the pet food market and new product development. However, some new protein sources (e.g., spray-dried chicken, rice protein concentrate, pea protein concentrate, and potato protein concentrate) have limited or no data available regarding their protein quality. The objective of this study was to evaluate several new protein ingredients used in the pet food industry for nutrient composition and protein quality using a chick protein efficiency ratio (PER) assay. Following proximate and amino acid analysis, 7-d old male Cobb x Cobb broilers were fed experimental diets for 10 d. Birds were allotted to pen ($n = 6$) by weight and randomly assigned to battery ($n = 4$). To the N-free basal ration test proteins were included to contribute 10% CP. The experimental protein sources included spray-dried egg (SDEG), spray-dried egg white (SDEW), spray-dried egg enriched with yolk (SDEY), chicken byproduct meal (CBPM), chicken meal (CKML), low temperature air-dried chicken meal (TACM), low temperature and pressure-fluid-bed-dried chicken (TPCK), spray-dried chicken (SDCK), whey protein

concentrate (WPCT), corn gluten meal (CGML), corn protein concentrate (CPCT), potato protein isolate (PPIS), rice protein concentrate (RPCT), pea protein isolate (PEPI), soy protein isolate (SPIS), and soybean meal (SBML). Data were analyzed using the GLIMMIX procedure of SAS (v9.4). Proximate analysis of all test ingredients were compatible with values reported previously except for the higher fat content of SDEG. Chicks fed SDEG, SDEY, and TPCK had the highest PER ($P < 0.05$; 5.18, 5.37, and 5.33, respectively) and the CBPM and CKML were the lowest among the poultry proteins for EAA:NEAA (0.79 and 0.74), PER (3.59 and 2.91), and Lys availability (84.1% and 78.0%). Among the vegetable proteins PPIS and SBML had the highest ($P < 0.05$) PER values (3.60 and 3.48) and Lys availability (95.4% and 93.4%). Whey protein concentrate and CPCT had the lowest PER values (−0.90 and −0.80), despite the high CP (76.10% and 78.83%) and Lys availability (95.2% and 88.9%). In general the chick PER method was effective at comparing the quality of protein sources and was consistent with the EAA:NEAA and Lys availability.

Key Words: protein ingredients, pet food, protein efficiency ratio, PER

0423 The effect of Miscanthus grass as a fiber source in cat diets on nutrient utilization and stool consistency. R. A. Donadelli*, C. G. Aldrich, and I. C. Alvarenga, *Kansas State University, Manhattan.*

High levels of insoluble fiber are commonly used in cat foods to increase energy dilution (weight loss) and to promote digesta flow (reducing hairballs). There are two commonly used fibers: cellulose (CE) and a beet pulp (BP). Miscanthus grass (MG) is a C4 forage grown for its cellulose content. Nutritional information for MG is scarce; therefore, the objectives of this study were to determine the effect of 10% fiber in cat diets on nutrients digestibility and stool consistency. Experimental diets were based on 90% of ration (low ash chicken byproduct meal, brewers rice, corn, wheat, corn protein concentrate, minerals and vitamins, both as recommended allowances NRC, 2006) plus 10% of each fiber source. The feeding trial was approved by Institutional Animal Care and use Committee at Kansas State University Research Compliance Office. Cats, 12 American shorthairs, were group-housed but fed individually in cages during 9-d adaptation and kept individually caged during the 5-d collection period. Animals were fed twice daily in a replicated Latin square design, with water available throughout the experimental period. Diets and feces were analyzed for proximate analysis and acid insoluble ash (AIA); additionally, apparent total tract digestibility (ATD) and urine pH were computed. Data was analyzed using statistical software (SAS v9.4) using the GLM procedure. Cats maintained body weight throughout the duration of the study (average 4.6 kg). Food intake, defecation frequency, fecal scores, and urine pH were not different ($P < 0.05$) (average 374.8g*d^{-1}, 1.2*d^{-1}, 3.1, 6.94, respectively). The DM and OM digestibility of BP were greater ($P < 0.05$) than for cats fed MG or CE for both TFC (DM; 81.14, 76.22, 75.45%, OM; 85.85, 80.47, 79.37%, respectively) and AIA (DM; 71.18, 69.54, 61.98%, OM; 77.5, 74.46, 67.49%, respectively) methods. The CP digestibility was not different among treatments for TFC (average 85.34%) and for AIA greater ($P < 0.05$) for MG than CE with BP intermediate (81.18, 74.59, 78.21%, respectively). The EE digestibility by TFC were similar for MG and CE and each greater ($P < 0.05$) than BP (89.15 and 89.64 vs. 84.96%, respectively) and by AIA there was no difference among the treatments (average 82.15%). While differences in ATD observed the values for MG were within the range of those for CE and BP for both methods of assessment. Miscanthus grass appears to be an effective alternative to BP and CE in high fiber cat diets.

Key Words: fiber, cat, Miscanthus grass, cellulose, beet pulp, digestibility

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0424 The effect of feed form on diet digestibility and cecal fermentation in rabbits. I. C. Alvarenga*[1], C. G. Aldrich[1], and M. Kohles[2], *[1]Kansas State University, Manhattan, [2]Oxbow Animal Health, Murdock, NE.*

Companion rabbits are commonly fed dry forages supplemented with formulated mixes based on finely chopped hay (alfalfa or timothy), grain and grain co-products, vitamins, and minerals. These may be offered as a muesli, a pellet, or extruded into kibbles; but, whether one form is beneficial relative to the other for companion rabbits has not been reported previously. Therefore, the objectives of this experiment were to determine the effects of diet form (muesli, pelleted, or extruded) on rabbit intake, weight, digestibility, and cecal fermentation. Fifteen New Zealand rabbits were randomly assigned to one of 3 treatment groups of 5 animals each and fed pelleted, extruded, or muesli diets in a completely randomized design experiment. Rabbits were placed in individual cages with ad libitum water and food for 45 d. Digestibility was calculated based on results from intake measurements and collection of feces by total collection (TFC) and by two methods for determining acid insoluble ash (AIA) as an internal marker (AIA1; Vogtman et al. (1975), and AIA2; Keulen and Young, 1977). Cecal fermentation was assessed at the conclusion of the experiment by measuring cecal pH, ammonia, and VFA following exsanguination and organ harvest. Feed intake was higher ($P < 0.05$) for pelleted and extruded diets (133.1g/d and 135.0g/d vs. 98.8g/d), but weight change was not different among treatments (average −1.2 g/d). By TFC the DMD of muesli and extruded were greater ($P < 0.05$) than pelleted (69.1, and 65.2 vs. 50.6%). DMD by AIA1 was not significantly different between treatments ($P > 0.05$; 58.1, 55.3, 64.4% for muesli, pelleted and extruded, respectively) and for AIA2 DMD was greater ($P < 0.05$) for pelleted followed by muesli and extruded (71.8 vs.

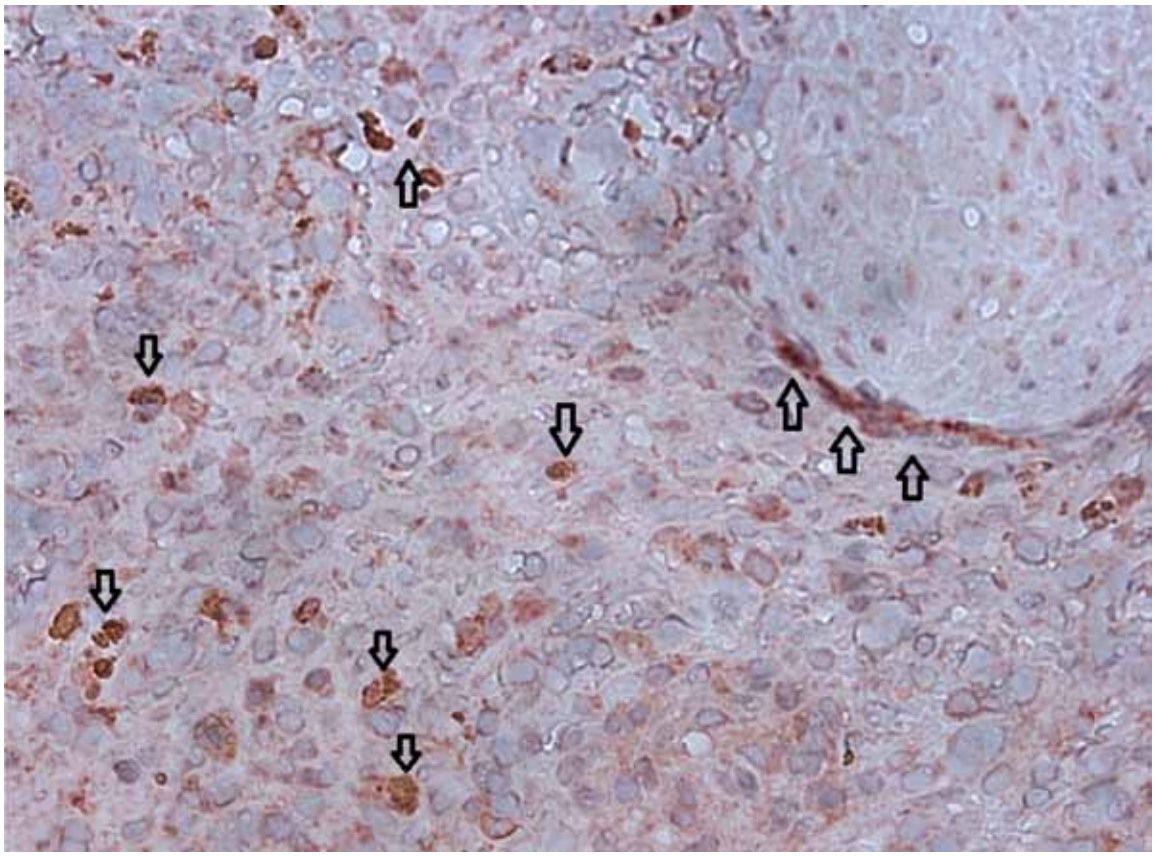
68.5 vs. 62.0%, respectively). Between the two AIA methods the AIA2 had much lower variation among each mean than AIA1 (SEM = 0.44 vs. SEM = 5.37). Rabbits fed pelleted and extruded diets had lower pH ($P < 0.05$) compared with muesli (6.38 and 6.42 vs. 7.02, respectively), the cecal butyrate concentration was higher ($P < 0.05$) in rabbits fed extruded and pelleted diets than muesli (12.4% and 11.38%, vs. 8.4%, respectively), and proprionate was higher ($P < 0.05$) in rabbits fed muesli than pelleted or extruded diets (10.2% vs. 7.7% and 6.6%, respectively). This would indicate higher fiber fermentation for extruded and pelleted diets. These results suggest that diet composition rather than processing had a greater impact on digestion and fermentation.

Key Words: rabbit, AIA, digestibility, extruded, pelleted

0425 Canine hemangiosarcoma expresses luteinizing hormone (LH) receptors. K. Zwida* and M. A. Kutzler, *Oregon State University, Corvallis.*

Throughout most of the developed world, surgical sterilization via gonadectomy has become a common tool for combating the overpopulation of unwanted dogs as well as to eliminate the risk of reproductive diseases in pet dogs. However, canine gonadectomy increases the risk of several non-reproductive long-term disorders, possibly due to a loss in negative feedback to the anterior pituitary, which results in supraphysiologic circulating concentrations of LH. In addition to its reproductive hormone action, LH is a powerful mitogen in extragonadal tissues with LH receptors. Studies have confirmed the presence of LH receptors in vascular endothelial and smooth muscle cells in humans. Hemangiosarcoma is a rapidly growing, highly invasive cancer arising from the lining of blood vessels (mostly commonly the spleen in dogs). Gonadectomized (spayed) female dogs have two times the risk for developing hemangiosarcoma compared with unaltered females. We hypothesized that LH receptors would be present in vascular cells of canine hemangiosarcoma. The aim of study was to investigate if LH receptors were expressed in primary and metastatic lesions of canine splenic hemangiosarcoma using immunohistochemistry. Formalin-fixed surgical biopsies submitted to the Oregon State University Veterinary Diagnostic Laboratory were paraffin-embedded and sectioned (6 μm) onto charged slides. Testicular tissue from a separate dog obtained following castration was used as a positive control. All slides were deparaffinized, rehydrated, subjected to heat-induced epitope retrieval (#S1700, Dako). Endogenous peroxidase activity was inactivated with 3% H_2O_2 and nonspecific binding was blocked with 1% horse serum. Goat polyclonal anti-human LHR antibody (SC-26341, Santa Cruz Biotechnology) was applied at a 1:50 dilution. Negative controls from each tissue were treated in the same way except in absence of primary antibody. Slides were then reacted with biotinylated horse

Fig 0425.



anti-goat IgG (Vector Laboratories, Burlingame, CA) and incubated with preformed avidin-biotin-peroxidase complex (#PK6105, ABC kit, Vector Laboratories) followed by Nova Red Peroxidase substrate (#SK4800, Vector Laboratories). Slides were counter-stained with hematoxylin, dehydrated, and mounted. Images were digitally captured at 400X magnification. LH receptor expression (cytoplasmic and granular) was found in splenic stromal cells of a primary tumor from one dog (identified by arrows on figure) but not in a primary splenic tumor or a mesenteric metastatic tumor from two other dogs. There was no positive staining in the negative sections. This is the first report shows that LH receptors are present in canine hemangiosarcoma and provides evidence for how gonadectomy may increase the incidence of cancer in dogs.

Key Words: dog, gonadectomy, immunohistochemistry

0426 Rabbit maternal pheromone delivered in ointment decreases heart rate in domestic dogs during a simulated thunderstorm. G. M. Pirner* and J. J. McGlone, *Texas Tech University, Lubbock.*

Thunderstorm-related anxiety is common in domestic dogs and is characterized by anxious behaviors such as pacing, vocalizing, or environment or self-destruction. Interomones are olfactory chemical cues released by one species that can elicit behavioral and physiological responses in a second species. Previous studies suggest that interomones can alter dog behavior. This study was designed to examine the effects of a rabbit maternal-neonatal pheromone (2-methylbut-2-enal; 2MB2) delivered via topical ointment on heart rate and behavior of domestic dogs. Twelve dogs of varying age, breed, and sex experienced two treatment ointments applied to the snout: a control ointment with no interomone (CON); or an ointment containing 1 µg/mL of 2MB2. Treatments were assigned using a completely random crossover design with two testing rooms and two treatments. Baseline heart rate (HR) and behavior (standing, lying, pacing, and vocalizing) were recorded throughout each trial. Trials consisted of a 15 min "before" period, at the end of which the designated treatment was administered and a simulated thunderstorm played for 15 min ("during"). This was immediately followed by a third 15-min recovery period ("after"). Data were analyzed using the General Linear Models Procedure of SAS (SAS Inst., Inc., Cary, NC) and Least Squares Means were compared. HR increased 9.5% at the onset of the simulated thunderstorm ($P < 0.05$); however, HR of dogs receiving 2MB2 returned to baseline approximately 5 min into the simulated thunderstorm compared with dogs receiving CON, whose HR remained elevated for most of the 15 min period. Throughout the "during" period, HR of dogs receiving 2MB2 was 13% lower than that of dogs receiving CON ointment (124 ± 4.02 vs. 143 ± 3.95 bpm, respectively; $P < 0.05$). Time dogs engaged in each behavior did not differ between treatments. The interaction between individual and treatment was significant ($P < 0.01$) for HR, indicating that 2MB2 influenced individuals differently. The rabbit maternal pheromone 2MB2 delivered in an ointment to the snout may act as an interomone in dogs, and provides a natural, fast-acting therapy for some dogs experiencing thunderstorm-related anxiety.

Key Words: dog, pheromone, thunderstorm

0427 Evaluation of nutrient digestibility and fecal scores in domestic dogs (*Canis lupis familiaris*) fed raw meat diets varying in protein source. C. A. Iennarella*, C. J. Iske, C. L. Morris, *Iowa State University, Ames.*

Few commercially available raw meat diets (RMD) formulated for exotic carnivores managed in zoological institutions, (typically beef or horse-based), are available. Recently, a 100% pork-based RMD was commercially developed and may provide an alternative dietary option for managing carnivores in the zoological community. The objective of this study was to evaluate the nutrient composition, fecal scores, and apparent total tract macronutrient and energy digestibilities of the pork diet compared with 3 existing RMDs commonly fed to zoologically managed carnivores using the domestic dog as a model. Four intact male dogs (*Canis lupis familiaris*) were utilized in a repeated 4x4 Latin square design consisting of 14-d periods including 10 d for diet transition followed by 4 d of fecal collection. Four raw meat dietary treatments varying in protein source were evaluated and included horse (H), pork (P), and two different beef diets (B1, B2). Diets and feces were analyzed for dry matter (DM), organic matter (OM), crude protein (CP), crude fat (fat) and energy according to AOAC methodology. Feces were scored using the following scale: 1 = very hard, dry feces to 7 = watery diarrhea (Nestle Purina). Dogs were individually fed to maintain body weight and body condition based on energy intake before initiation of the study. Data were analyzed using the mixed models procedure of SAS. Treatment nutrient concentrations ranged for DM (32.2–36.2%), OM (91.1–94.9%), CP (50.3–61.7%), fat (25.1–38.3%), and gross energy (5.8–6.4 Kcal/g). Fecal scores were lower ($P < 0.05$) when dogs were fed H (1.2) and B2 (1.9) diets compared with P (2.7) and B1 (3.1). Digestibility of nutrients and energy ranged from 83.3–92.4%, 88.4–95.3%, 93.8–97.7%, 94.9–98.2%, and 91.3–95.5% for DM, OM, CP, fat, and energy, respectively. Dogs fed B2 had greater ($P < 0.05$) DM (92.4%), OM (95.3%), CP (97.7%), and GE (95.5%) digestibilities but lower ($P < 0.05$) fat digestibility (94.9%) than all other diets evaluated. The results of this study suggest these RMDs were comparable in nutrient composition and apparent total tract digestibility, indicating dogs effectively digest RMDs containing various protein sources. Fecal scores were all 3.1 or less; therefore, RMDs did not result in reductions of digestibility or in diarrhea and all

diets utilized in this study may be effective options for managing exotic carnivores.

Key Words: raw meat diets, dogs, exotic canids

0428 Miscanthus grass utilization as a dietary fiber source for dogs. R. Antunes Donadelli*, C. G. Aldrich, and I. C. Alvarenga, *Kansas State University, Manhattan.*

Pet foods formulated to aid weight loss by energy reduction may include high levels of fiber (8 to 10%). This fiber may be added as beet pulp (BP), cellulose (CE), or other crop residues. *Miscanthus giganteus* (MG) is a purpose grown C4 grass that produces large quantities of fiber. However, there is no published data supporting the use of MG in dogs. The hypothesis of this study was that MG would be utilized as a fiber source similar to CE and BP in dog diets. Each experimental diet contained 10% test fiber and 90% basal ration (chicken byproduct meal, brewers rice, corn, wheat, corn protein concentrate, minerals, and vitamins) to meet the recommended allowance according to NRC (2006). The experimental protocol was approved by Institutional Animal Care and use Committee at Kansas State University. Twelve Beagle dogs (average weight 10.6 kg) were housed individually in metabolism cages in environmentally controlled rooms and fed experimental diets for 14 d (9-d adaptation and 5-d collection) in a replicated Latin square design. Diets and all feces (TFC) were analyzed for proximate analysis and acid insoluble ash (AIA) and apparent total tract digestibility (ATD) was computed. Data were analyzed with statistical software using the GLM procedure (SAS v9.4). Food was readily accepted by all dog and each maintained weight throughout the study. There were no differences in defecation frequency, but fecal scores (1 = soft, 5 = hard and firm) were lower (softer; $P < 0.05$) for BP (3.15) than MG (3.63) or CE (3.68). Dry fecal excretion was estimated at 46.9 and 63.1 g*d^{-1} for TFC and AIA, respectively. The DM and OM digestibility were greater ($P < 0.05$) for dogs fed BP than MG but less than those fed CE for TFC (DM; 81.32, 78.0, and 77.21%, OM; 86.06, 82.12, and 80.81%, respectively) and AIA (DM; 76.55, 72.20, 68.92%, OM; 81.58, 76.68, 73.56%, respectively). The CP digestibility was greater ($P < 0.05$) for MG than BP and CE for both TFC and AIA methods. The EE digestibility was greater ($P < 0.05$) for the MG and CE than BP for both TFC and AIA. The AIA method predicted nutrient digestibility with similar magnitude and rank to TFC. Further, differences among treatments for ATD occurred among treatments the results indicate that MG is a viable dietary fiber alternative to CE and BP in dog foods.

Key Words: fiber, dog, Miscanthus grass, cellulose, beet pulp, digestibility

429 The effect of milled sorghum fractions on diet utilization by dogs. I. C. Alvarenga*, C. G. Aldrich, and R. A. Donadelli, *Kansas State University, Manhattan*

Sorghum is an abundant starch source that has many potential health benefits. Some pet food companies have adopted whole sorghum in their formulations, however sorghum flour and (or) its seed coat which is rich in polyphenolics might provide added benefit to companion animal diets. The objective of this experiment was to evaluate diets utilizing sorghum flour (SFD), and sorghum mill feed (SMF) relative to whole sorghum (WSD), and conventional grains (rice, corn and wheat; CON) in a typical dog diet. Adult (1–3 yr) Beagle dogs ($n = 12$; 10.6 kg ± 1.4) were randomly assigned to individual pens with ad libitum access to water. Dogs were fed twice daily and adapted to diet (9 d) then feces and urine were collected for 5 d over 4 periods in a replicated Latin square design. Fecal excretion was estimated using Cr_2O_3as an external marker and apparent total tract digestibility was computed. Number of defecations and feces were scored on a subjective 5-point scale (1= runny, 5 = hard and dry). Results were analyzed with statistical software using GLM procedure of SAS (v 9.4). Dry matter digestibility (DMD) was greater ($P < .05$) for SFD than CON and WSD, which were greater ($P < 0.05$) than SMF (86.0, 83.0, 81.1, and 65.9%, respectively). The organic matter (OMD), energy (DED), and protein (PRD) digestibility followed a similar relationship among treatments (OMD 90.7, 88.1, 86.4, and 70.06%; DED 90.3, 87.2, 85.4, and 70.2%; PRD 81.8, 77.5, 77.2 and 67.2%, respectively). In contrast, fecal scores were highest ($P < 0.05$; 3.91) for SMF, intermediate for the WSD and SFD (3.74 and 3.77) and lowest ($P < 0.05$) for CON (3.58). As well the number of defecations per day was higher ($P < .05$) for SMF than all the other treatments (3.03 vs. average 2.21). While SMF may contain some beneficial phenolic compounds it decreased nutrient digestibility and yielded firmer stools relative to the other treatments. Mostly due to the higher fiber content of this milled sorghum component. In contrast, removing the fibrous cortical layer resulted in higher digestibility for SFD and may provide beneficial functional properties to modern pet food kibble.

Key Words: sorghum, pet food, digestibility, flour, mill feed

COMPANION ANIMAL SYMPOSIUM: BEHAVIOR AND THE HUMAN-ANIMAL BOND

0430 Cognitive assessment protocols for use with companion animals. B. Milgram*, *CanCog Technologies, Toronto, ON, Canada.*

This presentation will provide an overview of the three main technologies that have been used to train and assess cognitive ability in companion animals, will discuss the utility of each and their relationship between all three. The first technology utilizes an approach, known as Operant conditioning, and is a method of training animals that follows a sequence of distinct steps—each of which uses reward to motivate the animals to learn and a process referred to as shaping in which reward is provided for incremental responses. This approach can be used to shape a broad spectrum of behaviors, such as responding to specific commands or stimuli. In dogs, these behavioral testing protocols have long been used to train groups of animals to carry out specific behavioral functions, and include military working dogs and seeing eye dogs as examples. The procedures followed have been well established and there is a large population of animal trainers who are highly skilled in the art.

The second type of protocol, which is one that we have used extensively, is one in which animals are presented with a specific problem and over repeated testing learn to solve the problem, initially by a process of trial and error learning. We have used this procedurel to try to understand the cognitive structure of the canine (and feline) brain, how cognition develops, how it changes with age and how it compares with that of the human. The specific problems are referred to as neuropsychological tests, because their performance can be linked specific neural structures. These protocols are useful for safety and efficacy screening drugs and other interventions. They can also be used in developing interventions for use in humans, with the dog serving as a translatable animal model.

The final technology involves the development of standardized questionnaire to assess cognitive function and is a procedure used only for assessment. The rationale for developing this questionnaire came from the realization that cognitive function can decline dramatically with age in dogs. This cognitive decline has been labeled cognitive dysfunction syndrome (CDS). The actual functions, however, are not limited to behaviors linked to cognition, but also behaviorsthat could be linked to other aging processes. To date, there is little evidence that CDS as defined by questionnaires is a correlate of other measures of canine cognition.

Key Words: operant-condition, neuropsychologal testing, cognitive dysfunction syndrome

0431 Objective evaluation of affective states in dogs. R. T. S. McGowan*, *Nestlé Purina Research, St. Louis, MO.*

It has long been the impression of most pet owners that dogs have rich emotional lives and that their experiences affect them profoundly in ways similar to how humans are affected. However, there is a lack of methodology to objectively assess affective states in animals, especially positive states. It is widely accepted that there is more to good well-being than the absence of negative states and it is increasingly being accepted that the wellbeing of an animal is greatly influenced by its affective state. Animals continually experience "reward cycles" as they pass through appetitive, consummatory and post-consummatory phases during their daily activities (e.g., eating, playing, problem-solving). High arousal positive emotions (e.g., excitement, anticipation) are associated with appetitive phases, sensory pleasure (e.g., comforting touch, hedonic taste) occur during consumption and low arousal positive emotions (e.g., satisfaction, relaxation) accompany post-consumption phases. This talk will highlight methodology that can be used to evaluate these positive states in dogs, providing examples from studies in both research and shelter settings. Dogs are an ideal non-human model for studying positive affective states because they have traditionally lived in close contact with people (so we are good at reading them and they are even better at reading us), are capable of forming close attachments to people (providing opportunity to study the human animal bond from the animal's perspective) and are kept throughout the world as both companions and working animals (a better understanding of their affective states will help to promote optimal wellbeing). Using behavioral tests (e.g., human interaction, cognitive bias, problem solving) coupled with non-invasive physiological measures (e.g., cardiac activity, salivary cortisol, thermal fluctuations) we can glean new insights into how to measure affective states in dogs. By using a holistic approach that incorporates both behavioral and physiological measures, we can produce scientifically sound evidence to identify which emotions animals experience and how animals express these affective states through their behavior. With this holistic approach we can develop a more objective understanding of animal wellbeing.

Key Words: dogs, affective state, non-invasive physiological indicators

0432 The human-animal bond: Science-based approaches to improving companion animal welfare and adoption outcomes. C. C. Croney*, *Purdue University, W. Lafayette, IN.*

There is substantial literature documenting the myriad mutually beneficial effects of the human-animal bond. While such relationships typically enhance the health and well-being of both people and their animal companions, the bond can

weaken or fail to be established if the animals do not meet the expectations of the people with whom they interact. The behavioral component of animal welfare is particularly important in this regard, and requires significant attention, as owners of companion animals are often intolerant of behavior problems. These include behaviors characterized as nuisances, such as excessive vocalizations, those that result in aggression toward people or other companion animals, or behaviors that result in injury to the animal or damage to property. Problem behaviors are among the most commonly stated reasons for cat and dog relinquishment, abandonment and euthanasia. Thus, understanding key factors that impact behavioral well-being in these species is important whether the animals are maintained in or intended to be rehomed from breeding programs, shelters, rescues or elsewhere. Consequently, a comprehensive assessment plan for meeting the needs of animal companions that includes their mental and behavioral well-being is necessary to protect the human–animal bond. It is therefore imperative to develop and validate key metrics of companion animal welfare that are practical for field as well as laboratory purposes. Considerations and challenges in developing such metrics will be reviewed, using the development of care and welfare standards for breeding dogs for illustrative purposes.

Key Words: behavior, companion animal, well-being

0433 2015 Corbin Award Winner: Behavior and training of companion and zoo animals.

C. L. Morris*, *Iowa State University, Ames.*

Activity or behavior varies tremendously across taxa and activity itself separate plants from animals. Regardless if we consider a dog competing on an agility course or a hyena standing for voluntary jugular blood collection, we must understand the science of behavior, the natural history and the instinct of the animal in order for successful training to occur. Repeated behaviors result from either positive or negative reinforcement, whereas behaviors diminish with application of positive or negative punishment. Once we identify reinforcements or punishments relevant to the behavior and specific animal, training and behavior modification become more black and white. This science and theory of animal training are well rooted in the work of Skinner and Pavlov. However, difficulties in animal training occur when trainers or animal managers fail to understand what motivates or reinforces a specific animal or the relevant species-specific natural histories. Animal trainers typically use food to motivate or train animals; however, the animal must want that food item for it to be of value. Subjects of same species may not find similar value in reinforcement items. In addition, failure to understand instinctive behavior patterns typically related to obtaining food or social structures may lead to limitations in training or behavior modification. The term "Instinctive Drift" occurs when animals have been trained to a new learned behavior that ultimately drifts back toward an instinctive behavior. Often this behavioral drift can be mislabeled by animal trainers as disobedience or misbehavior but is frequently related to instinctive behaviors associated with feeding or obtaining food or other inate insticts such as herding. Similarly, some aggression issues in dogs may be prevented or mitigated at a young age if owners had increased awareness of the dynamic social structure of dogs. Stereotypic behaviors are typically thought of as negative repetitive behaviors that originate from artificial environments that do not allow animals to satisfy their normal behavior repertoire, and these behaviors can be difficult to modify. While the science and theory of animal training and behavior are critical to excelling as an animal trainer and manager, it is equally critical to understand natural history, instinctive behaviors and motivation. Therefore, great animal trainers not only understand the science and theory of behavior, they also consider the uniqueness of individual animals they manage.

Key Words: training, behavior, companion animals, zoo animals

COMPANION ANIMAL SYMPOSIUM: FUNDAMENTALS OF PROTEIN NUTRITION

0434 Global protein supply: Present and future considerations and availability.

D. L. Schaefer*, *Cargill, Wichita, KS.*

A key differentiator in the development and marketing of pet food is the source of protein. Producers and marketers are reaching further and using more creativity in product development. This presentation will focus on global trends in the availability of protein for the use in pet diets.

Key Words: protein, companion animal, global source

0435 Alternative protein supplies for petfood.

G. Bosch*, *Wageningen University, Netherlands.*

The combination of a growing human population, increasing standards of living and urbanization in developing countries fuels global demand of protein sources for consumption by humans and animals. Increasing food production is, however, highly challenging as required resources such as land, water and fossil energy are limiting and the environmental impact of crop and livestock production already needs to be minimized. Various efforts are focused on changing the demand as well as on the production of proteins. Global food supplies can be increased by improving production efficiencies. Production of underperforming crop and livestock production systems can be improved through management and new technologies. In addition to increased production of conventional foods, alternative and sustainable foods are being developed. It is therefore clear that also the landscape of available ingredients for the pet food industry will change further the coming years. The additional

alternative proteins can originate from biomass sources previously left as waste. Leaf proteins present in by-products from crops like sugar beet or from grass are already available in large volumes. Technologies are being developed that can extract these leaf proteins yielding colorless protein isolates for (pet)food applications. Various sources of organic waste can be converted by insects (e.g., black soldier fly larvae), which can be used as a high quality and sustainable protein source. Additionally, alternative proteins can also originate from "novel" ways of production. Production systems of aquatic protein sources (microalgae, duckweed, seaweed) are rapidly advancing and do not compete for good agricultural land. These protein sources have a high water content, however, and require separation technologies that are still costly and energy consuming, therefore, requiring further development. Acceptability of vegetable proteins can be facilitated by transforming them into fibrous structural patterns of meat. In the long run, laboratory cultured meat using muscle stem cells may even replace meat from conventional livestock. These examples illustrate that there are multiple alternative protein supplies for future petfoods, although still considerable time is required to further develop the products and reach production volumes for large-scale applications. Furthermore, ingredients still require evaluations beyond chemical characterization including in vivo testing of nutritional and (dys)functional properties as well as safety attributes. Finally, acceptance of alternative ingredients by pet owners may be difficult in some areas of the world. However, awareness of owners regarding global food security continues to grow, which will facilitate the application of these ingredients in petfoods.

Key Words: food security, novel proteins, sustainability

0436 Amino acid requirements and protein digestibility and assessment in dogs with considerations for cats. A. K. Shoveller*, *University of Guelph, ON, Canada.*

Dietary protein remains a key focus for pet food manufacturers; however, few properly designed amino acid (AA) requirement studies have been conducted in adult dogs. Data examining the effects of dietary protein in dogs exist, but few studies provide an understanding of the dietary AA provided or the digestibility and metabolic availability of those AA when different ingredients are utilized. Furthermore, there is a dearth of data on the effects of different food processing parameters on AA bioavailability in dogs. Effects of processing are important as new regulatory requirements for food safety have been implemented. Previous estimates of AA requirements used chemically defined diets and long adaptation periods and may have resulted in AA requirements that are lower than what is required to support protein synthesis. Carbon oxidation approaches have been developed to measure AA requirements of dogs using more appropriate adaptation periods and common ingredients. In addition, secondary measures of AA adequacy, such as taurine status and immune function, also should be investigated to further optimize dietary approaches for dogs. Greater knowledge of AA requirements will lead to better overall protein quality in commercial dog food and provide a better basis for formulation of diets for canine clinical cases.

Key Words: amino acid, requirements, protein, dogs, digestibility, metabolic availability

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0437 Idiosyncrasies of amino acid metabolism in dogs and cats. D. L. Harmon*, *University of Kentucky, Lexington.*

Both the dog and cat have been domesticated for thousands of years yet they retain some unique metabolic nuances. While both are classified as members of the order carnivora they each have nutritional and metabolic requirements that differ from the majority of domestic species. The dog is considered a nutritional omnivore adapting to a wide range of foods and nutrient sources, whereas the cat is a strict carnivore showing little nutritional or metabolic adaptation with changes in diet. The cat has little ability to adapt amino acid degrading enzymes to dietary protein restriction and conservation of protein and shows little change in urea cycle activity with changes in diet. This contrasting adaptability leads to differences in the nutrient profiles required by each. In addition to requiring greater quantities of dietary protein, the cat requires a dietary source of taurine because of its obligate use of taurine for bile acid conjugation and a limited ability to synthesize taurine from sulfur amino acids. Although taurine is not strictly required in the diet of dogs, it has been suggested that taurine may be required in the diets of certain large breed dogs. Like cats, dogs also use taurine for bile acid conjugation, but they have a greater taurine synthetic ability and can adapt for use of glycine for bile acid conjugation. Both the dog and cat require a dietary source of arginine with the cat being extremely sensitive to its absence. This occurs as a result of the limited ability of cats to endogenously synthesize ornithine and citruilline to maintain urea cycle activity because of low intestinal enzyme activities compared with omnivores. The cat also has a limited ability to use tryptophan to synthesize niacin. Again this occurs from evolutionary adaptations in enzyme levels. Additional nuances include higher requirements for sulfur amino acids in the cat because of needs for hair and felinine synthesis. Overall, the cat appears somewhat unique but metabolically and nutritionally it appears similar to other strict carnivores.

Key Words: feline, companion animal

COMPARATIVE GUT PHYSIOLOGY

0438 β-hydroxybutyrate and glucose concentrations in the blood of dairy calves. F. X. Suarez-Mena*, W. Hu, T. S. Dennis, T. M. Hill, J. D. Quigley, R. L. Schlotterbeck, *Provimi, Brookville, OH.*

This research was conducted to determine how blood β-hydroxybutyrate (BHBA) and glucose are impacted by age, time of day, voluntary starter intake, stress, weaning, and intake restriction in 1- to 9-wk-old calves and to see if either is an acceptable proxy for starter intake. Male Holstein calves were fed a 27% CP, 17% fat milk replacer at 660 g DM daily to weaning on d 42, along with free-choice starter (20% CP, 41% starch) and water. Jugular blood was sampled at 0800, 1200, and 1600 h and within 5 min of sampling BHBA and glucose concentrations were estimated using test strips (Nova Max® Plus meter, Nova Biomedical). Age effects were estimated by sampling blood weekly (d 6, 13, 20, 27, 34, 41, and 48). To determine vaccination stress, a *Pasteurella* vaccine was administered after blood sampling at 0800 h on d 36. Effect of voluntary starter intake was tested by selecting calves for low and high intakes (d 35 to 39) and sampling on d 40, 41, 43, and 44. Starter intake restriction was tested by restricting intake in 6 of 12 calves and sampling on d 60 and 61. Data were analyzed using several mixed model procedures (repeated measures, regression, etc.) in SAS. Time of day did not impact blood BHBA or glucose to wk 6, but did in wk 7 ($P < 0.05$). Blood glucose was greater ($P < 0.05$) in the first 5 wk compared with wk 6 and 7. Blood BHBA increased ($P < 0.02$; $R^2 = 0.28$) and glucose decreased ($P < 0.02$; $R^2 = 0.23$) with increasing starter intake. Blood BHBA declined ($P < 0.05$) due to vaccination but glucose was unaffected. Starter intake restriction reduced BHBA for 3 d ($P < 0.05$) and glucose for 2 d ($P < 0.05$) after intake restriction. Around weaning (d 40 to 44), BHBA and glucose increased ($P < 0.05$) with increasing starter intake. Blood BHBA was positively and glucose negatively related with starter intake; however, relationships were weak, variable, and impacted by time of day, stress, and intake restriction. Over 30% of calves tested ≤ 0.2 mmol/L BHBA when consuming > 1250 g/d of starter, and test strip increments were 0.1 mmol/L which represented > 25% of the mean blood BHBA concentration. In this study, neither blood BHBA nor glucose were an acceptable proxy for estimating starter intake.

Key Words: blood β-hydroxybutyrate, dairy calves, intake

0439 Comparison of intestinal goblet cell staining methods in turkey poults. S. O. Osho*, T. Wang, N. L. Horn, and O. Adeola, *Department of Animal Sciences, Purdue University, West Lafayette, IN.*

This study compared the intestinal goblet cell density of turkey poults at two different ages using Alcian blue-Periodic acid shiff (AB-PAS) and Mucicarmine stains. Neutral mucins are stained with PAS while acidic mucins are stained with AB. Mucicarmine is specific to the mucins of epithelial origin and it is currently used for human samples, Mucicarmine may have advantages for use in animals as a result of the methodological simplicity of staining as compared with AB-PAS. Jejunum samples were taken from 80 turkey poults at 21 and 28 d, and were assigned to two treatments which consisted of AB-PAS and Mucicarmine stains in a completely randomized design. A mid-section of jejunum from each bird was taken and placed in 10% buffered formalin for 48 h, dehydrated with ethanol, cleared with Sub-X and placed in a paraffin, prepared on two slides, and then tissues were briefly cleared and hydrated. Each slide was stained with either AB-PAS reagents or Mucicarmine reagents. Goblet cell counts were taken from four villi per slide and the villi height was measured and averaged. There was no difference in the goblet cell density between the staining methods AB-PAS and Mucicarmine at 21 or 28 d post-hatching. These results show that both staining methods are viable for assessment of goblet cell density in turkey poults.

Key Words: goblet cells, jejunum, stain

0440 The development of a cecum-cannulated gnotobiotic piglet model to study the human gut microbiota. N. D. Aluthge*[1], W. Tom[2], T. E. Burkey[2], D. E. Hostetler[2], K. D. Heath[2], C. Kreikemeier[2], and S. C. Fernando[2], [1]*University of Nebraska, Lincoln,* [2]*University of Nebraska, Lincoln.*

Research conducted over the past decade using high-throughput DNA sequencing technologies have provided valuable insights into the importance of the human gut microbiota in host health and disease. Most of these studies, however, have been associative and causality of the gut microbiota in human health-associated conditions has been difficult to demonstrate due to the lack of a suitable animal model which can faithfully recapitulate the interactions between the human host and the gut microbiota. The domestic pig (*Sus scrofa*) has been used as a clinically relevant model to study various aspects of human disease and shares a high degree of anatomical, physiological, and immunological similarities with humans, thus being a potentially valuable model for human gut microbiota studies. This study was conducted with the objective of establishing human gut microbial communities in gnotobiotic piglets and to investigate the potential of using cecum cannulation as a means of obtaining microbial community samples for time series and microbial gene expression studies. Six germ-free

piglets derived using cesarean section were transferred into isolator bubbles and at 7 d of age, 3 piglets were inoculated with fecal bacteria from high body mass index (BMI > 30) human donors and the remaining 3 animals were inoculated with fecal bacteria from low BMI (BMI < 25) donors. After weaning, the piglets with the high BMI microbiota were provided a high-fat (HF) diet while the piglets with the low BMI microbiota were fed a low-fat (LF) diet. At wk 7, the high BMI microbiota piglets were cecum-cannulated and the low BMI microbiota piglets were similarly cecum-cannulated at wk 8. A cecal sample was collected from each animal immediately before surgery for use as a control for comparing cecal bacterial communities. Cecal samples were collected via the cannulae from all animals at weekly intervals until wk 10 (when the animals were euthanized). The cecal samples were sequenced using the Illumina MiSeq™ DNA sequencing platform to characterize the bacterial community composition. Comparison of the cecal bacterial communities of the cannulated piglets before surgery and at later time points revealed similar composition (PERMANOVA, $p = 0.105$), indicating no negative impact of cannulation on cecal bacterial community structure. BMI-Diet type had a significant impact on structuring cecal bacterial communities (PERMANOVA, $p < 0.001$). These results point to the potential use of cecum-cannulated humanized piglets as a model system to study the human gut microbiota.

Key Words: human microbiota, high-throughput DNA sequencing, piglet model

COMPARATIVE GUT PHYSIOLOGY SYMPOSIUM

0441 Diet, gut microbiome, brain and behavior.

J. Bienenstock*, *McMaster Brain-Body Institute, Hamilton, ON, Canada.*

The gut microbiome consists not only of bacteria but also viruses (virome) and fungi (mycobiome). There is considerable evidence that gut bacteria influence the structure and function of both the enteric and central nervous systems and that changes in the microbiome can affect mood and cognitive functions. Dietary change alters the gut bacterial content and also the virome and these are in turn associated with changes in behavior and cognition. The pathways whereby these changes occur are multiple and interacting, and we are only just beginning to understand how these occur, but their importance to animal health is undoubted. This presentation will explore how microbes effect these changes and the pathways that may be involved in so doing from lumen to brain.

Key Words: microbiome, gut-brain axis, virome

0442 Butyrate increases tight junction protein expression and enhances tight junction integrity in porcine IPEC-J2 cells stimulated with LPS.

H. Yan*[1] and K. M. Ajuwon[2], *[1]Purdue University, West Lafayette, IN, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN.*

The intestinal mucosal barrier is maintained by tight junctions, which are intercellular adhesion complexes and prevent the passage of pathogens and toxins through the paracellular space. Dysfunction of tight junctions induced by endotoxin and mycotoxin is highly associated with a variety of gastrointestinal disorders in pigs. Butyrate has been shown to possess immunological and metabolic modulatory effects in various cells and tissues. Therefore, we investigated protective effect of butyrate on cell integrity and tight junction protein expressions during LPS stimulation in porcine IPEC-J2 cells. We found that butyrate (1mM) and LPS (10μg/ml) significantly induced TNFα, IL-1β, IL-6, IL-8 and MCP1 expression ($P < 0.05$) as well as IL-8 secretion. However, although LPS upregulated TLR4 expression, butyrate downregulated it ($P < 0.01$) indicating butyrate could inactivate LPS stimulation of TLR4 pathway. Barrier integrity was investigated with trans-epithelial electrical resistance (TEER) and fluorescein isothiocyanate-dextran (FITC-dextran) uptake based tests. Treatment with LPS for 24 h significantly decreased TEER ($P = 0.01$) and increased cell permeability ($P = 0.02$). On the contrary, butyrate (1 mM) significantly increased TEER ($P < 0.01$) and decreased cell permeability ($P < 0.01$), indicating that butyrate could increase cell integrity and enhance epithelial barrier against LPS-induced damage. Butyrate also induced *Claudin-1* ($P = 0.09$), *Claudin-3* ($P < 0.01$) and *Claudin-4* ($P < 0.01$) mRNA expression, and Claudin-3 protein expression ($P < 0.05$) in a dose-dependent manner, perhaps accounting for the increase in epithelial barrier integrity induced by butyrate. Butyrate also increased ($P < 0.01$) activation of Akt by phosphorylation, whereas LPS exerted the opposite effect. Taken together, butyrate increased basal immune response and enhanced the integrity of the intestinal mucosal barrier against LPS-induced damage through an upregulation of cytokine expression and an increase in the synthesis of tight junction proteins.

Key Words: Akt, butyrate, epithelial barrier integrity, IPEC-J2 cells, tight junction protein

0443 Understanding host-microbiota interplay using nutrimetabonomics.

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Gut microbiota are now recognized as fundamental partners of the host's health. Normally, the host-microbiota symbiosis results in a healthy metabolic phenotype. But as the

environment changes, our metabolism adapts to maintain homeostasis within an optimal metabolic space, and so do our microbiota. So how does this interplay result in an optimal metabolic state? And how can this be measured? Nutrimetabonomics is a useful tool to assess the metabolic state of the host in response to environmental perturbations. Here, we will illustrate how it was used to gain new understanding of the metabolic disruptions triggered by *Brachyspira pilosicoli*-induced spirochaetosis, a common condition in poultry farms. We will discuss how a better knowledge of the host metabolic response to the pathogen, and to the antibiotic treatment, can help design new therapeutic alternatives to antibiotics.

Key Words: gut microbiota, nutrimetabonomics, host-pathogen interaction

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0444 Effects of dietary fibers on obesity related physiological parameters in C57BL/6 mice.
C. Liu, A. K. Singh, M. Stewart, J. H. Uyehara-Lock, and R. Jha*, *University of Hawaii at Manoa, Honolulu.*

Obesity, a metabolic disease resulting from an imbalance between caloric intake and expenditure, is a global concern. Studies suggest that the intake of dietary fiber improves metabolic health; however, the amount of dietary fiber and the fiber type that contribute to this improvement is unclear. This completely randomized study investigated the effect of 1.25, 2.5, and 5.0% (w/w) glucomannan or oat β-glucan in the diet versus a control diet on metabolism. Obesity related variables such as liver steatosis, and short chain fatty acid (SCFA) production was evaluated in diet-induced obese male C57BL/6 mice. Six-wk-old mice (n = 84) were fed one of 7 diets for 12 wk. On d 84, whole blood was collected and serum metabolites were analyzed. Small liver lobe portions were used to examine steatosis severity and cecum samples were analyzed for SCFA concentration. The glucomannan diets had an interaction between fiber and their inclusion levels for relative liver weight ($P < 0.05$) and percent steatosis ($P < 0.001$). The oat b-glucan diet resulted in lower serum triglyceride concentrations ($P < 0.05$), whereas including glucomannan in the diet resulted in higher acetate and propionate levels ($P < 0.05$) in comparison to the other dietary treatments. In the liver, the inclusion of 2.5 and 5% of fiber caused a decrease in microvesicular fat in comparison to the inclusion of 1.25% of fiber. This study highlights that the inclusion of glucomannan and oat β-glucan fiber in the diet at specific inclusion levels is capable of having significant effects on relative liver weight, percent steatosis, and serum triglycerides in obese mice. Glucomannan decreased the severity of mediovesicular fat, while both fibers decreased severity of macrovesicular fat. Thus, supplementing a diet with an adequate amount of specific dietary fiber may be a strategic method to reduce obesity in animals, and this may eventually be translated toward treating human obesity to reduce obesity related health issues.

Key Words: fiber, obesity, mice

0445 The gut microbiome as a regulator of physiology, brain and behavior: Implications for the treatment of stress-related disorders.
G. Clarke*[1], T. F. O'Callaghan[1,2], P. Ross[1], and C. Stanton[1], *[1]University College Cork, Cork, Ireland, [2]Teagasc Food Research Centre, Cork, Ireland.*

It has become increasingly clear that multiple aspects of host physiology are heavily influenced by the gut microbiome. Included in this remit is not just host metabolism and body composition but also a marked influence on the stress response via the hypothalamic-pituitary-adrenal axis. This is clear from studies in microbiota-deficient germ-free animals who display exaggerated responses to acute stressors that can be normalized by monocolonization with certain bacterial species including *Bifidobacterium infantis*. Also coming into focus is microbial regulation of the metabolism of tryptophan, an essential amino acid and precursor to serotonin, a key neurotransmitter within both the enteric and central nervous systems. The gut microbiota may thus be a tractable target for treating or preventing stress-related microbiome-gut-brain axis disorders and metabolic diseases. Moreover, the implications of these findings need to be considered in the context of new control points for endocrine-immune-metabolic targeting in farm and domestic animal physiology and behavior.

Key Words: gut microbiome, stress, tryptophan

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446 The microbiota-gut-brain axis: A key regulator of neural function across the life span.
J. F. Cryan*, *University College Cork, Cork, Ireland.*

The microbiota-gut-brain axis is emerging as a research area of increasing interest for those investigating the biological and physiological basis of neurodevelopmental, age-related and neurodegenerative disorders. The routes of communication between the gut and brain include the vagus nerve, the immune system, tryptophan metabolism, via the enteric nervous system or by way of microbial metabolites such as short chain fatty acids. Studies in animal models have shown that the development of an appropriate stress response is dependent on the microbiota. Developmentally, a variety of factors can impact the microbiota in early life, including mode of birth delivery, antibiotic exposure, mode of nutritional provision, infection, stress as well as host genetics. At the other extreme of life, individuals who age with considerable ill health tend to show narrowing in microbial diversity and a proinflammatory phenotype. Stress can significantly impact the microbiota-gut-brain axis at all stages across the life span. Recently, the gut microbiota has been implicated in a variety of conditions including autism, schizophrenia and Parkinson's disease. Moreover, fundamental brain processes from adult

hippocampal neurogenesis to prefrontal cortex myelination to microglia activation have been recently shown to be regulated by the microbiome. Further studies will focus on understanding the mechanisms underlying such brain effects.

Key Words: myelin, neurodevelopment, psychobiotic, stress

0447 Microbial modulation of the neonatal immune system: Lessons from infants and piglets.

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Studies from germ-free and gnotobiotic animals clearly demonstrate that basic developmental features of the mammalian immune system depend on interactions with the microbiome. The objective of this presentation is to review how early life nutrition and the microbiome influence immune development and function in the neonate. Comparative aspects between different forms of nutrition (mother-fed versus artificially reared) on systemic and mucosal immunity and findings across species (human versus piglet) will be highlighted. Briefly, our laboratory has shown that the T cell and natural killer cell repertoire and cytokine secretion profiles differ by mode of nutrition in both species. In addition, although the composition of the microbiota differs between human infants, being bifidobacteria-predominant, and piglets, where lactobacilli predominate, the microbiome composition of both species responds to mode of nutrition and the addition of prebiotics to formula. Data from our group on the impact of transfaunation of breast-fed infant microbiome into piglets on piglet gut gene expression will be presented. Lastly, findings from our laboratory showing cross-talk between the bacterial metagenome and the intestinal epithelial transcriptome of human infants using shed epithelial cells will be described. Supported by NIH grant no. R01 HD061929 and Hatch ILLU-698–311.

Key Words: microbiota, human, swine, immunity, nutrition

0448 The growing importance of defining gut "health" in animal nutrition and health.

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Optimal gastrointestinal health (effective immune status, normal and stable microbiota, absence of inflammatory state) and functionality (digestion and absorption of feed) are essential for sustainable animal production (growth, milk yield, meat and egg quality). However, while gut health is an increasingly important topic in animal nutrition, a clear scientific definition is still lacking although it has been used repeatedly in animal health. A clear definition of gut health and how it can be measured is required to monitor animal health and to evaluate the effects of any nutritional intervention on animal performance. While in human medicine gut health is often associated with the "absence of clinical diseases," this definition cannot be applied to farm animals as it is well known that animal performance can be impaired without any clinical signs of disease. Perhaps a more comprehensive definition of gut health would be "a steady state where the microbiome and the intestinal tract exist in symbiotic equilibrium and where the welfare and performance of the animal is not constrained by intestinal dysfunction." This definition combines the principal components of gut health, namely diet, effective structure and function of the gastrointestinal (GIT) barrier and normal and stable microbiota, with effective digestion and absorption of feed and effective immune status. All these components play a critical role in GIT physiology, animal health, welfare and performance. Clarity of understanding of gut health will require the characterization of the interactions between all of these components. The development of biomarkers of gut health is imperative to gain clarity of understanding of the patho-physiological events that influence the intestinal barrier, its functionality and the ecology of the GIT microbiota. While there is considerable knowledge in biomarkers that are indicative of the GIT ability to digest, absorb, transport and secrete major macro and micronutrients, a large gap in the literature exists in relation to biomarkers of GIT permeability, GIT barrier function, or biomarkers that are indicative of the functional presence of beneficial microbiota or their metabolites. Therefore, future research should focus on the establishment of a reference panel of biomarkers of gut health to be used in farm animals and address the issue of standardization of techniques and methodologies to study gut health.

Key Words: biomarkers, gut health, microbiome

0449 The microbiome and animal health.

G. B. Penner*[1], T. A. McAllister[2], S. Li[3], J. C. Plaizier[3], E. Khafipour[3], and L. L. Guan[4], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, AAFC, AB, Canada, [3]Department of Animal Science, University of Manitoba, Winnipeg, Canada, [4]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

For monogastrics, the linkage between the microbiome and animal health has been established, and it is known that colonization of the gastrointestinal tract (GIT) stimulates development of the immune system. In ruminants, the microbiome has largely been evaluated to assess the potential contribution

toward feed digestion and adaptive responses as a consequence of dietary change. For example, previous research has shown a positive relationship between the Firmicutes:Bacteroidetes ratio and milk fat yield, and that the abundance of Clostridiales (family VIII) is negatively associated with feed conversion. A positive association for the systemic acute phase response caused by a severe form of subacute ruminal acidosis and the prevalence of *Escherichia coli* in the rumen has also been reported. Separating cause and effect continue to be a challenge with this area of research. The ruminal microbiome is responsive to diet and changes are particularly evident when comparing high-forage and high-grain feeding scenarios. That said, there is evidence to suggest that the microbial community is relatively resistant to change and can revert back to a composition similar to the original community structure after being disturbed. The microbiome robustness presents a challenge when modifications to the community structure may be desired. Moreover, differences between the digesta associated versus mucosa and epithelia associated communities are present and these communities change throughout the GIT. While understanding the rumen microbiome is important, more distal regions of the GIT have not been thoroughly examined. The change in microbial community structure along the GIT may not be that surprising given changes in retention time and substrate availability. In addition, microbial-host crosstalk mechanisms may differ among regions helping to explain why the microbial community structure differs. Understanding the regulation of the microbial-host communication may provide the necessary information to develop practical strategies to modulate the microbial community structure. Accordingly, evaluating strategies to manipulate microbial colonization and succession in pre-ruminants appears to be a logical intervention strategy. In addition to the core microbiome, diversity of the microbiome appears to be a critical aspect and calves that develop scours have been reported to have lower diversity when evaluating the fecal microbiome. Thus, a systematic approach to improve our understanding of the relationship between microbiome, or at least key species, is needed to advance this area. Such research will require an in depth understanding of both the microbiome and host gastrointestinal physiology.

Key Words: gastrointestinal tract, microbiome, cattle

0450 In vitro fermentation characteristics of agricultural products and coproducts and its effect on the large intestinal microbiota of swine.

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Dietary fibers and resistant starches are fermented in the gastrointestinal tract (GIT) and alter the microbial community. Specific microbes in the GIT are found to promote host health, the microbial population is also dependent on the type of fermentation substrates available in the GIT. Alternative feedstuffs are explored and evaluated to contribute in reducing feed costs of swine. These feedstuffs are typically rich in fiber and/or resistant starches which may provide prebiotic effects for the pigs. Six alternative feedstuffs were evaluated for their fermentation characteristics and effect on the microbiota of the large intestine of swine using an in vitro model. Three fibrous (macadamia nut cake, MNC; barley brewers grain, BBG; wheat millrun, WMR) and three starchy (Okinawan sweet potato, OSP; yam, and taro) feedstuffs along with inulin and blank as a positive and negative control, respectively were used in this study. After two-step enzymatic digestion assay, residues were fermented using fresh pig feces as microbial inoculum and gas production were recorded periodically. The residue after 72 h of microbial fermentation was used for genomic DNA isolation. The V3 region of the 16S rDNA of the genome was amplified using bacterial primers and the product used to generate banding profiles via temperature gradient gel electrophoresis (TGGE). The unique profile created by each sample was analyzed, and compared with determine similarities between samples. The fibrous feedstuffs (MNC, BBG and WMR) were most closely related to each other, and to inulin, indicating they may cause a health-promoting shift in the microbial community as inulin. The starchy feedstuffs (OSP, yam and taro) also showed similarities to each other, but were less related to inulin, with the exception of OSP, which had a similar profile to inulin. The MNC was least similar to the starchy feedstuffs. Total gas production of OSP (298), inulin (291) and taro (276) were significantly higher ($P < 0.01$) than MNC (87) and BBG (75 mL/g sample). In conclusion, some of the alternative feedstuffs tested may exert comparable prebiotic effects to inulin, thus may be included in swine diets to favorably impact the GIT microbiota.

Key Words: coproducts, fermentation, gut microbiota

0451 Analysis of the gut microbiome in beef cattle and its association with feed intake, growth, and efficiency.

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Next-generation sequencing has taken a central role in studies of microbial ecology, especially with regard to culture-independent methods based on molecular phylogenies of the small-subunit ribosomal RNA gene (16S rRNA gene). The ability to relate trends at the species or genus level to host/environmental parameters using 16S profiling has proven powerful. Within the rumen and lower gastrointestinal tract (GIT), the diverse microbial ecosystems present are essential for the host to digest plant material and regulate nutrient uptake and utilization. Their examination utilizing next-generation technologies has been instrumental to aid in the understanding of

the microbial-associated interactions throughout the gut with intake, growth, and feed efficiency. Using a feed efficiency design in which steers were selected from two contemporary groups and were ranked based on their standardized distance from the bivariate mean (ADG and ADFI), four steers with the greatest deviation within each Cartesian quadrant were sampled (n = 16/group; 2 groups) to examine the association of the microbiome throughout the gut with ADG, average daily DMI (ADFI), and feed efficiency. In addition, phylogenetic analyses of the ruminal bacterial community were compared based on varying sequencing technologies, 16S variable region selection, and short read 16S amplicons, near full-length 16S amplicons, and metagenomic sequence. In all studies, although no differences in bacterial diversity and richness metrics were revealed among the quadrants, finer changes in the relative abundance of microbial populations and operational taxonomic units did reveal differences between feed efficiency groups ($P < 0.05$), suggesting throughout the GIT, the microbial communities differ at the 16S level in cattle that vary in ADG, ADFI, and feed efficiency. However, additional phylogenetic analyses on the rumen bacterial community demonstrated that utilizing near full-length 16S reads may be useful in conducting a more thorough study, or for developing a niche-specific database to utilize in analyzing data from shorter read technologies when budgetary constraints preclude use of near-full length 16S sequencing. Partially funded by National Institute of Food and Agriculture Grant no. 2011–68004–30214, National Program for Genetic Improvement of Feed Efficiency in Beef Cattle.

Key Words: feed efficiency, microbiome, 16S rRNA

CONTEMPORARY AND EMERGING ISSUES SYMPOSIUM: COMMUNICATING ANIMAL SCIENCES EFFECTIVELY

0452 Public perceptions of animal-sourced genetically modified food products. W. K. Hallman*, C. L. Cuite, and X. K. Morin, *Rutgers University, New Brunswick, NJ.*

The success of agricultural biotechnology depends as much on consumer acceptance of Genetically Modified (GM) products as it does on the ability to create them. To explore public perceptions of GM food products, we surveyed a nationally representative sample of 1148 American adults during October 23–27, 2013. The data was collected by GFK Knowledge Networks from an internet panel recruited using proportional random sampling. The data was weighted to project to the U.S. population, and has a margin of error of ± 3%. The results show that despite the ongoing controversy over GM foods, 50% of Americans report having heard or read little or nothing about them, 55% report that they know very little or nothing at all about them, and two-thirds (66%) say they have never discussed the issue of GM foods with anyone. Estimates are that 75% of processed foods in the U.S. contain ingredients derived from GM crops. However, only 43% of Americans say that they believe that there are foods containing GM ingredients in supermarkets right now, while 4% say there are no such foods in U.S. supermarkets, and 51% say they don't know. Many of those who believe that there are GM foods in the supermarket are confused about which products are available. For example, while 75% correctly believe that there are products in U.S. supermarkets containing GM corn, and 59% correctly believe that there are products containing GM soy, nearly as many (56%) believe that GM tomatoes, GM Wheat (55%), and GM Chicken (50%) products are available and 35% believe that GM salmon are currently for sale. Moreover, even though GM food products have been on the market in the U.S. for more than two decades, only 26% of Americans believe that they have ever eaten a food containing GM ingredients. Yet, while most Americans say they have heard and read little about GM foods, know little about them, have never had a conversation about them, don't believe they are currently in the supermarket, and don't believe they have ever eaten them, most are willing to express an opinion about the acceptability of GM food products. When asked directly, only 10% of consumers say they approve of GM animal-sourced food products, 44% say they disapprove of them, and 43% neither approve nor disapprove of them, or are unsure. However, there is much greater public acceptance expressed when specific product benefits are described.

Key Words: public perceptions, genetically modified, animal-sourced foods

0453 What is the science of science communication for? And why should animal scientists care? D. Kahan*, *Yale Law College, New Haven, CT.*

The source of nearly every science-communication misadventure can be traced to a single mistake: the confusion of the processes that make science valid for the ones that vouch for the validity of it. The scientific knowledge that individuals rely on in the course of their everyday lives is far too voluminous, far too specialized for any—including a scientist—to comprehend or verify for herself. So how do people manage to pull it off? What are social cues they rely to distinguish the currency of scientific knowledge from the myriad counterfeit alternatives to it? What processes generate those cues? What are the cognitive faculties that determine how proficiently individuals are able to recognize and interpret them? These questions not only admit of scientific inquiry; they demand it. Unless we understand how ordinary members of the public ordinarily do manage to converge on the best available evidence, we will never fully understand why they occasionally do not, and what can be done to combat these noxious sources of ignorance. I will discuss these basic themes and relate them to the stake that the animal science community has in the

advancement of the new science of science communication.

Key Words: science communication

0454 Cracking the code: Making complex information understandable. A. Perry*, *The Center for Food Integrity, Gladstone, MO.*

Consumer beliefs do not always align with the scientific consensus. Consumers may not accept an idea even though science says it is true. Consumers do not fully understand the science that individuals in animal agriculture find so simple. Our challenge is to find better ways to bridge the communication gap by using shared values to earn consumer trust. In partnership with Iowa State University, CFI was the first to build a research-based consumer trust model. Our peer-reviewed and published model for building consumer trust in today's food system shows that shared values are more important than skills and technical expertise in building consumer trust. The social decision-making process is complex. Building trust is step one. Explaining the complex scientific concepts around animal agriculture is step two. The ability to break down existing communication barriers is critical to fostering informed decision making that leads to consumer confidence.

Key Words: consumers, complex, communication, food

0455 Communicating animal science effectively. D. R. Williams*, *National Cattlemen's Beef Association, Centennial, CO.*

Having spent the past 25 yr of my career helping companies and organizations communicate during crises ranging from Alar in apples to Pink Slime in ground beef, I have learned a number of lessons about what works and does not work in communicating science effectively. The first lesson is to not lead with science! People react to issues that could impact their family's health and well-being with emotion. Responding with facts and figures is unlikely to calm their fears. So the first step in communicating effectively is to acknowledge their concerns, whether you believe they are rational or not. By acknowledging that their concerns are legitimate you open the door to sharing factual information. I have a formula for responding effectively I call the "Two Cs." We care, and we're capable. We care about the same things they do: the safety of our food, the care of animals, the future of our planet and the health and well-being of our families. Once you have established that common ground, you can focus on addressing differing viewpoints on the "facts" of the matter. In this panel discussion I will share real-life examples of how this technique has been used to communicate animal science effectively.

CSAS GRADUATE STUDENT ORAL COMPETITION I

0456 Ensiling barley varieties selected for varied levels of in vitro NDF degradability. N. G. Preston*[1,2], J. Nair[1], P. Yu[1], D. A. Christensen[1], J. J. McKinnon[3], and T. A. McAllister[4], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, Agriculture and Agri-food Canada, AB, Canada, [3]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [4]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, AB, Canada.*

This study characterized the ensiling traits and digestibility of three barley varieties ranked for in vitro NDF degradability (NDFD). CDC Cowboy (H-NDF), CDC Copeland (I-NDF), and Xena (L-NDF) were ranked as high, intermediate, and low NDFD based on commercial silage samples ($n = 80$) collected over 2 yr. Barley varieties were planted the same day in one location and ensiled at the mid-dough stage in replicated mini or bunker silos. Silos were opened after 60 d of ensiling for chemical and microbial analysis. Silage from mini silos was exposed to air with temperature continuously measured and samples collected at 3, 7, 14, and 21 d. Silage was collected periodically from bunker silos during feed out. In vitro NDFD after 30 h of incubation in rumen fluid was estimated for silage collected after 60 d. Data were analyzed using the Proc Mixed procedure of SAS as a complete randomized design with fixed effect of variety and ensiling method, and random effect of silo within variety, and day as a repeated measure for aerobic stability. In vitro NDFD did not differ among varieties. Terminal pH was lowest ($P < 0.01$) for H-NDF in mini silos. The pH of H-NDF was higher ($P < 0.01$), and I- and L-NDF lower ($P < 0.01$) in bunker than mini silos. Lactate and acetate levels were higher ($P < 0.05$) in H-NDF mini silos, with acetate levels of all varieties being lower ($P < 0.01$) after ensiling in mini silos as compared with bunker silos. Day 60 I-NDF in mini silos had higher ($P < 0.01$) ADF and NDF levels, with method of ensiling affecting fiber levels ($P < 0.01$) with increased ADF and NDF in H-NDF and L-NDF in bunker as compared with the mini silos. The H-NDF silage was less aerobically stable than other silages as reflected by increasing ($P < 0.01$) temperature and pH ($P < 0.05$) and decreased levels of lactic acid ($P < 0.05$) and water-soluble carbohydrates ($P < 0.01$) over the exposure period. Using in vitro NDFD of field silage to select barley silage varieties for improved fiber digestibility proved difficult due to the effects of time of harvest and the fermentation process on this trait.

Key Words: barley silage, NDF degradability, aerobic stability0

457 Characterization of the variation in the daily excretion of fecal constituents and digestibility predictions in beef cattle fed feedlot diets using near infrared spectroscopy. L. J. Jancewicz*[1,2], G. B. Penner[3], M. L. Swift[4], J. J. McKinnon[1], C. L. Waldner[5], and T. A. McAllister[2], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, AB, Canada, [3]University of Saskatchewan, Saskatoon, Canada, [4]Hi-Pro Feeds, Okotoks, AB, Canada, [5]Department of Large Animal Clinical Sciences, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Canada.*

The 24-h variation in fecal nutrient excretion and accuracy of digestibility predictions using spot samples collected from feedlot cattle were evaluated using near infrared spectroscopy (NIRS). Six heifers were individually housed and randomly assigned to one of two feeding frequencies; once per day (0900), or twice per day (two equal feedings at 0900 and 1700), first over a backgrounding period, followed by a finishing period. Heifers were fed the backgrounding diet for 21 d, transitioned to the finishing diet over 20 d, which was fed for 21 d. During the last 4 d of both periods, total fecal collections were conducted at 4-h and 4-d-24-h intervals and NIRS calibrations were used to predict fecal organic matter (OM), starch, nitrogen (N), neutral detergent fiber (NDF), acid detergent fiber (ADF) and acid detergent lignin (ADL). Estimated total tract digestibility (eTTD) using NIRS predicted fecal nutrients and ADL and apparent total tract digestibility (aTTD) of DM, OM, starch, NDF, and ADF determined using previously derived NIRS calibrations were calculated at each 4-h interval as well as over 4 d. Fecal DM (%), NDF, and ADF varied among 4-h interval samples in the backgrounding period, and fecal DM, starch, NDF, ADF, and ADL varied in the finishing period. Fecal starch was able to predict aTTD during both feeding periods (backgrounding: R2 = 0.96, $P < 0.01$; finishing: R2 = 0.98, $P < 0.01$). Most 4-h interval samples could be used to predict eTTD of nutrients and aside from starch in the finishing period, there were no differences for eTTD using fecal samples collected at any of the 4-h intervals versus those collected over 4 d. The NIRS calibrations for predicting aTTD coefficients using the 4-h interval samples or the 4 d-24-h composite were least accurate for NDF and ADF. Spot fecal samples collected at any time point from multiple cattle have potential to predict digestibility. However, timing of sampling after feeding must be standardized to predict starch digestibility during the finishing period, with samples between 0–4 h and 8–16 h generating estimates of both starch concentration and digestibility that were closest to that derived from 4-d-24-h composite samples.

Key Words: fecal nutrients, fecal starch, 24-h variation, feedlot cattle, near infrared spectroscopy

0458 Effect of energy substrate and days on feed on plasma insulin response in finishing beef heifers. F. Joy*, K. M. Wood, and G. B. Penner, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to determine the effect of dietary energy source and days on feed (DOF) on plasma insulin concentration and insulin responsiveness when subjected to an arterial glucose challenge. Eight heifers were randomly allocated to 1 of 2 finishing diets consisting of a barley-based control (CON; $n = 4$; 75.2% barley grain, 6% barley silage, 9.8% canola meal and 9% vitamin and mineral supplement on a DM basis) or a diet where a high-lipid byproduct-pellet replaced 60% of the barley grain and canola meal relative to CON (HLP; $n = 4$). Diets were formulated to be iso-caloric and iso-nitrogenous, but the CON had greater starch (46.6 vs. 39.5%) and lower ether extract (3.8 vs. 5.7%) than HLP. The 160-d study period was divided into four 40-d periods (P1, P2, P3, and P4). On the final day of each period, 7.57 mmol/kg $BW^{0.75}$ of dextrose was infused and the insulin response was analyzed in plasma collected at 0, 5, 10, 15, 20, 25, 30, 45, 60, 90, and 120 min post-infusion. Data were analyzed using a mixed model (fixed effects of treatment, period, and the treatment × period interaction). Period was included as a repeated measure. The 12-h fasting plasma insulin concentration did not differ ($P = 0.40$) between the treatments averaging 1.51 μg/L. However, insulin concentration increased from P1 (1.17 μg/L; $P < 0.01$) to P3 (1.81 μg/L) and P4 (1.60 μg/L) with the latter not differing. Area under the curve for insulin following the glucose challenge tended ($P = 0.08$) to increase with DOF, but did not differ by diet. The peak insulin concentration following the glucose challenge increased from 8.42 during P1 to 11.3 μg/L during P3 ($P = 0.048$) and the time to attain the peak tended to increase ($P = 0.09$) with DOF, but was not affected by treatment ($P > 0.1$). A tendency ($P = 0.07$) for a treatment × period interaction was observed for peak insulin concentration with HLP attaining a greater peak than CON in all periods except P2. The results of this study indicate that insulin concentration and the insulin insensitivity to a glucose challenge in growing beef heifers increase with advancing DOF and this increase is independent of energy substrate fed. Increasing insulin resistance may be one factor leading to reduced energetic efficiency associated with advancing DOF in finishing cattle.

Key Words: beef, insulin, finishing

0459 Effect of digestible fiber content of barley silage on lactation performance and chewing activity of lactating dairy cows in comparison with corn silage. B. Refat[*1,2], D. A. Christensen[3], J. J. McKinnon[4], J. Nair[1], A. D. Beattie[5], T. A. McAllister[6], W. Yang[7], and P. Yu[1], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]Animal Production Department, Faculty of Agriculture, Zagazig University, Egypt, [3]University of Saskatchewan, Saskatoon, Canada, [4]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [5]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Canada, [6]Lethbridge Research and Development Centre, AAFC, AB, Canada, [7]Lethbridge Research and Development Centre, AAFC, AB, Canada.*

There is a limited knowledge on evaluating barley silage with different digestible fiber content on dairy cow performance. The objective of this study was to evaluate the effects of barely silage varieties selected for varying rates of in vitro NDF digestibility on DM intake (DMI), milk production, and total chewing activity of high-yield dairy cows in comparison with corn silage. Four early lactating multiparous Holstein cows (average body weight = 703 ± 78 kg; days in milking = 101 ± 25; parities = 2.75 ± 0.83) were used in a 4 × 4 Latin square design. The cows were fed diets that contained 49% barley-based concentrate and 51% forage (DM basis). The forage consisted of 10% alfalfa hay and 41% silage. The four whole plant silages were: corn silage (P7213R), CDC Cowboy barley silage, CDC Copeland barley silage, and Xena barley silage. The diets were formulated to meet the nutrient requirements by lactating dairy cows producing 40 kg of milk using NDS software. The in vitro 30 h NDF digestibility (NDFD) of CDC Cowboy, CDC Copeland and Xena varieties were 37, 31, and 29%, respectively. The experiment consisted of 18 d of adaptation and 5 d of data collection. Statistical analyses were performed using PROC MIXED procedure of SAS 9.4 with significance declared at $P < 0.05$. The results indicate that barley silage variety did not influence DMI, milk production and chewing activity ($P > 0.1$). The CDC Cowboy with higher NDFD did not result in an improvement in milk yield (averaged 35.3 ± 1.71 kg/d, $P > 0.1$), feed efficiency (averaged 1.37 ± 0.07 DMI/milk yield, $P > 0.1$), and total chewing activity (averaged 892 ± 23 min/d, $P > 0.1$) compared with other barley silage varieties. Cows fed the corn silage had similar DMI (averaged 26.3 ± 1.4 kg/d, $P > 0.1$) but produced more milk than those fed barley silage (40.1 vs. 35.3 ± 1.71 kg/d, $P < 0.05$). As a result, the cows fed corn silage had improved feed efficiency compared with those fed barley silage (1.57 vs. 1.37 ± 0.07 DMI/milk yield, $P < 0.05$). The results of this study indicate that feeding barley silage with higher digestible fiber content does not necessarily result in greater milk production performance. However, feeding corn silage has potential to produce more milk and better feed efficiency compared with barley silage.

Key Words: fiber digestibility, chewing activity, milk yield

0460 Daytime pasture vs. free-stall barn access: What do dairy cows with year-long outdoor experience prefer? E. R. Shepley[*1], E. Vasseur[2], and R. Bergeron[3], *[1]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [2]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [3]University of Guelph, ON, Canada.*

Provision of regular exercise to dairy cows is a topic that has received an increasing amount of interest in recent years. Pasturing cows not only addresses the current issue of restricted movement found in many production units, but also has positive effects on health and welfare. The objective of the current study was to investigate cow preference for day-pasture access or a free-stall barn under Eastern Canadian summer climatic conditions. Two important components were introduced in the current study: the use of a herd with year-round outdoor experience and the provision of the same feed options (fresh forage and silage) inside and on pasture. Thirty-two lactating organic Holstein cows were submitted to a 6-d preference cycle comprised of three 2-d phases. Cows were restricted to a free-stall barn (forced-indoor), restricted to pasture (forced-outdoor), or provided the choice between staying in a free-stall barn or going to pasture (free-choice) for a 7-h period in between morning and evening milking. Live observations of activities (feeding from the feeder, grazing, lying down, and other) were conducted every 2 min by scan sampling during the forced-outdoor and choice phases. A group level *t* test was used to test whether preference of cows to be outdoors differed from 0% (choice to stay in free-stall), 50% (indifference), and 100% (choice to go to pasture). An independent 2-sample *t* test was used to compare time spent in conducting the observed activities inside to those outside. Cows spent more time at pasture when provided the choice (range h 1 to h 6 across wk: 68.4 to 87.4%), displaying partial preference for the outdoors in h 1, and h 3 to h 6 (difference from 0%; $P < 0.01$) and complete preference for outdoor in h 2 (difference from 0 and 50%; $P < 0.01$), when the percentage of cows choosing to be outside was the highest. Cows conducted the same levels of activities on pasture as in the free-stall barn ($P > 0.05$), with cows grazing more than eating silage from the feeder on pasture (33.1 vs. 10.2%, respectively) and eating fresh forage over silage when indoors (33.6 vs. 4.2%, respectively). This study showed that when provided with year-long outdoor access, dairy cows

chose day-time pasture access over free-stall barn, and freshly-cut forage or pasture over silage.

Key Words: dairy cow, preference test, outdoor access

0461 Can regular exercise and more comfortable stalls improve cleanliness and lameness in tie-stall dairy cows? S. Palacio*[1,2], S. Adam[3], R. Bergeron[4], D. Pellerin[5], A. M. de Passillé[6], J. Rushen[6], D. B. Haley[7], T. J. DeVries[8], and E. Vasseur[1], *[1]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [2]McGill University, Ste.-Anne-de-Bellevue, QC, Canada, [3]Valacta, Ste.-Anne-de-Bellevue, QC, Canada, [4]University of Guelph, ON, Canada, [5]Universite Laval, Quebec, Canada, [6]Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada, [7]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Canada, [8]Department of Animal Biosciences, University of Guelph, ON, Canada.*

Tie-stall dairies are still one of the major housing systems around the world and with growing industry requirements to meet animal welfare standards, providing options to help producers meet these animal welfare standards is a priority. The objective of the study was to evaluate how minor stall modifications and/or regular exercise (access to pasture and winter exercise) affected the welfare of Holstein cows housed in tie-stalls. Twenty lactating cows/farm on 12 tie-stall farms were visited and assessed 4 times over 1 yr. Visit 1 was conducted toward the end of the pasture season, visit 2, 9–30 d after modifications were applied, visit 3, toward the end of the winter, and visit 4, 1 yr after visit 1. Stall modifications were applied to half of the study cows on each farm with most modifications being a re-adjustment of the tie-rail. Assessments of animal welfare consisted of animal and housing-based measures, as well as a management questionnaire. Farms were separated on whether they provided exercise (Exc) or not, as well as cows that were kept on modified (Mods) stalls or in unmodified stalls; differences in cow cleanliness, BCS and lameness were analyzed with a mixed model. Farm was nested in Exc and was included as a random effect and Exc, Mods and their interaction were treated as fixed effects. On visit 2 (in winter) 20% more cows had dirty udders when kept in modified stalls with exercise compared with unmodified stalls with exercise (30 vs. 10% respectively, $P < 0.05$). On visit 3, there were 20% fewer lame cows in the herds with exercise (18%) compared with herds with no exercise (38%) ($P < 0.05$). On visit 4, there were 9% more cows with dirty udders in modified stalls (16%) compared with unmodified stalls (7%) ($P < 0.05$). Results show that exercise can have a beneficial effect on lameness, especially during the winter months, and that modifications intended to improve stall comfort might cause some increase in cow dirtiness. However, this increase in dirtiness must be weighed against the potential benefits of a providing dairy cows with more adequate and comfortable stalls.

Key Words: regular exercise, tie-stall improvement, dairy cow

0462 *Saccharomyces cerevisiae* boulardii improves acute phase response and phagocytosis during weaning in dairy calves. B. Fomenky*[1,2], J. Chiquette[1], P. Y. Chouinard[3], and É. M. Ibeagha-Awemu[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada, [2]Département des Sciences Animales, Université Laval, Québec, Canada, [3]Département des Sciences Animales, Université Laval, Québec, Canada.*

The use of direct fed microbials (DFM) as alternatives to antibiotic growth promoters in farm animal production continues to stimulate research and commercial interest. During the early period of life, inadequate immune development and weaning stress contributes to increase susceptibility to infectious diseases in calves. Currently, it is less clear how DFM elicit acute phase immune response in calves. This study aimed to investigate the effect of *Saccharomyces cerevisiae* and *Lactobacillus acidophilus* on acute phase response and phagocytosis during the early period of calf growth.

Forty eight Holstein calves (2–7 d old) were grouped according to body weight and circulating IgG and randomly assigned to four treatments as follows; Control (CTRL)-fed milk replacer with starter diet introduced gradually in the third week of the experiment; CTRL supplemented with *Saccharomyces cerevisiae boulardii CNCM I-1079* ($7.5x10^9$ cfu/L milk replacer + $3x10^9$ cfu/kg feed) (SCB); CTRL supplemented with *Lactobacillus acidophilus BT1386* ($2.5x10^8$ cfu/L milk replacer + $1x10^9$cfu/kg feed) (LA); and CTRL supplemented with tetracycline (528 mg/L milk) and neomycin (357 mg/L milk) before weaning and chlortetracyclin (55 mg/kg) after weaning (ATB). After weaning calves received hay in addition to starter diet and their respective treatments. Serum samples on experiment d 29 and 43 (pre-weaning), 46, 49, 51, and 54 (weaning) and 58 and 65 (post-weaning) were used for measurements of C-reactive protein and haptoglobin. Likewise, polymorphonuclear neutrophils (PMN) were isolated from plasma on d 15 and 43 (pre-weaning), 47 and 54 (weaning), 59, 66, and 87 (post-weaning), stimulated with lipopolysaccharide and phagocytosis beads pH rhodo Green *E. coli* bio particles. Phagocytosis was then measured using flow cytometry. The effects of treatments were analyzed using a complete randomized block design with repeated measures and PROC MIXED of SAS with Tukey adjustments for multiple comparisons.

Serum concentrations of C-reactive protein and haptoglobin in SCB-treated calves increased during weaning (d 54; $P < 0.05$) when compared with CTRL, LA and ATB-treated calves. Concentrations of C-reactive protein tended to increase on d

65 (post weaning; $P < 0.10$) with SCB compared with CTRL or ATB. The PMN from calves on SCB increased ($P < 0.05$) phagocytosis during weaning (d 47) as compared with CTRL.

Data show that SCB has immunomodulatory effects in calves and a possible role in enhancing innate immune and inflammatory responses of calves during the critical stress period of weaning. Direct fed SCB might play a role in innate immunity as an early defense system against infections in calves.

Key Words: calf, *Saccharomyces cerevisiae*, C-reactive proteins, haptoglobin, innate immunity

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0463 Effect of lipid supplementation and type of lipid on fatty acid composition of the ruminal epithelium and short-chain fatty acid transport.

A. C. Verdugo* and G. B. Penner, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to evaluate the effect of lipid supplementation and the type of lipid on the fatty acid (FA) composition of the ruminal epithelium and short-chain fatty acid (SCFA) transport. Twenty-one Holstein steers (194 ± 10.7 kg) were blocked by BW and randomly assigned to 1 of 3 treatments differing in FA supply and composition. The control treatment (CON) contained 2.9% ether extract whereas the FA treatments contained 6.2% ether extract with the lipid coming from saturated (SAT; tallow and palmitic acid) or unsaturated sources (UNSAT; flax and Megalac). All calves were fed at 3% BW on a DM basis. After a 30-d feeding period, steers were killed and samples of the ruminal tissue were collected for FA analysis and to evaluate SCFA uptake and flux in Ussing chambers. Data were analyzed as a randomized complete block design using a mixed model with orthogonal contrasts to evaluate the effect of FA supplementation and the type of the FA supplement. There was a tendency for increased FA concentration in ruminal tissue for supplemented calves ($P = 0.10$), and SAT calves tended to have less FA than UNSAT (15.1 vs. 20.1 g/100 g; $P = 0.06$). Ruminal tissue from SAT had a tendency for greater monounsaturated FA (37.5 vs. 32.0; $P = 0.08$) and had less polyunsaturated FA (17.0 vs. 23.0; $P = 0.03$) than UNSAT. The changes in major FA classifications were largely due to an increase for C16:0 (25.2 vs. 24.2%; $P = 0.02$), decrease in C16:1 (1.65 vs. 10.32%; $P = 0.02$), and a decrease in EPA (0.19 vs. 0.38; $P < 0.01$) for SAT relative to UNSAT. Acetate uptake was not affected by FA supplementation ($P \geq 0.25$), but providing supplemental FA increased propionate [0.61 vs. 0.37 nmol/(cm2 × min); $P = 0.05$] and butyrate uptake [0.82 vs. 0.45 nmol/(cm2 × min); $P = 0.03$)] by the ruminal epithelium. Moreover, feeding SAT increased butyrate uptake relative to UNSAT [1.06 vs. 0.59 nmol/(cm2 × min); $P = 0.01$)]. There was a tendency for an increase in propionate flux across the ruminal epithelium with FA supplementation [0.65 vs. 0.56 μ mol/(cm2 ×h)], but there were no differences between SAT and UNSAT. The results from this study indicate that providing supplemental FA may alter ruminal epithelial FA composition and enhance SCFA transport relative to non-supplemented calves.

Key Words: short-chain fatty acid, absorption, palmitic

0464 Degradation kinetics and bypassed nutrients of value added pellet products based on combination of new co-products from bio-fuel/bio-oil processing, low grade of peas, and lignosulfonate chemical compound at different levels for ruminants.

V. Guevara*, D. A. Christensen, J. J. McKinnon, and P. Yu, *Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

New co-product, carinata meal, from bio-fuel processing is ready to be used as animal feed nowadays. Conventional co-product, canola meal, has high levels of methionine and cysteine, but limiting in lysine. Low grade of peas contains high starch content and also has high levels of lysine and tryptophan. There is little information available on nutrient profile, as well as degradation kinetics, especially when it blends with other feedstuff as a pellet. The aim of this project was to test and develop eight high value added pellet products (BPP) based on combination of co-products from bio-fuel/bio-oil processing, low grade of peas and lignosulfonate at different levels for ruminants. Statistical analyses were performed using PROC NLIN and PROC MIXED procedures of SAS 9.4 with significance declared at $P < 0.05$. The results showed that BPP1 (low level of carinata meal, high level of peas and no lignosulfonate), BPP2 (low level of carinata meal, high level of peas and lignosulfonate), BPP5 (low level of canola meal, high level of peas and no lignosulfonate), BPP6 (low level of canola meal, high level of peas and lignosulfonate) and BPP8 (high level of canola meal, low level of peas and lignosulfonate) had the higher rate of degradation (Kd) ($P < 0.05$). There were no significant differences between all blend pellet products (BPP) on soluble fraction in situ (S), insoluble but potentially degradable fraction in situ (D) and undegradable fraction in situ (U) ($P > 0.10$). BPP3 (high level of carinata meal, low level of peas and no lignosulfonate), BPP4 (high level of carinata meal, low level of peas and lignosulfonate) and BPP7 (high level of canola meal, low level of peas and no lignosulfonate) and BPP8 had the higher rumen undregradable dry matter (BDM) ($P < 0.05$); while BPP1, BPP2, BPP5 and BPP6 had the higher effective degradability of dry matter (EDDM) ($P < 0.05$). In conclusion pellet products with high level of co-products had the higher rumen undegradable dry matter. Further study on intestinal digestion of nutrients is needed.

Key Words: canola, carinata, lignosulfonate

0465 The different effects of ferrous glycine chelate and ferrous sulfate to intestinal porcine epithelial cells. Z. Zhuo*, *College of Animal Science, Zhejiang University, Hangzhou, China.*

This study was conducted to investigate the effects of ferrous glycine chelate and ferrous sulfate on cell proliferation and gene expression of iron related transporters in intestinal porcine epithelial cells (IPEC-J2). When IPEC-J2 cells covered 80~90% of the Petri dish, they were treated with different concentration of $FeSO_4$ and Fe-Gly (0, 50, 100, 200 μ mol/L as the low concentration; 16,000, 32,000, 64,000, 128,000 as the high concentration) for 12 h and 2 4h to determine the cell survival rate. Besides, IPEC-J2 cells were also treated with $FeSO_4$ and Fe-Gly (50 μ mol/L as iron) for 2 h, and then quantitative Real-time PCR was applied to detect the mRNA expression of DMT1, FPN1, Dcytb and PepT1. The results showed that both $FeSO_4$ and Fe-Gly nearly have no toxicity to cells in low concentration; however, high concentration of iron solution could significantly affect cell survival. The influence on cell viability caused by $FeSO_4$ was more obvious in high concentration compared with Fe-Gly. The qRT-PCR results revealed that Fe-Gly had significant lower expression of DMT1, FPN1 and Dcytb than FeSO4 ($P < 0.05$), while there was no difference on the expression of PepT1. For the physiological function of Dcytb, DMT1 and FPN1 are related with iron ions transportation, it reminded us that $FeSO_4$ may own more free iron ion than Fe-Gly in the same concentration. Fe-Gly had a better stabilization than FeSO4, which means it can prevent iron toxicity to cell when in a high concentration.

Key Words: ferrous glycine chelate, ferrous sulfate, IPEC-J2, cell proliferation, gene expression

0466 The effect of SNPs in the promoter on expression of CYP2E1 gene and boar taint. H. E. Archer*[1], M. Jafarikia[2], B. Lillie[3], F. Schenkel[2], and E. J. Squires[1], *[1]Department of Animal Bioscience, University of Guelph, ON, Canada, [2]Center for Genetic Improvement of Livestock, University of Guelph, ON, Canada, [3]Department of Pathobiology, Ontario Veterinary College, Canada.*

Boar taint, an unfavorable odor detected in the meat of intact male pigs, is caused by the accumulation of two compounds: androstenone and skatole. Despite mounting welfare concerns, surgical castration of all male piglets is still the most common control method in production systems. The need for new methods to control boar taint is therefore a necessity. Genetic selection represents one such alternative. Among the genes known to be involved in boar taint metabolism, CYP2E1 has repeatedly proven influential. The aim of this study was to identify SNPs within the CYP2E1 promoter affecting gene expression and boar taint. Genotypes were obtained from a previously developed list of 7 single nucleotide polymorphisms (SNPs) on 66 boars from three major swine breeds: Duroc, Landrace and Yorkshire. RNA was isolated from liver tissue and quantitative PCR was performed to measure CYP2E1 gene expression. Association analysis was run correlating genotype and CYP2E1 expression (ΔCT) using PROC GLM (SAS Version 9.4). Weight was included as a fixed effect. The effect of breed, androstenone and skatole concentrations on CYP2E1 expression were also tested. All SNPs had a MAF > 0.05. Results indicated that 1 SNP within the CYP2E1 promoter was significantly associated with CYP2E1 expression at $\alpha < 0.05$. An additional 3 SNPs demonstrated association at $\alpha < 0.10$. While weight was significantly associated with gene expression, breed was found to have no effect. Significant within breed variation in CYP2E1 expression was observed, indicating significant differences in gene expression among individuals. Androstenone and skatole were significantly associated, with means of 1.33 ug/g and 0.58 ug/g, respectively. Though SNPs were significantly associated with gene expression, no associations were observed between gene expression and androstenone or skatole in fat. Due to this lack of association between expression and boar taint, results indicate that CYP2E1 mRNA expression alone is not a key indicator for boar taint.

Key Words: boar taint, CYP2E1, SNP

0467 Nutritional evaluation of barley varieties grown for silage. J. Nair*[1], D. A. Christensen[2], P. Yu[1], A. D. Beattie[3], T. A. McAllister[4], D. Damiran[1], N. Preston[1,5], L. Fuhr[6], and J. J. McKinnon[7], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]University of Saskatchewan, Saskatoon, Canada, [3]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Canada, [4]Lethbridge Research and Development Centre, AAFC, AB, Canada, [5]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, AB, Canada, [6]Dairy Smart Nutrition, Saskatoon, SK, Canada, [7]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

This study evaluated the nutritional and neutral detergent fiber (NDF) digestibility characteristics of common barley varieties grown for silage by beef and dairy operations in western Canada. Of 135 silage samples collected over two crop years (2012 and 2013), 80 samples harvested at the mid-dough stage, representing seven varieties (Conlon, CDC Copeland, CDC Cowboy, Falcon, Legacy, AC Metcalfe and Xena) were selected for analysis. Chemical composition, NDF digestibility (NDFD) and indigestible NDF (INDF) content were analyzed as randomized complete block design with year as random blocking factor using mixed model procedure of SAS (9.4). Average pH

and dry matter (DM) were 4.05 ± 0.17 and 36.8 ± 4.1, respectively. AC Metcalfe had higher ($P < 0.05$) CP content relative to CDC Copeland and Xena with intermediate values for the other varieties. Acid detergent fiber (ADF) content was higher ($P < 0.05$) for CDC Cowboy and AC Metcalfe relative to Conlon. Similarly, CDC Cowboy had a higher ($P < 0.05$) NDF content relative to Conlon, Falcon and Legacy. AC Metcalfe had a higher ($P < 0.05$) lignin content than CDC Copeland. Starch content of Legacy and Conlon was higher ($P < 0.05$) than that of CDC Cowboy with intermediate values for the other varieties. Neutral detergent fiber digestibility (%NDF) after 6 ($NDFD_{6h}$) and 30 h ($NDFD_{30h}$) of incubation in an ANKOM Daisy^{II} system indicated that Legacy and Falcon had a higher ($P < 0.05$) $NDFD_{6h}$ relative to the other varieties; while CDC Cowboy had the highest ($P < 0.05$) $NDFD_{30h}$ followed by CDC Copeland, AC Metcalfe, Falcon and Conlon with Xena and Legacy being the lowest. Rumen in situ incubation for 288 h to determine the INDF (% NDF) content of barley varieties indicated that CDC Cowboy had a higher ($P < 0.05$) potentially digestible NDF (pdNDF) content relative to AC Metcalfe with other varieties being intermediate. Silage fermentation parameters including VFA, lactate and ammonia concentrations did not differ among varieties. These results indicate that barley varieties grown for silage in western Canada vary with respect to chemical composition, NDFD and pdNDF content and suggest that nutritional as well as agronomic characteristics are important for producers to consider when selecting barley varieties for silage. Selection pressure by plant breeders for increased NDFD may help lead to new or improved forage barley varieties for ruminant production systems.

Key Words: barley silage, variety, NDFD

0468 The repeatability of gonadotropin releasing hormone-induced release of luteinizing hormone and its association with fertility in dairy cattle.

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Objectives were to: (1) determine repeatability and variability of plasma LH concentrations in response to exogenous GnRH administration and (2) examine associations among categories of LH release, plasma estradiol, ovulatory response and first service conception rate in dairy cattle. Lactating Holstein cows (35 primiparous, 65 multiparous) received one injection of $PGF_2\alpha$ (cloprostenol, 500 µg, d 0) followed by GnRH (gonadorelin, 100 µg, d 3; Presynch) and were subjected to an Ovsynch protocol starting on d 10, with timed-AI (TAI) occurring at ~75 d postpartum. Blood samples were collected immediately before (0 h) and 2 h after the GnRH of Presynch and the second GnRH of Ovsynch to determine plasma LH concentrations. Cows were ranked based on LH concentrations after the second GnRH of Ovsynch, from highest to lowest, and those in the top ($n = 33$) and bottom ($n = 33$) thirds were classified into HIGH- and LOW-LH categories. Differences in plasma LH and estradiol concentrations among parity and LH categories were analyzed using MIXED procedure of SAS. Repeatability was analyzed using the CORR procedure and binomial data using the GLIMMIX procedure of SAS. Mean (± SEM) LH concentrations (ng/mL) before GnRH were 0.4 ± 0.04 and 0.6 ± 0.03, while, the mean LH 2 h after GnRH were 8.3 ± 0.7 (range 1.0 to 27.4, CV 80.7%) and 10.0 ± 0.7 (range 0.7 to 28.4, CV 67.3%), during Presynch and Ovsynch assessments, respectively. The correlation between GnRH-induced LH concentrations during Presynch and Ovsynch assessments was $r = 0.19$ ($P = 0.06$). The proportion of cows that remained in HIGH- and LOW-LH categories during both Presynch and Ovsynch assessments was 35.3 and 33.3%, respectively. The mean plasma LH concentration (ng/mL) after GnRH was significantly greater ($P < 0.01$) for HIGH-LH (17.6 ± 0.6) than LOW-LH (2.8 ± 0.6) category. Similarly, cows in the HIGH-LH category had greater plasma estradiol than those in LOW-LH category (2.7 ± 0.3 vs. 1.1 ± 0.3 pg/mL; $P < 0.01$). In addition, cows in the HIGH-LH category had greater ovulatory response (97.0 vs. 78.8%; $P = 0.03$) and increased first service conception rate (44.1 vs. 24.2%; $P = 0.04$) than cows in the LOW-LH category. The mean plasma LH concentration in multiparous cows was significantly greater at Presynch assessment (9.3 ± 0.8 vs. 6.3 ± 1.1; $P = 0.03$) and numerically greater at Ovsynch assessment (10.7 ± 0.8 vs. 8.7 ± 1.1; $P = 0.16$) than in primiparous cows. In summary, GnRH-induced LH concentrations were highly variable and weakly repeatable. However, cows with higher GnRH-induced plasma LH concentrations 2 h after second GnRH of Ovsynch had greater ovulatory response and conception rates.

Key Words: LH variability, repeatability, fertility

0469 Use of low-cost, non-nutritive adsorbents as intestinal binding agents to sequester the boar taint compound androstenone.

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Boar taint is an unpleasant odor and taste detected from pork of some intact males when cooked, caused by high accumulation of the testicular steroid androstenone and the indole skatole. Currently available research exploring dietary approaches to control androstenone is scarce. The objective of this study was to evaluate for the efficacy of binding agents in vivo against androstenone and its impacts on performance in intact male pigs, following up on previous works in vitro.

The study aims to capitalize on a hormone-recycling phenomenon which takes place in the gastrointestinal tract of animals, called enterohepatic circulation. Four adsorbents have been assessed for their binding effectiveness against androstenone in our laboratory; these were previously used in studies which successfully mitigated negative effects associated with mycotoxin ingestion in production animals. All additives bound androstenone in high efficacies in vitro, which warranted evaluation of the effectiveness of these binders in swine diets to reduce its levels in plasma and fat. Ninety ($n = 90$) purebred Duroc boars (123 ± 6 d of age at start of experiment) were equally allocated ($n = 18$) and fed 1 of 4 diets added with 2% bentonite (BNT), 3.5% diatomaceous earth (DE), 15% spent filter aid (SFA), or 0.7% hydrated sodium-calcium aluminosilicate (HSCAS) for at least 28 d followed by 14 d of recovery. All groups were compared with a control entire male group ($n = 18$) fed a typical corn-soybean meal finisher diet. Plasma samples and backfat biopsies were collected at d 0, 14, 28, 42, and 56 of trial. Pigs were weighed weekly and calculated for growth performance parameters. Estrone-1-sulfate in plasma was analyzed as a positive control for enterohepatic circulation. Analysis of trends during the treatment period were performed using the PROC MIXED repeated measures procedure in SAS (SAS Institute, Cary, NC, USA). There were no differences in ADG, ADFI, or FCR across diets ($P > 0.05$) throughout the treatment period. In addition, there were no significant decreases in backfat or plasma androstenone and estrone-1-sulfate across pigs fed treatment diets by d 28 ($P > 0.05$). However, there was a wide variation in plasma and fat androstenone concentration, which may result from the process of transporting the pigs into a novel environment and mixing. Further research using of crossbred pigs that will not be mixed and/or transported into unfamiliar groups is needed to conclusively evaluate the efficacy of these treatments.

Key Words: boar taint

0470 The effect of sorting wheat or barley, based on the predicted CP of individual seeds, on physical characteristics and in vitro dry matter digestibility.

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Nutrient values are based on sample averages, ignoring variability among seeds. The objective of this experiment was to determine if fractions obtained by separating kernels based on predicted CP (PCP) have different physical characteristics and DM digestibility (DMD). Second, we determined if grinding method and intensity influence digestibility of each fraction. The BoMill TriQ (TriQ), which uses near infrared transmittance spectroscopy (NIT), was used to separate individual kernels based on PCP. In the first study, the TriQ was used to sort 6 wheat sources into 10 fractions. Sixty kernels from each fraction were randomly chosen for measurement of length, width, height, area, geometric mean diameter, perimeter, sphericity, color, and mass. Data were analyzed using a mixed model with the fixed effect of fraction. Physical characteristics were similar among fractions ($P > 0.10$), except color, where lower PCP content had greater L* (54.12 vs. 50.95; $P < 0.05$). In the second study, 2 fractions [high CP (HCP) vs. low CP (LCP)] were produced from 5 sources of wheat and barley. The unsorted grain and each fraction were ground through a hammer mill (0.188 or 0.375 mm screens) or a roller mill to produce coarse and finely ground treatments. The roller mill was adjusted to produce samples with a similar processing index (wt/v) to the hammer mill. In vitro DMD and total gas production (TGP) were determined after a 12-h incubation. Data were analyzed independently by grain source including the effect of fraction, grinder, degree of processing, and interactions. The TGP (ml) and DMD (%) were similar among fractions ($P > 0.10$). The TGP and DMD of barley ground using a hammer mill was greater ($P < 0.10$) than when processed using a roller mill (59.4 ± 2.0 and 24.0 ± 2.0; 41.8 ± 1.0 and 24.0 ± 1.0, respectively) and a similar response was observed for wheat ($P < 0.10$; 63.8 ± 1.4 and 27.8 ± 1.5; 42.3 ± 0.8 and 26.3 ± 0.8, respectively). Increasing the degree of processing increased TGP ($P < 0.10$; 47.4 ± 2.0 and 35.9 ± 2.0; 48.9 ± 1.5 and 42.7 ± 1.4, respectively) and DMD ($P < 0.10$; 36.2 ± 1.0 and 29.6 ± 1.0; 36.4 ± 0.8 and 32.2 ± 0.8, respectively) of barley and wheat. Sorting individual seeds for PCP produces fractions with comparable physical characteristics, DMD, and in vitro TGP.

Key Words: grinding, near infrared transmittance spectroscopy, single seed sorter

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0471 The effect of binding feed emzymes to spores of *Bacillius subtlis* and *Bacillius coagulans* on in vitro NDF digestibility in ruminal batch cultures.

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Immobilization of enzymes on *Bacillus* spores has been shown to enhance enzyme stability. Binding feed enzymes to spores may therefore protect them in the rumen environment and improve enzyme efficacy. The objective of this study was to determine whether a xylanase feed enzyme bound to the surfaces of *Bacillus subtilis* or *Bacillus coagulans* spores would improve in vitro ruminal NDF digestibility compared with free

enzyme. Three separate in vitro ruminal batch cultures were performed on different days using the following treatments: *B. subtilis* spore-bound enzyme (BsubE; 1.0×10^9 *B. subtilis* spores + 0.1 mg xylanase enzyme protein); *B. coagulans* spore-bound enzyme (BcoaE; 1.0×10^9 *B. coagulans* spores + 0.1 mg xylanase enzyme protein); free enzyme (ENZY; 0.1 mg xylanase enzyme protein); and control (CON; water). The treatments were applied to alfalfa hay (2-mm particle size) 4 h before incubations. Rumen fluid was collected from two cannulated heifers and mixed with Menke's buffer (3:1) under anaerobic conditions to make inoculant. Serum vials containing pre-treated alfalfa hay (0.5 g) were filled with 60 mL of inoculant and then incubated on a shaker (39°C) for 0, 3, 6, 12, 24, and 48 h. Triplicate vials were removed at each time point to measure gas production, methane emission, and alfalfa digestibility. Gas production (ml/g dry matter (DM)) at 48 h was not different between BsubE, BcoaE, or ENZY ($P > 0.05$); however, it was reduced in CON vials compared with the other treatments ($P < 0.001$). Methane emissions at 24 and 48 h (ml/g DM) were least for CON (25.2 and 29.8 mL/g, respectively), intermediate for the spore treatments (25.8 and 30.5 g/ml for BsubE; 25.9 and 30.7 g/ml for BcoaE), and greatest for ENZY (35.4 and 39.0 mL/g, respectively; $P = 0.011$). In vitro DM digestibility was not different at 24 h ($P = 0.36$), but at 48 h there was a difference between CON (78.9%) and BsubE, BcoaE and ENZY (average 80%; $P = 0.018$). There was a tendency for greater NDF digestibility at 48 h in the enzyme treatments, compared with CON ($P = 0.075$). These data showed that the feed enzyme enhanced digestion of alfalfa. However, there was no difference when the enzyme was applied in free-form or bound to spores. Protection of feed enzymes through absorption to *Bacillus* spores may be more effective when the enzymes are unstable in a ruminal environment.

Key Words: feed enzyme, rumen digestibility, spores

0472 Characterization of bovine nasopharyngeal lactic acid bacteria and their in vitro antimicrobial activities against the respiratory pathogen *Mannheimia haemolytica*.

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Most research on bacteria in the bovine nasopharynx has focused on pathogens implicated in respiratory disease. There is limited information on commensals, such as lactic acid bacteria (LAB), which are important to mucosal health and have been investigated as probiotics to inhibit pathogens. The purpose of this study was to characterize the bovine nasopharyngeal LAB and their in vitro antimicrobial activities against *Mannheimia haemolytica*. The diversity of nasopharyngeal LAB was investigated in two separate studies using DNA– or culture-based techniques. In the first study, nasopharyngeal samples were collected from calves ($n = 14$) on a farm before shipment to a feedlot (d 0), and then 2, 7, and 14 d after feedlot placement. Swabs were processed for DNA extraction and the 16S rRNA gene was PCR-amplified and sequenced using the MiSeq platform. In the second study, nasopharyngeal swabs were collected from calves ($n = 70$) sampled at feedlot entry and 60 d afterward. The swabs were processed for the isolation of LAB using selective media. A subset of LAB ($n = 66$) was identified by sequencing the full-length 16S rRNA gene and isolates were subsequently screened for inhibition of *M. haemolytica* using the agar slab method. From the first study, high–throughput sequencing showed that the total LAB (defined as the order *Lactobacillales)* constituted 4.2% of the nasopharyngeal bacterial microbiota and consisted of 23 genera. Within LAB, 6 different families were identified that included *Streptococcaceae* (49.2%), *Carnobacteriaceae* (23.9%), *Aerococcaceae* (16.0%), *Enterococcaceae* (5.6%), *Lactobacillaceae* (5.3%), and *Leuconostocaceae* (0.26%). The relative abundance of total LAB increased by 97% from d 0 to 2 and remained greater for the 14 d of feedlot placement, compared with d 0 ($P < 0.05$). Interestingly, however, the *Lactobacillaceae* family decreased ($P < 0.05$) from d 0 to 2, demonstrating that not all *Lactobacillales* members increased after feedlot arrival. Using culture–based methods, only 6 genera of LAB were isolated: *Streptococcus* (39.2%), *Lactobacillus* (37.1%), *Enterococcus* (10.3%), *Aerococcus* (9.3%), *Corynebacterium* (3.1%), and *Pediococcus* (1.0%). Among the screened LAB isolates, species within *Lactobacillus* exhibited the strongest inhibition against *M. haemolytica*, with zones of inhibition ranging between 16 and 23 mm. Our results show that the relative abundance of nasopharyngeal LAB can change after cattle are transported to a feedlot and that some LAB are able to inhibit the respiratory pathogen *M. haemolytica*. These LAB may have potential as nasal probiotics for the mitigation of bovine respiratory pathogens.

Key Words: lactic acid bacteria, probiotic, bovine nasopharynx

0473 Severity and prevalence of ruminal acidosis during the diet transition for commercial feedlot cattle. B. I. Wiese*[1], S. Hendrick[2], J. J. McKinnon[3], J. Campbell[1], and G. B. Penner[4], *[1]Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, Canada, [2]Coaldale Veterinary Clinic, Coaldale, AB, Canada, [3]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [4]University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to determine the severity and prevalence of ruminal acidosis in commercial feedlot cattle during the transition to a finishing diet. Previously backgrounded steers (n = 907) and heifers (n = 998) were chosen as a source population and housed separately in 8 pens with an average of 227 ± 13 and 249 ± 6 hd/pen, respectively. Within the source population, 16 steers (mean BW ± SD = 435.1 ± 32.8 kg) and 16 heifers (mean BW ± SD = 382.7 ± 49.4 kg) were used to measure reticulo-ruminal pH using an orally administered pH measurement system; however, 3 systems were not recovered on slaughter. Cattle were fed 3 times daily and were transitioned from a diet containing (forage:concentrate; F:C) 62:38 to 20:80 (DM basis) over 40 d. Dry matter intake was assessed at the pen level. The effect of diet and day within diet were analyzed using the MIXED procedure in SAS, with diet and sex as fixed effects. Dry matter intake was greater for steers than heifers (10.2 vs. 9.3 kg/d; $P < 0.01$) and increased from diet 1 to diet 3, reaching a peak of 10.2 kg/d, before declining to 9.4 kg/d in diet 6. Mean reticulo-ruminal pH ($P < 0.01$) declined from pH 6.45 in diet 1 to pH 6.10 in diet 6. Heifers had greater mean pH than steers (6.38 vs. 6.33) when averaged over the diet transition ($P = 0.04$). Area (pH min)/d) and duration (min/d) that pH was < 5.6 increased with decreasing F:C ($P < 0.01$), as did the standard deviation from mean pH ($P < 0.01$). Over the entire transition period 24/29 study animals experienced at least one bout indicative of acidosis (pH < 5.6 for > 180 min) but the average daily prevalence was 5.4%. The prevalence of reticulo-ruminal acidosis increased with decreasing F:C (peak of 13.5%). When days within a diet were evaluated, lowest mean pH was observed 2-d post diet change ($P < 0.01$). Results indicate that daily prevalence for ruminal acidosis ranges between 1 and 13% with the risk increasing with decreasing F:C. The susceptibility to ruminal acidosis may differ between steers and heifers and the second day relative to a diet change appears to be the day with the greatest risk.

Key Words: diet transition, feedlot cattle, ruminal acidosis

0474 Comparison of digestion and particle-associated bacteria after in situ incubation of different barley varieties in the rumen of cattle. H. E. Yang*[1,2], C. A. Zotti[2], J. J. McKinnon[1], and T. A. McAllister[2], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]Lethbridge Research and Development Centre, AAFC, AB, Canada.*

The chemical composition of barley grain, including the structure of starch, can vary among barley varieties and result in different digestion efficiencies. It is not known if compositional differences in barley can affect the particle-associated bacteria (PAB) involved in digestion. Therefore, the objective of this study was to characterize the in situ rumen digestion and PAB of four barley grain varieties. Three ruminally-cannulated cattle were fed a diet of 60% barley silage, 37% barley grain and 3% supplement. Four different barley varieties (Fibar, Xena, McGwire and Hilose) and corn as a control were included in the experiment. Ground grains (3 g) were placed in nylon bags and incubated in the rumen of cattle for 0, 2, 4, 12, 24, and 48 h. At each time point, triplicate bags were removed from each animal and analyzed for dry matter (DM), starch and crude protein (CP) disappearance. A second set of bags (n = 3) containing 5 g of each grain were incubated for 2, 4, and 12 h and DNA was extracted to characterize PAB via 16S rRNA gene sequencing. McGwire had the highest effective degradability (ED) of DM ($P < 0.01$), followed by Xena, Fibar, Hilose, and corn, respectively. The ED of starch was highest ($P < 0.01$) for Xena, followed by McGwire, Fibar, Hilose, and corn, while CP disappearance was not affected by grain type. Overall, 15 phyla were identified after analysis of 16S rRNA genes. Barley variety did not affect the relative abundance of phyla however they did differ with incubation time. *Firmicutes* (19.2%), *Bacteroidetes* (18.27%) and *Proteobacteria* (8.89%) were the dominant phyla after 2 h of incubation. By 12 h, *Bacteroidetes* decreased to a relative abundance of 4.3%. In contrast, *Firmicutes* increased in abundance over time, accounting for 45.9 and 82.1% of PAB after 4 and 12 h of incubation, respectively. Principal Coordinate Analysis showed that bacterial populations clearly grouped according to incubation time. At the family level, *Lactobacillaceae* increased over time, with a relative abundance of 0.76, 6.49, and 76.3% at 2, 4, and 12 h, respectively, reflecting an increasing presence of lactic-acid producing bacteria. This study found that the diversity of PAB on barley grain was not affected by barley variety, despite there being differences in digestion kinetics. However, time affected PAB, illustrating that the bacterial biofilm involved in the digestion of grains clearly undergoes compositional shifts during ruminal digestion.

Key Words: barley, rumen, microbiota

0475 Carbohydrate spectroscopic features of bio-oil co-products in relation to rumen degradation kinetics in ruminants. X. Li[*1,2], W. Xu[1], J. Yang[1], Y. Zhang[1], and P. Yu[2], *[1]College of Animal Science and Technology, Northeast Agricultural University, Harbin, China, [2]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

The objectives of this study were to investigate the carbohydrate structure makeup associated with dry matter (DM) rumen degradation kinetics of three commonly used bio-oil co-products in ruminants. Three bio-oil products (rapeseed meal, canola meal and soybean meal) from three different sources in both Canada and China were collected in 2014. The carbohydrate spectral features were investigated using attenuated total reflectance-Fourier transform infrared spectroscopy instrument. The rumen degradation kinetics was determined according to the in situ nylon bag method with 3 rumen cannulated lactating Holstein cows at Rayner Dairy Teaching and Research Facility, University of Saskatchewan, Canada. The PROC MIXED procedure of SAS 9.3 was used for spectral data and degradation kinetics data analyses. The PROC CORR procedure of SAS was used to investigate the relationship between carbohydrate structure makeup and metabolic characteristics. Significances were declared at $P < 0.05$.The results showed that the peak area intensities of structural carbohydrate related region and its multiple peaks height were all lower in rapeseed meal and canola meal compared with soybean meal ($P < 0.05$). The cellulosic compound related spectral region had lower peak area and peak height intensities in rapeseed meal and canola meal than soybean meal ($P < 0.05$). Additionally, structural carbohydrate to total carbohydrate ratio and cellulosic compound to total carbohydrate ratio were all lower in rapeseed meal and canola meal than soybean meal ($P < 0.05$). For in situ DM rumen degradation kinetics, rapeseed meal had significantly lower soluble fraction than soybean meal. Rapeseed meal and canola meal had significantly lower potentially degradable fraction and higher undegradable fraction in comparison with soybean meal ($P < 0.05$). Compared with soybean meal, rapeseed meal and canola meal had higher rumen bypass DM content, and lower rumen effectively degradable DM content. There is a close relationship between carbohydrate spectral parameters and nutrient metabolic characteristics. The peak area intensity of functional group such as structural carbohydrate, cellulosic compound related region and their ratio to total carbohydrate were all positively related with DM degradable fraction and negatively correlated with DM undegradable fraction ($P < 0.05$). In conclusion, canola meal genetically developed from rapeseed meal shares similar carbohydrate structure and nutrition availability with rapeseed meal. The unique carbohydrate molecular spectral bands in the mid-IR region are highly associated with the nutrient utilization of bio-oil co-products in ruminants.

Key Words: carbohydrate molecular structure, vibrational spectroscopic profiles, nutrient metabolic characteristics

0476 Low protein diets produce divergent effects on energy balance. R. C. Zapata[*1], A. Pezeshki[2], A. Singh[1], N. J. Yee[1], and P. K. Chelikani[1], *[1]University of Calgary, AB, Canada, [2]Oklahoma State University, Stillwater.*

Background: The protein leverage theory postulates that diets low in dietary protein increase total energy intake due to overconsumption of carbohydrates and fat in an attempt to meet protein requirements. However, little is known of the mechanisms by which protein deficiency elicits such behavioral and metabolic adaptations, promotes positive energy balance and increases the risks for obesity and associated metabolic disorders.

Objectives: Our objectives were to determine the effects of graded degrees of protein restriction on (1) energy balance, body composition, glucose tolerance, gut hormones, (2) sympathetic signaling and, (3) key regulatory markers of thermogenesis in liver, skeletal muscle and brown adipose in diet-induced obese (DIO) rats.

Methods: The DIO rats were randomized to receive one of 4 isocaloric high-fat diets with graded concentrations of protein (n = 8/group; 4.40 kcal/g): Control (15% protein, CON), 10% (10P), 5% (5P), 0% (0P) for 2 wk, followed by realimentation to CON for 2 wk. Food intake, energy expenditure, body composition, glucose tolerance, plasma hormone concentrations, and tissue gene and protein expressions were measured. Data were analyzed by linear mixed models or ANOVA.

Results: We found that during protein restriction, compared with CON, 0P decreased energy intake but increased energy expenditure which led to reduced body weight, fat and lean mass, 5P increased energy intake and energy expenditure which led to reduced body weight and lean mass, and 10P increased energy intake but did not affect body weight and composition. These diet-induced alterations in energy expenditure are in part mediated through enhanced β-adrenergic signaling coupled with upregulation of key thermogenic markers (UCP1, β-Adrenergic receptors, fibroblast growth factor-21, irisin) in the brown adipose, liver and skeletal muscle. The 0P decreased plasma peptide YY, leptin, insulin, C-peptide and tended to decrease amylin and glucose-dependent insulinotropic peptide. The 0P and 5P induced fatty liver, reduced energy digestibility, and decreased lean mass and body weight that persisted beyond the restriction period. In contrast, moderately low protein diets promoted gain in body weight and adiposity following the period of protein restriction.

Conclusion: In summary, our novel findings demonstrate that low protein diets produce divergent effects on energy balance by engaging sympathetic signaling. Importantly, moder-

ately low protein diets could exacerbate preexisting susceptibility to weight gain and obesity. Funding: NSERC, ALMA

Key Words: low protein, energy balance, obesity

CSAS GRADUATE STUDENT POSTER COMPETITION

0477 Effect of high dietary canola meal inclusion in lactating sows on nutrient digestibility and sow and piglet performance. D. E Velayudhan* and C. M. Nyachoti, *University of Manitoba, Winnipeg, Canada.*

The aim was to determine the effects of high canola meal inclusion levels in sow lactation diets on nutrient digestibility, reproductive performance, milk composition and piglet performance. Forty five sows (n = 15) with an average parity of 1.8 (SD = 0.83) were randomly assigned to 1 of 3 dietary treatments; corn soybean meal control diet with 0, 15, and 30% canola meal (Diet A, B and C, respectively). All diets were formulated to be similar in standardized ileal digestible amino acids and NE, and were formulated to meet or exceed NRC (2012) nutrient requirement recommendations for lactating sows with an average post-farrowing BW of 210 kg, an expected average BW loss of 5.8 kg, and an expected piglet ADG of 230 g. Sows were moved to farrowing rooms and given the experimental diets from d 111of gestation until weaning on d 21. All sows were weighed and backfat thickness measured on d 111 of gestation and also on d 0, 7, and 21 post-farrowing. Litters were weighed on d 0, 7, and 21. Weaning to estrous interval in sows was also recorded. Blood samples, 2 h post feeding and milk samples were collected from sows on d 0, 7, and 21 to analyze plasma urea nitrogen (PUN) and milk composition, respectively. Fecal samples were collected on d 10, 11, and 12 post-farrowing to determine energy and nutrient digestibility. All data were analyzed as a randomized complete block design using mixed procedures of SAS 9.3 (SAS Inst., Cary, NC). There were no effects of higher levels of dietary canola meal inclusion on lactation feed intake, sow BW and backfat change, and weaning to estrous interval ($P > 0.10$). Also, there were no dietary effect on piglet mortality and piglet ADG ($P > 0.10$). There were no differences in the sow milk composition among dietary treatments ($P > 0.10$). However, sows fed 15 and 30% canola meal had lower ($P < 0.05$) PUN values compared with those fed control diet, on d 0, 7, and 21 post-farrowing. Also, apparent total tract digestibility of DM, GE, CP and P declined ($P < 0.05$) with increasing levels of canola meal inclusion. It was concluded that inclusion of up to 30% canola meal in lactation diet can support satisfactory sow and litter performance.

Key Words: canola meal, performance, sow

0478 Transcriptome analysis of the intestinal tissues of cattle suggests an association among host immune responses, lipid metabolism and the super-shedding of *E. coli* O157. O. Wang*[1], T. A. McAllister[2], G. Plastow[3], B. Selinger[4], K. Stanford[5], and L. L. Guan[6], *[1]University of Alberta, Edmonton, Canada, [2]Lethbridge Research and Development Centre, AAFC, AB, Canada, [3]Livestock Gentec, Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [4]University of Lethbridge, AB, Canada, [5]Alberta Agriculture and Forestry, Lethbridge, Canada, [6]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Super-shedder cattle, which are defined as cattle shedding > 4 log of CFU of *Escherichia coli* O157 (O157) per g of feces, are responsible for the majority of O157 excretion into the farm environment. Colonization of the rectal anal junction by O157 is integral to super shedding. The objective of current study was to further understand the molecular mechanisms of colonization during super-shedding through investigating the transcriptome of the whole intestinal tract of cattle. We hypothesized that the difference in gene expression profiles between the anterior and distal part of intestine underlies the tropism of O157 toward the distal colon, and that transcriptomes of intestinal tissues differ between super-shedders and steers fecal-negative for O157 (non-shedders). RNA-sequencing (Illumina HiSeq 2000, 100 bp paired-end) was performed for intestinal tissues, including duodenum, proximal jejunum, distal jejunum, cecum, spiral colon and descending colon collected from 5 super-shedders and 5 non-shedders. Sequencing data were processed using a Tophat2, HTseq and edgeR pipeline, and gene function analysis was performed using Ingenuity Pathway Analysis. The number of genes detected in tissues ranged from 16,846 ± 639 (cecum) to 18,137 ± 696 (distal jejunum), and the functional analysis indicated that cell-mediated and humoral immune functions were enriched for the transcriptomes of small intestinal tissues, reflecting their greater immune activity. The number of differentially expressed genes between super-shedders and non-shedders ranged from 1 (duodenum) to 248 (distal jejunum) (false discovery rate < 0.05). Up-regulated genes in super-shedders, including F3, GPR123 and CCR9 in distal jejunum, and GP2 and CD36 in descending colon, indicated possible increased activation of cell-mediated immune responses in these two intestinal regions of super-shedders. Up-regulated APOA1, GPAM, PLIN1 and APOB in descending colon of super-shedders suggested altered lipid metabolism. This is the first report of transcriptome analysis for intestinal tissues of cattle, and our current findings indicate that the tropism of O157 toward the distal part of the colon may be due to less active immune protection in the large intestine. Furthermore, both host

immunity and lipid metabolism may play a role in the interaction between the cattle host and O157. The identified genes may be potential genetic indicators for O157 super-shedding in cattle.

Key Words: *E. coli* O157, super-shedder, transcriptome

0479 Determination of standardized total tract digestibility of phosphorus in flaxseed meal fed to finishing pigs without or with phytase supplementation. J. W. Kim* and C. M. Nyachoti, *University of Manitoba, Winnipeg, Canada.*

This experiment was conducted to determine the phosphorus (P) digestibility of flaxseed meal (FM) fed to finishing pigs and effect of phytase supplementation on P digestibility for finishing pigs. A total of 18 growing barrows [(Yorkshire × Landrace) × Duroc] with an average body weight (BW) of 78.7 ± 2.4 kg (mean ± SD) were randomly allotted to 3 treatments to give 6 replicates per treatment. Pigs were housed for 10 d in adjustable metabolism crates (1.80 × 0.6 m) with 5 d of adaptation periods and 5 d of total collection periods in a temperature-controlled room (22 ± 2°C). A semi-purified diet based on corn starch-sucrose containing 320 g/kg of FM as the sole source of P was fed without or with phytase supplementation at the level of 500 FTU/kg. A P-free diet mainly based on corn starch, sucrose, and gelatin was also prepared to estimate the endogenous P losses (EPL). Pork gelatin was added to the diets for maintaining similar crude protein in all experimental diets. Vitamins and all minerals except P were included in the diets according to requirements for finishing pigs (NRC, 2012). Pigs were fed at 40 g/kg BW at the beginning of experiment. The daily feed allowance was offered in two equal portions at 0800 and 1600 h. Pigs had free access to water. Results indicated that total feed and P intake were not different between diets without or with phytase supplementation. However, phytase supplementation increased ($P < 0.01$) apparent total tract digestibility (ATTD) and standardized total tract digestibility (STTD) of P in FM diet. The ATTD of P and STTD of P were increased from 31.4% to 45.8% and from 37.3% to 51.8%, respectively. Phytase supplementation also decreased ($P < 0.05$) P concentration (1.95 vs. 1.62%) in feces. Total P output was tended to decrease ($P = 0.08$) in pigs fed diets containing FM with phytase. The basal EPL was calculated at 151 ± 20 mg/kg of DMI in pigs fed the P-free diet. In conclusion, dietary phytase supplementation may increase P digestibility in FM fed to finishing pigs.

Key Words: flaxseed meal, phosphorus, phytase

Table 0479.

Table 1. Digestibility of phosphorus (P) in experimental diets fed to finishing pigs[1]

	Flaxseed meal[2]			
	-	+	SEM	P-value
Feed intake, g/d				
Total feed intake	2877	3108	93.4	0.111
P intake	6.85	7.34	0.222	0.157
Fecal output				
Total feces, g/d	244	247	15.9	0.902
P in feces, %	1.95[a]	1.62[b]	0.081	0.017
P output, g/d	4.72	3.97	0.276	0.081
Digestibility, %				
ATTD[3] of P	31.4[b]	45.8[a]	2.90	0.006
STTD[3,4] of P	37.3[b]	51.8[a]	2.90	0.005

[1] Each value represents the mean of 6 replicates per each treatment.
[2] -, without phytase; +, with phytase (the activity of microbial phytase added to the diets was 500 FTU/kg).
[3] ATTD = Apparent total tract digestibility; STTD = Standardized total tract digestibility.
[4] Values for the STTD were calculated by correcting the ATTD values for the basal endogenous loss of P. The basal endogenous loss of P was estimated in pigs fed the P-free diet at 151 ± 20 mg/kg of DMI.

0480 The effects of partial replacement of barley starch with lactose on production and ruminal fermentation characteristics in dairy cows. E. De Seram*[1], G. B. Penner[1], and T. Mutsvangwa[2], [1]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada,* [2]*University of Saskatchewan, Saskatoon, Canada.*

Previous studies have reported improved DMI and milk production when dietary starch was replaced with sugars in corn-based diets, but there is limited work with barley-based diets. Because corn and barley starch differ in their rates and extents of ruminal degradation, it is important to determine if replacement of barley starch with sugars is beneficial as has been reported for corn. The objective of this study was to determine the effects of partial replacement of barley starch with lactose (as dried whey permeate; DWP) on DMI, milk yield and composition, and ruminal fermentation characteristics. Eight lactating Holstein cows (97 ± 10 d-in-milk; 733 ± 63 kg BW)

were used in a replicated 4 × 4 Latin square design experiment with four dietary treatments. Experimental periods consisted of 18 d of adaptation and 10 d of measurements. Four cows in one Latin square were ruminally cannulated. Cows were fed a barley-based diet (3.6% total sugar [TS]; control), or diets that contained 6.6, 9.6 or 12.6% TS on a DM basis. Dietary TS content was increased by the replacement of barley grain with DWP, which contained 83% lactose. Diets were isonitrogenous (17.2% CP) and starch contents of the control, 6.6, 9.6, and 12.6% TS diets were 24.3, 22.2, 21.2 and 19.1%, respectively. The inclusion of DWP did not affect DMI (mean = 26.6 kg/d) and milk yield (34.3, 35.0, 35.6, and 34.6 kg/d for the control, 6.6, 9.6, and 12.6% TS diets, respectively); however, milk lactose content tended to increase quadratically ($P = 0.07$) as TS content increased. There was a linear decrease ($P = 0.03$) in ruminal NH_3–N concentrations as TS content increased. Ruminal pH tended to decrease linearly as TS content increased ($P = 0.06$; 6.32, 6.31, 6.34, and 6.22 for the control, 6.6, 9.6, and 12.6% TS diets, respectively). Total ruminal VFA concentrations were not affected ($P > 0.05$) by diet; however, there was a linear increase ($P = 0.04$) in butyrate concentration as TS content increased. Plasma urea-nitrogen concentrations were not affected by diet, but milk urea-nitrogen concentrations tended to change in a cubic manner as TS content increased ($P = 0.08$; 14.1 15.1, 14.0, and 13.7 mg/dL for control, 6.6, 9.6, and 12.6% TS diets, respectively). These results suggest that partial replacement of barley starch with lactose improves ruminal N efficiency by decreasing ruminal NH_3–N concentration, but production performance was unaffected

Key Words: barley starch, lactose, production, ruminal fermentation

0481 Potential to improve fiber digestion in the rumen of cattle through inoculation with bison rumen contents.

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We hypothesized that inoculating the rumen of cattle with bison rumen contents would improve the ruminal degradability of forage by enhancing the cellulolytic capacity of the rumen microbiome. Sixteen ruminally cannulated beef heifers were fed a diet of 70% barley straw (78.0 ± 3.89 neutral detergent fiber [NDF]) and 30% supplement (36.6 ± 0.76 CP, 37.6 ± 1.41 NDF) on a dry matter (DM) basis. Cattle were inoculated with bison rumen contents twice, 2 wk apart. Intact bison rumens were obtained from an abattoir and transported in insulated containers in a heated truck. Rumens were opened and contents mixed in a heated tub under CO_2. Rumen contents were removed from the cattle, weighed and approximately 72% of the contents (DM basis) were replaced by mixed bison rumen contents in each transfer. The in situ technique was used to measure ruminal degradation of canola straw, barley straw, timothy hay, and alfalfa hay before inoculation and 11 d after the second inoculation. Duplicate bags (10 × 20 cm; 6 g DM/bag) were incubated in the rumen of each heifer for 0, 4, 8, 12, 24, 48, 96, 120 h. The percentage NDF disappearance (NDFD) from the bags was analyzed as: $NDFD = A + B(1\text{-}e^{-k\text{-}d(time\text{-}lag)})$, where A = soluble fraction, b = slowly digestible fraction, K_d = rate of digestion of fraction b, and lag = time before digestion began; and effective ruminal degradability (ERD) = A+B(kd/(kd+kp)) where kp = rate of passage (measured for each animal). Transfer of rumen contents decreased ($P < 0.05$) the potentially digestible fraction (A+B) in barley straw, but increased it in alfalfa hay ($P < 0.05$) (Table 1). No effect of inoculation on ERD were observed, suggesting fiber utilization by cattle was not substantially improved by introducing

Table 0481.

		Pre-inoculation		Post-inoculation		
Feed	Variable	Mean	STD	Mean	STD	*P* value
Canola straw	ERD	21.9	2.59	22.0	1.56	0.92
	A+B	37.4	1.31	36.3	2.20	0.12
Barley straw	ERD	38.5	3.87	37.5	2.55	0.21
	A+B	60.1	1.14	58.5	1.29	0.002
Timothy hay	ERD	45.0	3.87	44.4	3.46	0.50
	A+B	69.2	1.60	68.6	1.45	0.14
Alfalfa hay	ERD	40.8	2.76	40.1	2.64	0.49
	A+B	52.2	0.87	54.1	1.29	<0.001

A+B = % total digestible NDF fraction, ERD = % effective ruminal degradability of NDF; STD = standard deviation

microbes from bison rumen contents.

Key Words: bison, effective ruminal degradability, microbiome

0482 CNCPS fractions of value added pellet products based on combination of new co-products from bio-fuel/bio-oil processing, low grade of peas and lignosulfonate chemical compound at different levels for ruminants. V. Guevara*, D. A. Christensen, J. J. McKinnon, and P. Yu, *Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

Carinata meal, new co-product from bio-fuel processing, is ready to be used as animal feed nowadays. Canola meal has high levels of methionine and cysteine, but limiting in lysine. Pulse products contain high starch, also have high levels of lysine and tryptophan. There is little information available on chemical profile, as well as its nutritive value especially when it blends with other feedstuff as a pellet. The aim of this project was to test and develop eight high-value added pellet products (BPP) based on combination of co-products from bio-fuel/bio-oil processing, low grade of peas and lignosulfonate at different levels for ruminants. Statistical analyses were performed using PROC MIXED procedure of SAS 9.3 with significance declared at $P < 0.05$. The results from CNCPS 6.5 system indicated all canola based pellet products BPP5 (low level of canola meal, high level of peas and no lignosulfonate), BPP6 (low level of canola meal, high level of peas and lignosulfonate), BPP7 (high level of canola meal, low level of peas and no lignosulfonate) and BPP8 (high level of canola meal, low level of peas and lignosulfonate) showed higher levels of indigestible protein (PC, $P < 0.05$) and higher soluble true protein (PA2, $P < 0.05$). All carinata based pellet products showed the higher fiber bound protein (PB2, $P < 0.05$). BPP3 (high level of carinata meal, low level of peas and no lignosulfonate), BPP4 (high level of carinata meal, low level of peas and lignosulfonate), BPP7 and BPP8 had the higher levels of water-soluble carbohydrates (CA4, $P < 0.05$); BPP1 (low level of carinata meal, high level of peas and no lignosulfonate), BPP2 (low level of carinata meal, high level of peas and lignosulfonate), BPP5 (low level of canola meal, high level of peas and no lignosulfonate) and BPP6 showed the higher levels of starch (CB1, $P < 0.05$), while BPP1, BPP3 and BPP4 had higher digestible fiber (CB3, $P < 0.05$). In conclusion, carinata meal can be used as a potential feed ingredient for ruminants.

Key Words: canola, carinata, lignosulfonate

0483 Comparison of barley silage with varying digestible fiber content to corn silage on rumen fermentation characteristics and microbial protein synthesis using RUSITEC technique. B. Refat*[1,2], D. A. Christensen[3], J. J. McKinnon[4], J. Nair[1], A. D. Beattie[5], T. A. McAllister[6], W. Yang[7], and P. Yu[1], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]Animal Production Department, Faculty of Agriculture, Zagazig University, Egypt, [3]University of Saskatchewan, Saskatoon, Canada, [4]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [5]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, Canada, [6]Lethbridge Research and Development Centre, AAFC, AB, Canada, [7]Lethbridge Research and Development Centre, AAFC, AB, Canada.*

The effect of barley silage with enhanced in vitro fiber digestibility on rumen fermentation characteristics and microbial protein synthesis has not been well investigated in barley grown in western Canada. The objective of this study was to evaluate the effects of barely silage with varying in vitro NDF digestibility (IVNDFD) in comparison to corn silage on rumen fermentation characteristics and microbial protein synthesis using rumen simulation technique (RUSITEC). The experiment was a completely randomized design with four treatments. The experimental diet contained 49% barley-based concentrate and 51% forage (DM basis). The forage consisted of 10% alfalfa hay and 41% silage. The four whole plant silages were: T1 = P7213R corn silage, T2 = CDC Cowboy barley silage, T3 = CDC Copeland barley silage, and T4 = Xena barley silage. The experiment consisted of 10 d of adaptation and 6 d of data collection. Statistical analyses were performed using the PROC MIXED procedure of SAS 9.4 with significance declared at $P < 0.05$. The 30 h IVNDFD of corn silage, CDC Cowboy, CDC Copeland and Xena varieties were 27, 37, 31, and 29%, respectively. Barley silage T2, with the highest IVNDFD, had no effect on rumen fermentation characteristics ($P > 0.10$) when compared with T3 and T4 barley silage. However, corn silage vs. the average of T2, T3 and T4 barley silage ($P < 0.05$) had lower ruminal pH (6.65 vs. 6.73), greater molar proportion of propionate (28 vs. 23%) and lower C2/C3 acid ratio (1.8 vs. 2.2). Nutrients disappearance of total mixed ration (DM and CP) were not affected by the treatments. On the other hand, corn silage in T1 had the highest DMD compared with the average DMD of barley silages in T2, T3 and T4 (69.1 vs. 64.8%, $P < 0.05$). There was no significant effect of higher digestible fiber content in T2 on bacterial protein production compared with T3 and T4 (averaged 49.5 mg/d) while T1 diet had a higher bacterial protein

production than the average of T2, T3 and T4 (53.5 vs. 49.5 mg/d, $P < 0.05$). These results imply that higher in vitro NDF digestibility of barley silage might not necessarily correspond with greater impact on rumen fermentation and microbial protein synthesis. However, feeding the corn silage had a higher microbial protein produced in the rumen and may enhance the dairy cattle performance compared with the barley silages.

Key Words: bacterial N production, rumen fermentation, RUSITEC

0484 Phosphorus utilization on dairy farms in Manitoba. V. P. Senaratne*, E. J. McGeough, K. H. Ominski, and J. C. Plaizier, *Department of Animal Science, University of Manitoba, Winnipeg, Canada.*

A survey was performed on 19 dairy farms in Manitoba representing a range of sizes, feeding, housing and management systems to identify factors that affect the utilization of dietary phosphorus (P) by lactating dairy cows. Each farm was visited once to collect milk, blood, feed and feces samples as well as production data from 10 early/peak, 10 mid-lactation, and 10 late lactation cows. Phosphorus content of feed (FEED P), feces (FECAL P), milk (MILK P), blood (BLOOD P) and calcium content of feed (Ca) were determined. Pearson correlation analysis among the various measures was conducted using SAS 9.4 software. The average P contents (DM basis) of FEED P, FECAL P, MILK P, and BLOOD P was 0.41% (0.34 and 0.53%), 0.76% (0.30 and 1.35%), 0.09% (0.05 and 0.12%) and 2.04 mmol/L (1.34 to 3.04 mmol/L), respectively. The output of P in milk (P OUT) which is obtained by multiplying MILK P with daily milk yield (MY), was positively correlated with the MILK P, FEED P, MY, Parity, Ca and negatively correlated with days in milk (DIM). But no correlation was observed with the BLOOD P and FECAL P. FEED P was positively correlated with the MILK P, FECAL P, MY, and negatively correlated with Ca and DIM. BLOOD P was positively correlated with Ca and DIM, but not correlated with any other measures (Table 1). Results show that the P content of diets, and feces vary considerably among cows and among farms, suggesting that the P contents in diets and feces can be reduced. Furthermore, more than 50% of the animals received diets which contain excess P levels than the NRC (2001) recommendations. The P content of blood was not indicative of P output in milk, nor the P contents of the diet or feces. The output of P in milk was highly correlated with the yield and P content of milk, but a 1% increase in the dietary P content lead to a 0.21% increase in P OUT. Better understanding of the dynamics between these dietary and cow factors can help to develop efficient P management strategies to improve P utilization and avoid excess P use.

Key Words: phosphorus, dairy, cow

0485 Effect of variety and level of inclusion of barley grown for silage on performance and carcass characteristics of growing and finishing beef steers. J. Nair*[1], D. A. Christensen[2], P. Yu[1], T. A. McAllister[3], D. Damiran[1], and J. J. McKinnon[4], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada, [2]University of Saskatchewan, Saskatoon, Canada, [3]Lethbridge Research and Development Centre, AAFC, AB, Canada, [4]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, Canada.*

This study was designed as a 3 × 2 factorial to evaluate three barley silage varieties when included at two (high and low) inclusion rates on performance and carcass characteristics of beef steers. Barely varieties CDC Cowboy (CB), CDC Copeland (CL) and Xena were chosen based on results of a preliminary study for high (CB, 37.0%), medium (CL, 31.1%) and low (Xena, 28.8%) NDF digestibility (NDFD; % NDF). For the present trial, the three varieties were seeded and managed identically including harvesting at the mid-dough

Table 0484.

Table 1: Pearson correlation coefficients *P<0.05

	MILK P	FECAL P	BLOOD P	FEED P	MY	DIM	Parity	Ca	P OUT
MILK P	1	0.019	-0.032	0.149*	-0.055	-0.028	-0.017	-0.018	0.847*
FECAL P	0.019	1	0.047	0.206*	-0.074	0.142*	-0.063	0.019	-0.026
BLOOD P	-0.032	0.047	1	0.075	0.060	0.130*	-0.061	0.168*	-0.001
FEED P	0.149*	0.206*	0.075	1	0.166*	-0.118*	0.051	-0.131*	0.208*
MY	-0.055	-0.074	0.060	0.168*	1	-0.430*	0.352*	0.223*	0.455*
DIM	-0.028	0.142*	0.130*	-0.118*	-0.430*	1	-0.070	-0.040	-0.251*
Parity	-0.017	-0.063	-0.061	0.051	0.352*	-0.070	1	0.069	0.168*
Ca	-0.018	0.019	0.168*	-0.131*	0.223*	-0.040	0.069	1	0.086*
P OUT	0.847*	-0.026	-0.001	0.208*	0.455*	-0.251*	0.168*	0.086*	1

stage for ensiling. Crossbred steers (n = 288; 320 ± 23 kg) were allotted to one of 24 pens (12 steers/pen) with each pen assigned to one of 6 treatments for a 68-d backgrounding (BK) and 148-d finishing program. Diets with the low inclusion level during BK consisted of 40.1% BS, 9.4% brome grass hay (hay), 40.1% barley grain (BG), 5.6% canola meal (CM) and 4.8% mineral-vitamin supplement (supplement; %DM), while high inclusion diets consisted of 53.5% BS, 9.4% hay, 26.7% BG, 5.6% CM and 4.8% supplement. During finishing, low inclusion diets consisted of 5.0% BS, 87.0% BG, 3.5% CM and 4.5% supplements while high inclusion diets consisted of 15.0% BS, 77.0% BG, 3.5% CM and 4.5% supplement (%DM). Actual NDFD averaged 37.6 ± 3.5, 34.7 ± 3.8 and 36.9 ± 3.0% for CB, CL and Xena, respectively. Data were analyzed as completely randomized design with pen as the experimental unit and treatment as the fixed effect using the mixed model procedure of SAS (9.4). During BK, cattle fed CB exhibited lower ($P < 0.01$) ADG and end of period BW (EBWT) than cattle fed CL or Xena. Low BS inclusion resulted in greater ($P < 0.01$) ADG and EBWT relative to high inclusion diets. The DMI during BK was less ($P < 0.01$) for steers fed CB relative to those fed CL, with Xena being intermediate. Low BS inclusion resulted in greater ($P < 0.01$) DMI than high inclusion. Feed efficiency was greater ($P = 0.02$) for steers fed low, relative to high inclusion diets. During finishing, ADG and DMI were greater ($P < 0.01$) for steers fed high BS inclusion diets. However, over the entire trial, performance and carcass characteristics were not impacted by treatment except for carcass weight where steers fed CL had heavier ($P = 0.04$) carcasses relative to those fed CB or Xena. These results indicate that barley variety and inclusion level will impact performance of growing cattle. Barley variety has a minimal impact on finishing performance.

Key Words: barley silage, cattle, performance

0486 Development of a genetic marker panel for ketosis in dairy cattle. V. Kroezen[*1], F. Miglior[1,2], F. S. Schenkel[1], and J. Squires[1], *[1]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, ON, Canada, [2]Canadian Dairy Network, Guelph, ON, Canada.*

During the transition period high-yielding dairy cattle are susceptible to ketosis, a metabolic disease which has negative impacts on the health, fertility and milk production of the cow. Genetic selection of animals resistant to developing ketosis is a potential solution to the economic losses faced by producers, as well as the reduced herd health and welfare associated with this disease. Genetic evaluations for ketosis, a health trait with low heritability, would benefit from the additional information provided by genetic markers. The objective of this study is to identify novel single nucleotide polymorphisms (SNP) within candidate genes for ketosis to be incorporated into a custom marker panel. Investigating candidate genes provides the opportunity to discover SNP with a functional role that are not currently included on commercially-available marker panels. A list of 123 candidate genes, selected based on biological relevance, were selected for in silico investigation; this includes genes which encode key enzymes and regulatory factors involved in metabolic pathways, genes that have been shown to be differentially expressed in ketotic animals, and genes that have been proposed by genome-wide association studies (GWAS). A preliminary GWAS from our group identified 462 SNP from high-density genotypes that are associated with de-regressed estimated breeding values for ketosis. These SNP were mapped to genes involved in pathways that were expected to be involved in ketosis (i.e., PPAR signaling pathway, CoA biosynthesis), as well as unexpected (i.e., T and B cell receptor signaling, apoptosis). Within the candidate genes, putative SNP were identified by aligning sequence data from online cDNA libraries with the gene reference sequence. The variant calling program, Sequencher 4.9, was used to identify SNP and their corresponding amino acid substitutions. SNP were prioritized for inclusion in the panel based on their Sorting Intolerant From Tolerant prediction score, to select polymorphisms which would most likely alter the function of the encoded protein. A set of 1081 SNP were incorporated onto a custom low-density panel. To our knowledge, this is the first custom panel composed of markers found in candidate genes that are specific to ketosis. The second phase of this project will use this panel to genotype several thousand cows from herds originating from Quebec, Canada; these data to be collected spring 2016.

Key Words: ketosis, SNP, candidate gene

0487 Taxonomic assessment of the rumen microbiome of bulls under backgrounding and finishing diets. E. O'Hara[*1,2], M. Zhou[1], S. M. Waters[2], M. E. Walpole[3], P. Gorka[4], M. Woodbury[5], G. B. Penner[6], and L. L. Guan[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [2]Teagasc Grange Animal and Bioscience Department, Dunsany, Co. Meath, Ireland, [3]Department of Animal and Poultry Science, University of Saskatchewa, Saskatoon, Canada, [4]University of Agriculture in Krakow, Poland, [5]Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon, Canada, [6]University of Saskatchewan, Saskatoon, Canada.*

To examine the effect of backgrounding and finishing diets on the rumen microbial community in beef cattle, 16 healthy beef bulls were blocked by BW and randomly assigned to 1 of 2 dietary regimes: a backgrounding diet (BCK: 45% grain) or a high-grain finishing diet (FIN: 80% grain). Initiation of both diets was staggered such that both groups received their final diets for 30 d. At the end of the treatment period, bulls were

slaughtered and samples of mixed ruminal digesta were collected for microbial analysis. A 454 pyrosequencing was performed on DNA amplicons, targeting the bacterial/archaeal partial 16S rRNA genes and protozoal partial 18S rRNA gene. Taxonomy was assigned using QIIME, with only those OTUs represented at > 0.05% in more than 4 bulls/treatment considered for downstream analysis. As a whole, the bacterial community of BCK was more diverse than FIN ($P < 0.01$). The bacterial phyla *Firmicutes, Bacteroidetes,* and *Proteobacteria* dominated regardless of treatment, with *Spirochaetes* (0.83% vs. 0.29% total bacteria) and *Fibrobacteres* (2.36% v 0.09%) higher in BCK ($P < 0.05$). *Choloroflexi* (0.44%; $P < 0.05$) was only found in in the BCK group. Twenty-four genera were affected by treatment, with *Ruminococcus* (6.92% vs. 2.13%) and *Fibrobacter* (2.36% vs. 0.09%) greater in abundance in BCK ($P < 0.05$) than FIN. *Succinivibrio* was among the genera that increased in FIN (2.12% vs. 0.025%; $P < 0.05$) relative to BCK, and *Megasphera* appeared exclusively in FIN (1.45%). Archaeal composition was not affected, with the *Methanobrevibacter gottschalkii* clade predominating in both groups. However, the methanogen community for BCK was more diverse ($P < 0.01$) than for FIN. The protozoal genus *Epidinium* predominated under both treatments (74–77% abundance), and the genus *Eudiplodinium* appeared exclusively in FIN bulls (6.42%, $P < 0.05$). Our results revealed that the responses to treatment differed across the three microbial groups, suggesting that future studies are needed to define their respective roles in rumen function during diet change.

Key Words: rumen microbiome, backgrounding diet, finishing diet

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0488 The transition cow: May the odds be ever in her favor. Y. Schuermann*[1], A. St-Yves[1], N. Dicks[1], R. C. Bohrer[1], R. Mondadori[2], G. Welsford[1], V. Boyer[1], M. Taibi[1], V. Higginson[1], S. Hartley[1], E. Madogwe[1], V. Bordignon[1], B. Baurhoo[1], and R. Duggavathi[1], *[1]McGill University, Ste.-Anne De Bellevue, QC, Canada, [2]Federal University of Pelotas, Capão do Leão, Brazil.*

Longevity is a key component of sustainable dairy farming. High-yielding dairy cows often suffer from ovarian dysfunction and infertility leading to reduced reproductive and productive longevity. Infertility has been attributed to the metabolic stress during the transition period. However, potential metabolic alterations that may dysregulate ovarian functions have not been completely cataloged. Our objective was to characterize metabolic parameters of dairy cows during the transition period. In the first experiment, we examined the metabolic profiles in circulation to pinpoint time-points of major changes. We collected weekly blood samples from Holstein cows ($N = 15$) from 3 wk before until 12 wk after calving. As expected, glucose levels reduced during pre-calving weeks to reach a nadir at 3 wk post-calving ($P < 0.05$) and the first increase in glucose concentration occurred at 10 wk post-calving ($P < 0.05$). Also, β-hydroxybutyric acid levels increased from calving until wk 3 of lactation ($P < 0.05$) and subsequently returned to baseline. Levels of triglycerides decreased during pre-calving weeks, while significant increase occurred at 5 wk post-calving ($P < 0.05$). Total cholesterol concentrations increased from the third to seventh week post-calving ($P < 0.05$). Total bile acid levels increased from 3 wk to 2 wk before calving and stayed elevated throughout the transition period ($P < 0.05$). Oxidative stress indicator, glutathione, decreased to reach a nadir by 7 wk in lactation ($P < 0.05$), while the ferric reducing ability of plasma remained constant ($P > 0.05$). Thus, post-calving wk 3 to 7 are associated with major changes in metabolic indicators in circulation. In the second experiment, we evaluated changes in liver mRNA levels and circulating metabolic indicators during the periods of major metabolic changes above. We collected blood and liver biopsy samples from Holstein dairy cows at 3 wk pre-partum, during the calving week and 7 wk post-partum ($N = 13$). Quantitative PCR analyses ($N = 4$) did not reveal any changes in the hepatic mRNA abundance of genes indicative of liver functions including acyl-CoA:cholesterol acyltransferase 1 (*ACAT1)*, Paraoxonase-1 (*PON1*) and sterol regulatory element-binding factor-1 (*SREBF1*) during wk 6–7 post-calving compared with peri-calving period. Taken together, transition period in dairy cows features increasing cholesterol, triglycerides, total bile acids and decreasing glucose and glutathione compared with pre-calving period. However, these changes appear to be independent of alterations in mRNA levels in the liver. Further studies, including liver function assays, are required to thoroughly investigate the relationship between liver health and alterations in circulating metabolic indicators during transition period in dairy cows.

Key Words: cow, liver, infertility

0489 Effect of dietary wheat bran inclusion on nutrient digestibility in weaned pigs. B. Koo*, M. M. Hossain, and C. M. Nyachoti, *University of Manitoba, Winnipeg, Canada.*

Wheat bran (WB) as a source of insoluble fiber has been shown to confer gut health benefits in weaned piglets. However, there is limited data on the influence of WB inclusion in weaner pig diets on digestibility. Thus, the aim of this study was to assess the effect of a 4% dietary inclusion of coarsely milled (1088 µ of particle size) WB on nutrient digestibility in weaned pigs. Six barrows (7.3 ± 0.1kg BW) fitted with a T-cannula at the distal ileum were fed one of two test diets consisting of: (1) a barley-wheat-corn-soybean meal-based diet (Control) and (2) a WB diet with 4% coarsely milled WB. Diets were assigned according to a 2x2 Latin square design repeated three times. At the end of the second period, all pigs were fed a 5% casein-corn starch-based diet to estimate basal endogenous amino acid (AA) losses. Each period lasted 9 d consisting of

5 d for adaptation followed by 2 d for fecal collection and 2 d for ileal digesta collection (12 h/d). All pigs were fed diets mixed with 0.3% titanium dioxide as an indigestible marker to calculate apparent total tract digestibility (ATTD), apparent ileal digestibility (AID) and standardized ileal digestibility (SID) of nutrients. Treatment means were compared using the Student *t* test procedure of SAS (SAS Inst. Inc., Cary, NC). Piglets fed the WB diet had lower ATTD of organic matter and AID of dry matter (DM) compared with those fed the control diet (89.4 vs. 88.3% and 60.8 vs. 66.4%; $P < 0.05$). However, piglets fed the WB diet had higher ATTD of fat compared with those fed the control diet (70.4 vs. 62.6%; $P < 0.05$). There were no differences in the AID and SID of nitrogen (N) and AA between the two diets ($P > 0.10$). Average AID values (%) were 66.3, 80.5, 41.5, 79.9, 80.4, 80.9, 87.2, 81.3, 71.6, and 76.0 for N, Arg, His, Ile, Leu, Met, Phe, Thr, and valine, respectively. Respective average SID values (%) were 79.7, 88.9, 66.4, 86.3, 84.5, 85.2, 90.3, 84.8, 80.2, and 82.7. In conclusion, results indicated that dietary inclusion of WB increased ATTD of fat and reduced ATTD of OM and AID of DM in weaned piglets. Further research is warranted to evaluate effects of WB, especially on growth and health performance, gut microbiota and fecal and/or ileal digesta volatile fatty acids production.

Key Words: digestibility, piglets, wheat bran

0490 Effect of steam flaking and seed type on carbohydrate molecular structure features associated with nutrient availability of legume seed in ruminants.

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The objectives of this study were to evaluate the effect of steam flaking processing and different seed type on carbohydrate spectroscopic features in relation to degradation kinetics. Six different sources of peas from Duck Lake and COOP were processed at Canadian Feed Research Center (CFRC, University of Saskatchewan, North Battleford, Canada). The carbohydrate molecular structure makeup was detected using attenuated total reflectance-Fourier transform infrared spectroscopy instrument at molecular spectroscopy lab, Department of Animal and Poultry Science, University of Saskatchewan. Three rumen-cannulated lactating Holstein cows were used to determine the in situ rumen degradation kinetics of DM and starch at Rayner Dairy Teaching and Research Facility (RDTRF). Statistical analyses were performed using the PROC MIXED procedure of SAS 9.3. The Tukey method was used for multi-treatment comparison. Difference was declared at $P < 0.05$. The results of univariate molecular spectral analyses showed that the whole pea seed had a significantly higher ratio of structural carbohydrate to total carbohydrate area than split pea seed (0.313 vs. 0.307; $P < 0.05$). The spectral ratio of cellulosic compound to structure carbohydrate area was significantly affected by steam flaking treatment, which was higher in flaking pea seed than the control (0.153 vs. 0.135; $P < 0.05$). Additionally, steam flaking treated pea seed also had a significant higher spectral ratio of cellulosic compound to total carbohydrate area than control untreated pea seed as a control (0.047 vs. 0.042; $P < 0.05$). In conclusion, steam flaking affected the inner molecular makeup of pea seed, which may be highly associated with the nutrient utilization.

Key Words: flaking, pea seed type, molecular structure

0491 Dynamics of progesterone concentrations and insemination outcomes in dairy cows.

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The objective was to evaluate the association between milk progesterone (P4) concentrations and its dynamics with insemination outcomes. In-line milk P4 records (Herd Navigator, DeLaval Inc.) relating to 605 inseminations (AI) were assessed from two dairy farms. Only cows that had confirmed luteolysis (P4 declined to < 5ng/mL) and ovulation (P4 increased to > 5 ng/mL) were included. The day of luteolysis was considered d 2 and AI occurred on d0. Progesterone at d 2, 5, 10, 14, and maximum P4 (Peak) within d 21 were considered, in addition to the rate of increase in P4 (e.g., d 2 to d 5). Insemination outcomes were defined as open (P4 > 5 ng/mL for < 20 d; $n = 357$), pregnant (P4 > 5 ng/mL for > 45d; $n = 170$) or pregnancy loss (P4 > 5 ng/mL for > 20 to $\leq$ 45 d, $n = 78$). Progesterone concentrations were modeled against outcomes of AI and parity, while herd and AI (first or second) were considered random variables, and data analyzed using MIXED procedure of SAS. Milk P4 at d 2 tended to be lower ($P = 0.10$) in pregnant (3.33) than in open (3.44) or cows that suffered pregnancy loss (3.44). Pregnant cows had greater P4 ($P < 0.01$) than open cows at d 10, 14 and at Peak (9.6, 18.3 and 23.4 vs. 8.3, 16.7 and 20.3, respectively). Rate of P4 increase (ng/mL/d) was also greater ($P < 0.01$) in pregnant than in open cows from d 2 to 14, d 2 to Peak, d 5 to 10, d 5 to 14 and d 5 to Peak (0.9, 1.0, 1.1, 1.6 and 1.5 vs. 0.8, 0.9, 0.9, 1.4 and 1.3, respectively). However, the aforesaid dynamics of P4 did not differ among cows that remained pregnant or suffered pregnancy loss. Primiparous cows had higher P4 ($P < 0.03$) than multiparous cows at d 2, 5, 10, 14 and at Peak (3.5, 4.8, 10.8, 19.7 and 23.6 vs. 3.3, 3.0, 7.7, 16.0 and 21.2 ng/mL, respectively). Furthermore, primiparous cows had a greater rate of P4 increase ($P \leq 0.05$) than

multiparous from d 2 to 5, d 2 to 14, d 2 to Peak, d 5 to 10, d 5 to 14, d 5 to Peak and d 10 to 14 (0.2, 1.0, 1.0, 1.2, 1.6, 1.4 and 2.2 vs. −0.1, 0.8, 0.9, 0.9, 1.4, 1.3 and 2.0, respectively). Cows that conceived, regardless of whether or not they suffered pregnancy loss, had greater P4 concentrations (except on d 2) and a greater rate of P4 increase than open cows. Also, primiparous cows consistently had greater P4 concentrations and rate of increase than multiparous cows.

Key Words: in-line milk progesterone, estrous cycle, fertility

CSAS SYMPOSIUM: REDUCING THE USE OF ANTIBIOTICS IN LIVESTOCK PRODUCTION

0492 Alternatives to antibiotics in swine and poultry.

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To reduce the risk for the spread of antibiotic resistant bacteria from livestock to humans, the European Union banned the use of antibiotics as growth promoters in animal feeds for pigs and poultry since January 2006. As a result, the use of veterinary prescribed antibiotics increased in a sort of compensation phenomenon. In intensive husbandry systems, veterinary prescribed antibiotics are mainly used around birth and in newborn animals.

To study the effects of antibiotic usage during early life stages, we performed several experiments in piglets and poultry. We analyzed both the short-time and long-term effects at the level of intestinal microbiota and intestinal mucosal functions. To this end, we applied metagenomics, transcriptomic and immunologic analytical approaches on intestinal tissues and luminal contents, taken at different intestinal locations and at different time-points after treatment. These studies clearly demonstrated both short-term and long-term effect on the expression of immune related genes. We hypothesized that that these long-lasting effects are due to differences in the programming of the gut immune system as induced by the temporary early life perturbation of the gut microbiota.

To search for alternatives for antibiotic growth promoters, a large variety of farming approaches are proposed, including organic acids, probiotics and prebiotics, enzyme, clays and minerals, trace elements, and botanicals. In this presentation, we will show the effect of the administration of fructooligosaccharides (FOS) to suckling piglets on intestinal microbiota and gene expression. Twelve days of intervention with FOS resulted in a bifidogenic effect in the colon of treated piglets. Furthermore, after 23 d of intervention with FOS, decreased expression in immune related gene sets was observed in treated piglets.

In this context, it is also important to identify major intrinsic and extrinsic factors that (co)determine the early life gut microbial colonization of livestock species. From literature it is already known that several extrinsic factors are important, including the sow/mother-hen and the environment. Here we show data that indicate that also the genetic make-up of host is an important factor in the early life microbial colonization of the gut and consequently for immune system development.

In conclusion, during early life, the interplay between the host (genetics), environment (nutrition and/or management), in association with the microbiota modulate bacterial colonization, drives gut development and immune maturation. The use of antibiotics during early life stages perturbs this interplay significantly with serious consequences for the functionality of the host immune system.

0493 Management of dairy cows to improve resistance to infectious diseases.

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The incidence of infectious diseases varies greatly during the lactation cycle. Most new cases of clinical mastitis appear at the beginning of lactation (transition period), and the incidence increases with the level of milk production. In addition to mastitis, the majority of other infectious diseases becomes clinically apparent during the first 2 wk of lactation. During this time, cows are in negative energy balance and they must mobilize body reserves to balance the deficit between food energy intake and energy required for milk production. Cows undergoing energy deficit have a weakened immune system, which increases their susceptibility to infections. Therefore, we evaluated the effects on blood metabolite concentrations and immune functions of limiting milk production in early lactation to reduce the negative energy balance. In a first experiment, multiparous Holstein cows were milked either once a day or twice a day for the first postpartum week. In a second experiment, the amount of milk harvested was limited by milking cows incompletely (about one-third of expected milk production was collected) twice a day until d 5 after calving. In a third experiment, first-wk milk production was limited by administering a prolactin secretion inhibitor, quinagolide, during the first days of lactation. Globally, the results of these studies indicate that reducing the amount of milk harvested postpartum while maintaining milking stimuli reduces metabolic stress and immunosuppression without compromising productivity of high-yielding dairy cows. The second period that has the highest incidence of new intramammary infections

(IMI) is the period immediately following drying-off, during early mammary gland involution. The importance of the dry period is often underestimated as many of these new infections are only detected after the next calving. A cow's risk of acquiring a new IMI during the dry period increases with milk production at drying-off but decreases as mammary gland involution progresses. In this context, we tested whether prolactin inhibition could be used to reduce milk production at drying-off and to accelerate the rate of mammary involution after cessation of milking. In late-lactation cows, quinagolide decreased milk production within the first day of treatment and induced more rapid changes in concentrations of several markers of mammary gland involution after drying-off. In addition, quinagolide improved the resistance to IMI suggesting that prolactin inhibition could be a new strategy for facilitating drying-off. Innovative management can be used to reduce dairy cow's susceptibility to infection and antibiotic utilization.

Key Words: mastitis, transition period, blood metabolites

0494 Selection for disease resistance in swine.

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Infectious disease is a major problem for swine production around the world despite successes in terms of biosecurity and vaccination. Perhaps the best known examples of disease resistance pertain to infection with *E. coli* F4 (K88) or F18, which cause scours in young pigs and can result in significant morbidity and mortality. In other cases, there is variation in susceptibility but all pigs become sick. Porcine respiratory and reproduction syndrome (PRRS) is an example of a disease where all pigs are infected by PRRSV but the impact on the host varies. For example, the amount of virus produced and the growth of the infected pigs varies significantly between individuals. Genome wide association studies identified a relatively large effect on chromosome 4 (SSC4) and Boddicker et al. (2012 *J. Anim Sci* 90:1733) reported that this region explained 15.7% of the genetic variance for viral load and 11.2% for gain. Subsequently a putative functional variant in *GBP5* was identified as the likely causative mutation (Koltes et al., 2015 *BMC Genomics* 16:412). Two regions of the genome were identified as explaining a similar amount of variation in PCV2 susceptibility (Engle et al., 2014 *Proc. 10th WCGALP).* Although these findings offer potential tools to reduce the impact of these two major viruses through genomic assisted selection, it would be very difficult to combine such tools for all of the important diseases. One option may be to select for animals that respond better to infection, maintaining growth and/or rapidly recovering. This is described as resilience or robustness. A new study is underway to investigate resilience using a "natural challenge" model consisting of a number of different agents including PRRSV as well as Swine Influenza Virus, *Haemophilus parasuis* and *Streptococcus suis*. A number of approaches are being used to try to identify biomarkers that will predict resilience in high health status pigs to reduce the impact of infection and contribute to reducing the use of antimicrobials in production. For example, Kommadath et al. (2015 *BMC Genomics* 15: 452) used RNaseq to identify gene expression patterns before infection with *Salmonella* that predict different outcomes in terms of carriage of the pathogen. A second option in the future may be to use gene editing to manipulate the early stages of infection and develop novel resistance as was recently demonstrated so remarkably for PRRSV by Prather and colleagues (Whitworth et al., 2016 *Nature Biotechnology* 34:20).

Key Words: health, pigs, resilience

0495 Genomic approaches to characterizing and reducing antimicrobial resistance in beef cattle production systems.

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The current rate of resistance development against antimicrobials (AMR) available for use in human medicine is a global health threat. The discovery and design of new antibiotics is nearly at a standstill and as a result, the approximately 700,000 global deaths attributed to AMR infections yearly is expected to rise. Intensive livestock operations, including beef production systems require the use of antimicrobials to ensure animal health and to optimize growth efficiency. As a result the microbes present in the feedlot environment can be exposed to multiple classes of antimicrobials and have the potential to harbor, acquire or develop resistance. To understand the magnitude and risk of AMR in this setting, it is important to assess the prevalence and diversity of AMR determinants in the microbial population. AMR bacteria are traditionally identified by isolation and growth in the presence of selective antibiotics. However, more recent advances in genomics have enhanced the precision of AMR characterization. Whole-genome, metagenomic, and RNA sequencing provide new avenues for the rapid detection of AMR determinants in microbial communities, including unculturable organisms. Metagenomic approaches can be used to identify both previously characterized and novel AMR mechanisms in recalcitrant bacteria which may serve as an environmental reservoir of resistance genes. Metagenomic approaches can also be used to place AMR genes within the context of mobile genetic elements, providing information with regard to the likelihood of their dissemination among microbial communities. Genomics may also play a key role in mitigating and developing alternatives to antimicrobials such as probiotics. RNA-seq-based

transcriptomics and Tn-seq may also provide new ways to examine the cellular mechanisms that may promote AMR or prevent it. Finally, CRISPR-Cas gene-editing shows promise as a tool to directly reduce AMR by killing AMR-resistant organisms without harming beneficial microbes. All these technological developments provide new opportunities to better identify, quantify, and mitigate resistance to antimicrobials as well as develop alternatives.

Key Words: antimicrobial resistance, bacteria, beef, cattle, CRISPR-Cas, genomics, metagenomics

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0496 Nurturing healthy gut microbiome: route to increased disease resistance in ruminants.

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Perturbations in gut microbiota colonization during early life have been shown to present long lasting influences to the host immune responses, health and metabolism as well as subsequent microbial succession. These perturbations can be caused by nutritional imbalances, differing feeding methods, nutritional regimes and antibiotic treatments during the early life. Management of ruminants can vary significantly due to different feeding practices and it relies heavily on antibiotics prevention/treatments for diarrhea and pneumonia in pre-ruminants. However, our understanding on the influence of such management practices on gut microbiome as well as ruminant health and metabolism is very limited. Our recent study has revealed that feeding of heat-treated colostrum soon after birth enhances the colonization of beneficial bacterium, bifidobacteria, which is well-studied using mouse models and has been shown to have greater impact on mucosal immune system development as well as weight gain in children. Besides, the colonization of bifidobacteria in calf gut has been suggested as a preventive mechanism of pathogenic *E. coli* that causes neonatal calf diarrhea. The use of next generation sequencing approaches to study calf gut microbiome and linking the early microbial composition with that of calf phenotypes have reported that higher abundance of *Fecalibacterium* is associated with decreased diarrhea incidences and increased body weight, suggesting linkages between gut microbiome, calf health and growth. Moreover, diet-driven changes in rumen microbiome are related to the development of subacute ruminal acidosis, a prevalent metabolic disorder in adult cattle. Thus, understanding on gut microbiome and their link to gut/rumen development and metabolism will provide means to improve health in ruminants via microbial manipulation. Such manipulation methods toward nurturing a healthy gut microbiome not only improve the disease resistance in ruminants, but may also decrease the heavy antibiotic usage that is in practice in the industry.

Key Words: disease resistance, gut microbiome

0497 Pre- and probiotics for increased disease resistance in the nonruminant animal.

C. M. Nyachoti*, *University of Manitoba, Winnipeg, Canada.*

In addition to formulating diets for poultry and swine to optimize performance outcomes, an equally important goal is to apply nutritional interventions to support a healthy and functional gastrointestinal tract. The latter has gained considerable interest as the utilization of in-feed antibiotics and some ingredients (such as those derived from animals) has come under increased scrutiny and may no longer be an option. To this end, feed additives such as pre- and probiotics have been suggested as feed additives with potential to mitigate enteric diseases in poultry and swine raised under antibiotic-free feeding programs. Prebiotics are ingredients that are selectively fermented and lead to specific changes in the composition and (or) activity of gut microbiota (e.g., bifidobacteria and lactobacilli) that confer beneficial effects to the host. Various carbohydrate components, including fructooligosaccharides and transoligosaccharides and other fiber types (e.g., inulin, sugar beet pulp, and coarsely ground wheat bran) have been reported to cause prebiotic effects in poultry and swine. Moreover, it has been reported that dietary supplementation with carbohydrases may generate carbohydrate components in the gut that could enhance gut health and function partly by acting as prebiotics. Probiotics are live microorganisms which when administered in adequate amounts confer a health benefit on the host. The beneficial effects of these additives are mediated through one or more of the following mechanisms in the gut: stimulation of a healthy microbiota, prevention of enteric colonization by pathogens, improving digestive capacity and lowering the pH, improving mucosal immunity, or enhancing gut tissue maturation and integrity. Bacillus, yeast and lactic acid-producing bacteria such as *Lactobacillus*, *Bifidobacterium*, and *Enterococcus* are the most common groups of organisms used as probiotics. This presentation will highlight recent studies on the utilization of pre- and probiotic utilization in the nutritional management of gut health and function in the nonruminant animal. Also, the mechanisms underlying the effects of these additives will be discussed along with the possible reasons for the inconsistencies often seen among studies with regards to the efficacy of these additives.

Key Words: prebiotics, probiotics, poultry, swine

DAIRY FOODS DIVISION

0498 Investigating the antimicrobial activity of pasteurized and raw camel milk against foodborne pathogens: Listeria monocytogenes and *E. coli* O157:H7. M. Ayyash*, *UAE University, Al-Ain, United Arab Emirates.*

The objectives of this study were to investigate the antimicrobial activity of pasteurized camel milk against foodborne pathogens (*L. monocytogenes* and *E. coli* O157:H7) at different incubation temperatures, and to examine the influence of pasteurization on antimicrobial activity of camel milk at different incubation temperatures. Pasteurized or raw camel milks were inoculated with a cocktail of *L. monoctogenes* or a cocktail of *E. coli* O157:H7, separately. Inoculated camel milk was incubated at 10°C, 25°C, and 37°C and sampled at 0, 2, 4, 8, and 24 h of incubation time. This procedure was exactly applied using pasteurized bovine milk as a control for this experiment. All experiments were repeated at least three times. Chemical compositions of all milks were determined. pHs during incubation, total bacterial count in raw camel milk, and thermoduric bacteria in pasteurized milks were monitored. During incubation time, *L. monocytogenes* growth increased dramatically after 2 h when incubated at 25°C and 37°C but no significant growth observed at 10°C. *E. coli* O157:H7 showed similar behavior. Interestingly, growth of *L. monocytogenes* and *E. coli* O157:H7 in pasteurized camel milk were significantly lower than in pasteurized bovine milk. In general, the growth of *L. monocytogenes* in camel milk was suppressed by 15–18% and 8–10% after 8 and 24 h of incubation, respectively. However, growth suppression of *E. coli* O157:H7 ranged from 5–21% and 6–14% after 8 and 24 h of incubation time, respectively. Growth suppression of *E. coli* O157:H7 was influenced significantly by temperature but not suppression of *L. monocytogenes* growth. In conclusion, our results showed that camel milk possesses antimicrobial activity against foodborne pathogens (*Listeria monocytogenes* and *E. coli* O157:H7). Moreover, pasteurization process has insignificant effect on antimicrobial activity of camel milk. Further investigations are need to identify and characterize antimicrobial agents in camel milk.

Key Words: camel milk, *Listeria monocytogenes*, *E. coli* O157:H7, antimicrobial activties

0499 Application of fluorescent probes to determine localized salt concentrations within cheese matrices and their influence on metabolic activity of entrapped bacterial cells. C. D. Hickey[1], V. Fallico[1], Z. Burdikova[1], M. G. Wilkinson[2], and J. J. Sheehan[*1], *[1]Teagasc Food Research Centre Moorepark, Co. Cork, Ireland, [2]University of Limerick, Ireland.*

The influence of salt on microbial growth and activity in cheese has received much prior attention. However, the way in which salt within cheese matrices affects bacterial physiology to control cell growth is not fully elucidated. Application of advanced microscopy techniques to determine salt concentration at a localized level is of interest to understand interactions between cheese matrix physico-chemistry and microbial activity before, during and post-brining of cheese. The objective of this study was to determine the presence of and effects of localized salt gradients associated with brine salting on microflora physiology and metabolic activity of the individual starters, *S. thermophilus* and *L. helveticus* used in cheese manufacture. Cheeses were manufactured in 3 replicate trials, brined for 66 h and sampled at the high-salt outside and low-salt inside layers before, during and post-brining. Localized salt concentrations were determined using CoroNa Green Sodium Indicator by Confocal Laser Scanning Microscopy. The average salt content in the outside layer post brining was ~3.8%. The response of cytoplasmic membrane integrity of bacterial cells and levels of free reactive oxygen species to salt concentrations were assessed using fluorescent probes combined with Flow Cytometry. There were greater levels of membrane damage and oxidative stress observed in *L. helveticus* compared with *S. thermophilus* at all times. Confocal imaging clearly identified localized variations in salt concentrations and illustrated the penetration distance of the brine solution into the matrix during and post-brining. Overall, this study showed a differing impact of varying salt levels on cheese starter physiology and metabolic activity in vivo, dependant on starter type and confirmed that the methodologies used have the potential to identify ripening hotspots at a localized level. It opens up further opportunities to apply fluorescent probes to gain a deeper understanding of the influence of cheese matrix physicochemistry on the metabolic activity of entrapped bacteria and thus to control cheese manufacture processes to achieve greater consistency in ripened cheese quality.

Key Words: cheese, salt gradients, metabolic activity

0500 Inducing HT-29 colon cells apoptosis by the extracellular polymeric substances isolate from *L. casei* strains. W. Di[*1], L. Zhang[1], X. Han[2], [1]*Harbin Institute of Technology, China,* [2]*Harbin Institute of Technology, China.*

Nine *Lactobacillus* strains (*L. casei* X11, *L. casei* X12, *L. casei* K11, *L. casei* J5, *L. rhamnosus* J10, *L. casei* M5, *L. casei* M23, *L. rhamnosus* IN4125, and *L. casei* SB27) were obtained from the Chinese traditional fermented foods of minority nationalities or infant feces based on the previous research in our laboratory (4 strains from Sinkiang, 3 strains from Gansu, 1 strain from Tibet, 1 strain from infant feces). Fermentation broths from skim milk produced by the nine *Lactobacillus* strains were screened for anti-proliferation activity on HT-29 cells by MTT assay. The results showed that four strains exerted higher anti-proliferation activity on HT-29 effects than positive control ((*Lactobacillus rhamnosus GG, LGG*). Crude and acidic exopolysaccharides isolated from the 4 strains (*L. casei* K11, *L. casei* M5-L, *L. casei* SB27, *L. casei* X12) at different concentrations (10, 20, 100, 200, and 500 μg/mL) were systematically assessed for the anti-proliferation activity on human colon cancer HT-29 cells. Further the apoptosis induced by exopolysaccharides (EPSs) were analyzed by flow cytometry (FCM) on HT-29 cells. The colon cancer cells treated with *L. casei* SB27 acidic exopolysaccharides achieved the highest rate of apoptosis, 24.3% cells were found apoptosis and 1.4% cells in necrosis. The results of cell cycle analysis on HT-29 cells cycle treated with exopolysaccharides showed that *L. casei* SB27 acidic exopolysaccharides could slow the conversion rate of HT-29 cells from G phase to S phase, prolong the cell cycle and reduce the proliferation of colorectal cancer cells. The results of HT-29 cells Caspase-3 activity treated with *L. casei* acidic SB27 fraction showed that Caspase-3 was activated and achieve the significantly highest of all the samples at 2.79- fold compared with control group at 1.2- fold. The result of Hoechst 33258 staining shown that HT-29 colon cells treated with *L. casei* SB27 acidic exopolysaccharides appeared bright condensed dots compared with untreated with exopolysaccharides samples.

Key Words: *L.casei* strains, exopolysaccharides, HT-29 colon cancer cells apoptosis

0501 Comparative genomics of *Lactobacillus brevis* uncovers its common capability for efficiently synthesizing neuroactive γ-aminobutyric acid. Q. Wu[*1], H. M. Tun[2], Y. S. Law[1], E. Khafipour[2], and N. P. Shah[1], [1]*School of Biological Sciences, University of Hong Kong, Pokfulam, Hong Kong,* [2]*Department of Animal Science, University of Manitoba, Winnipeg, Canada.*

γ-Aminobutyric acid (GABA) is the chief inhibitory neurotransmitter in mammalian central nervous system and has shown anti-hypertensive and anti-depressant activities to the host after oral administration. However, its content in natural animal and plant products is too low to deliver benefits to human. Thus, GABA synthesized by food-grade bacteria such as *Lactobacillus* and *Bifidobacterium* is an important source and its producers could be used for manufacturing GABA-rich fermented dairy foods. Many GABA-producing *Lactobacillus* and *Bifidobacterium* strains have been isolated and characterized in the last decade and have shown strain-specific capability in the synthesis of GABA. Among these GABA producers, *Lactobacillus brevis* seems to be the most common cell factory for synthesizing GABA. In this study, comparative genomic approach was used to identify which LAB species have the common ability to produce high amount of GABA and to identify the essential genetic elements for GABA production. It was found that gene encoding glutamic acid decarboxylase (GAD) and an intact *gad* operon were present in all the sequenced strains of *L. brevis* at the species level, but not all the strains of other *Lactobacillus* and *Bifidobacterium* species possess an intact *gad* operon including a regulator *gadR*, a *gadA*- or *gadB*-encoding GAD, and an antiporter *gadC*. This suggests the common capability of *L. brevis* to synthesize GABA. Moreover, enzyme assay for two GADs from *L. brevis* indicated that both enzymes are functional with high activities. Carbohydrate utilization by model strain *Lb. brevis* NPS-QW-145 generated different lactic acid production, which showed strong positive correlation with its GABA yields suggesting that intracellular lactic acid production triggers its GABA biosynthesis, which was also evidenced by the intracellular pH level of the cells. Moreover, among all of acid resistance (AR) pathways in *Lb. brevis*, GAD pathway contributed to late acid resistance whereas tyrosine decarboxylation (TDC) and arginine deimination (ADI) pathways were activated during lag and log phases, which were confirmed by transcriptional profiles and concentrations of the end metabolites of each AR. The present study highlights the common capability of *Lb. brevis* for highly efficient biosynthesis of GABA.

Key Words: comparative genomics, γ-aminobutyric acid, *Lactobacillus brevis*

0502 Effect of incubation temperature on yield and molar mass of EPS during fermentation of milk by *Streptococcus thermophilus* DGCC 7785 and the impact on the rheological properties of acid milk gels. S. N. Khanal[*1] and J. A. Lucey[2], [1]*University of Wisconsin, Department of Food Science, Madison,* [2]*Wisconsin Center for Dairy Research, Madison.*

Some strains of *Streptococcus thermophilus* produce exopolysaccharides (EPS) during milk fermentation. It is unclear if there is any change in the yield, or properties, of EPS when milk is fermented at different temperatures. We investigated the yields of both ropy and capsular forms of EPS, and the

physical properties of ropy EPS that were isolated during the fermentation of milk by *S. thermophilus* strain DGCC 7785. Reconstituted skim milk was fermented at 33, 39, and 45°C until pH reached 5.2, 4.9, 4.7 and 4.5. Fermented milk was then heated to 80°C for 10 min and whey (containing bacterial cells) was obtained by decantation. Whey was ultrafiltered with sufficient diafiltration using 100 kDa membrane at 45°C to remove soluble sugars and proteins. The UF retentate was centrifuged and the supernatant and pellet were analyzed for ropy and capsular EPS, respectively. Ultrafiltration of whey from a non-EPS producing strain was also performed as a control for estimating the amount of capsular EPS. Molar mass of ropy EPS samples were analyzed using size exclusion chromatography multi-angle laser light scattering (SEC-MALLS). Rheological properties of fermented milk gels were analyzed using small-strain dynamic oscillatory measurements. The yield of ropy EPS was 102, 108, and 55 mg/L when milk was fermented at 33, 39, and 45°C respectively, whereas the yields of capsular and total EPS were 102, 132, and 102 mg/L, and 204, 241, and 157 mg/L for these fermentation temperatures (33, 39, and 45°C). Significantly higher ($P < 0.05$) yields of capsular and total EPS were produced at 39°C. Total EPS content significantly ($P < 0.05$) increased from 150 mg/L to 257 mg/L when the pH of milk decreased from 5.2 to 4.5. Molar mass of ropy EPS ranged from 2.0×10^6 to 2.8×10^6 g/mol, exhibiting no significant ($P > 0.05$) effect of temperature or pH values during fermentation. Gelation pH (~ 5.3) of milk did not change with incubation temperature, whereas storage modulus values of the final gel (at pH 4.5) significantly ($P < 0.05$) increased (58, 135, and 410 Pa at 45, 39, and 33°C, respectively) with a decrease in fermentation temperature.

Key Words: exopolysaccharides, fermented milk, *Streptococcus thermophilus*

0503 Probiotic-fermented maillard reaction products: New functional food for cardiovascular health.
S. Kim*, *Korea University, Seoul, Korea (The Republic of)*.

Cardiovascular diseases (CVDs) are the leading contributors to adult mortality worldwide and will continue to dominate mortality trend in the future. Unhealthy dietary practices of consuming foods which are high in calories and/or cholesterol are commonly associated with elevated oxidative stress and accompanied by an increased risk of CVDs. Recently, dietary approach using probiotic intervention is increasingly recognized as a natural health improving supplement, attributed to their long history of safe use with beneficial effects on gastrointestinal health. Probiotic *Lactobacillus* strains are frequently incorporated in yogurts and fermented milk products, but other dairy products are also widely available and potentially developed as functional dairy probiotic foods. Maillard Reaction Products (MRPs) are compounds that can be produced through non-enzymatic reaction between lactose and milk protein (whey protein concentrates or sodium caseinate), which possess antioxidant activity and may exert protective effect in CVDs. Despite these suggestions, no attempt has been made to incorporate probiotics into MRPs and to evaluate their potential applicability on cardiovascular health. Thus, the potential cardiovascular health benefits of MRPs fermented by *Lactobacillus* strains were determined in the present study. In vitro studies demonstrated that hydrolysates of MRPs fermented by *L. gasseri* or *L. fermentum* strain exhibited significantly higher proteolytic, antithrombotic, and radical scavenging activities compared with unfermented MRPs. Hydrolysates of these fermented MRPs also significantly inhibited the 3-hydroxy-3-methylglutaryl-CoA reductase activity, which is the rate-liming enzyme in the cholesterol biosynthetic pathway. In animal studies, feeding of *Lactobacillus* fermented MRPs to acute pulmonary thromboembolism-induced mice were shown to attenuate serum cholesterol levels and thrombotic activity, improve liver enzymes activity, as well as overcome severe body paralysis or death. Additionally, *Lactobacillus* fermented MRPs were also capable of regulating mRNA expression level of cholesterol metabolism related genes and modulating gut microbiome in rats fed with high-cholesterol diet. My talk highlights on the recent findings and biological mechanisms by which probiotic fermented MRPs exert their beneficial effects on cardiovascular health.

Key Words: probiotics, functional food, cardiovascular health

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0504 An ancient, species-specific tagatose-6-phosphate pathway in *Lactobacillus casei* group for galactose reduction in cultured dairy foods.
N. P. Shah* and Q. Wu, *School of Biological Sciences, University of Hong Kong, Pokfulam.*

Residual lactose and accumulated galactose in cultured dairy foods lead to several medical and industrial concerns such as lactose intolerance, galactosemia, and browning of pizza during baking. Our previous comparative KEGG study on galactose metabolism pathways in sequenced LAB strains has uncovered the presence of tagatose-6-phosphate (T6P) pathway in all of the completely sequenced *Lactobacillus casei* group strains including *Lb. casei*, *Lb. paracasei* and *Lb. rhamnosus*. In this study, we have demonstrated that T6P pathway, but not Leloir pathway, in *Lb. casei* group is more efficient for lactose and galactose catabolism than Leloir pathway in selected strains of *Lb. acidophilus* group, *Streptococcus thermophilus* and *Lb. bulgaricus* cultured in galactose- or lactose-based MRS media. However, the activity of β-galactosidase, which is a key enzyme in Leloir pathway in *Lb. casei* group strains, was not detected. In the milk, *Lb. casei* group strains catabolize less lactose than *Str. thermophilus*, *Lb. bulgaricus* and *Lb. acidophilus* group, but very limited galactose was accumulated in milk. Moreover, co-cultivation

of *Lb. casei* group with *Str. thermophilus* or *Lb. bulgaricus* generated less galactose or lactose in the cultured milk. In addition, comparison of *lac-gal* gene cluster in sequenced *Lb. casei* group strains has shown the presence of an unknown PTS (PTS^{Unk}) in this region. The EIIC of PTS^{Unk} has conserved protein domain found in EIIC of PTS^{Gat} (galactose-specific PTS) and its gene expression was also highly up-regulated (> 200 fold changes) in the presence of galactose suggesting its possible role for galactose phosphorylation. In addition, it was found that *lac-gal* clusters in the genomes of *Lb. casei* group strains are not associated with any HGT events suggesting that this cluster may be an ancient pathway. This study demonstrates the use of *Lb. casei* group strains as functional dairy starter for lactose or galactose depletion in milk. Further characterization of PTS^{Unk} in *Lb. casei* group using genetic manipulation has been performed.

Key Words: galactose catabolism, *Lactobacillus casei* group, tagatose-6-phosphate pathway

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0505 Characterization of the fatty acid composition of retail bovine milk and vegetable milk in Chile.

E. Vargas-Bello-Pérez*, P. Toro-Mujica, D. Enriquez-Hidalgo, M. A. Fellenberg, *Pontificia Universidad Católica de Chile, Santiago.*

In Chile, there is a lack of information regarding the lipid quality of bovine and vegetable milks and this can cause consumer confusion. The objective of this study was to characterize and compare the fatty acid (FA) composition between bovine (whole, semi-skimmed and skimmed) and vegetable milks that are offered in Chile. To maximize representativeness, the availability of bovine and vegetable milks in the three biggest stores located in five of the main cities of Chile was assessed in February 2015, before sampling. Santiago's stores presented the greatest offer of those beverages and therefore the analysis of the beverages found in Santiago's stores were evaluated. During a 4-wk period in March and April (summer) 2015, retail bovine milk (n = 62) and vegetable milk (n = 27) samples were collected. A multivariate analysis was performed to determine which FA were responsible for the differentiation between milk by origin and type of milk. The multivariable analysis included a correlation matrix, a factorial analysis (by principal components (PC) method) and a cluster analysis. Three PC were selected from factorial analysis, those explained 0.72 [PC 1 (0.54); PC 2 (0.11); and PC 3 (0.07)] of the overall variance in the data. PC 1 was related to the saturated FA and some monounsaturated FA such as C18:1 trans-11. High scores for this PC were associated with whole milk samples. PC 2 was represented by n-3 FA and the higher scores were found in semi-skimmed milk samples. PC 3 was related with C18:2 trans-9, trans-12 and C20:4 n-6 and skimmed milk samples; and vegetable milk showed the higher scores. C18:1 trans-11 and C18:2 cis-9, trans-11 were only found in retail bovine milk. Data were analyzed by using ANOVA and when significant differences were detected, means were separated using Tukey test. Compared with semi-skimmed, skimmed and vegetable milks, whole milk was higher (P < 0.05) in contents of saturated FA (10.3, 1.48 and 2.23 vs. 21.9 g/L) and monounsaturated FA (3.6, 0.48 and 5.4 vs. 7.3 g/L). Compared with bovine retail milk, vegetable milk had the highest (P < 0.05) contents of polyunsaturated FA (0.78 vs. 5.9 g/L) and this was related to its high content of C18:2 cis-9, cis-12. Data from this study can serve as a reference for estimating dietary intake for future studies. This study showed evidence that vegetable milk have a more "polyunsaturated FA profile" than retail bovine milk.

Key Words: milk fat composition, milk quality, oleic acid, linoleic acid, bovine

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0506 Effect of milk protein intake and casein: Whey ratio in breakfast meals on postprandial glucose, satiety ratings and subsequent meal intake.

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Novel satiating dairy-based breakfast products have potential to reduce the risk of developing and improve management of type 2 diabetes and obesity. Whey and casein proteins may induce different physiological effects on blood glucose, induction of satiation and satiety. Whey proteins have been associated with acute satiation, compared with the prolonged feelings of satiety from casein. The purpose of this work is to investigate the impact of breakfast meal milk casein:whey ratio and protein concentration on postprandial blood glucose, appetite ratings, and subsequent food intake. In a randomized, controlled, double-blinded study, healthy young adults (n = 32, 16 m/f, 23.4 ± 3.1 y, BMI 22.2 ± 2.5 kg/m^2) consumed milk (250ml) with normal (80:20) or modified (40:60) casein:whey protein ratio at normal (3.1%) or high (9.3%) protein concentration, or water (control), along with 2 servings of breakfast cereal. Following an overnight fast and up to 120 min following the breakfast meal, participants had their plasma glucose concentrations determined from finger-prick samples, completed a series of scale ratings to assess satiety and consumed a weighed ad libitumpizza lunch. Repeated measures ANOVA followed by Tukey-Kramer's post hoc testing was performed. Incremental area under the curve (AUC) glucose values showed significant attenuations in postprandial plasma glucose concentration for all milk treatments, relative to control (P < 0.05). Also, the high protein treatments (9.3%) had significantly attenuated glucose concentrations compared with those with lower protein (3.1%). However, there was no effect of casein:whey protein ratio on blood glucose. Treatments were not associated with differences in total area under the curve for individual scale ratings of Hunger, Desire to Eat, Fullness, and Prospective Consumption. Nor were differences observed in mean appetite score (P = 0.86) or subsequent

lunch intake ($P = 0.06$). Therefore, since consumption of high protein milk treatments with breakfast cereal was associated with the lowest plasma postprandial glucose concentration, new high-protein dairy breakfast products should be considered for product development.

Key Words: appetite, dairy protein, glycemia

0507 Influence of sodium reduction on the rheological characteristics of cottage cheese cream dressing.

H. L. Damiano*, *University of Idaho, Moscow.*

Once a popular dairy product, creamed cottage cheese consumption has decreased over the past several decades. There are a number of reasons for this, including free whey formation during storage, which consumers find unappetizing. Free whey formation is often a result of cream dressing separation. Cream dressing is added to provide flavor and texture to the curd, and its appearance, texture, and stability during storage is an important factor in consumer acceptance of creamed cottage cheese. Despite this, there is little published data on cottage cheese cream dressing; the bulk of the literature focuses on cottage cheese curd and its physicochemical properties. The objective of this study was to evaluate the effect of sodium reduction on the rheology of cottage cheese dressing over time. Dressing samples were prepared with 2.2%, 1.48%, and 0.73% w/w NaCl, with the 2.2% NaCl formulation acting as a control. Samples were acidified to pH 4.5, 5, and 5.5. Rheological tests (shear rate, strain, and frequency sweeps) were conducted in triplicate at 8°C and 25°C. Tests were conducted within 48 h after acidification and again after 14 d of storage at 4°C. Dressing viscosity increased over time regardless of salt amount and type; dressings had greater viscosity at 8°C compared with 25°C. As NaCl was reduced from 2.2% to 0.73%, viscosity generally decreased. Interactions among the hydrocolloids, proteins, and salt led to the formation of a three dimensional network, causing all formulations to display weak gel behavior under oscillatory shear. This structure increased during storage because the hydrocolloids had more time to interact with the milk proteins. Dressing pH had the most significant effect on structure, with a greater degree of solid-like behavior occurring closer to the isoelectric point of casein (pH = 4.6). Dressing made with lower salt concentrations generally saw a greater increase in G' over the 14-d storage period. Although changing NaCl concentration led to rheological differences, they were generally not significant. Thus, these results indicate that manipulating NaCl concentration in cottage cheese dressing can be made to mimic full salt formulations in terms of rheological properties by simultaneously adjusting pH

Key Words: cottage cheese, rheology, salt reduction

0508 A rapid and nondestructive fluorescence-based analyzer for monitoring the changes in deproteinized whey powder during storage.

K. Sajith Babu* and J. K. Amamcharla, *Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan.*

Deproteinized Whey (DPW) is a co-product obtained during ultrafiltration of whey. Subsequently, it undergoes unit operations like evaporation, crystallization, and spray drying resulting in a non-hygroscopic, free-flowing powder containing more than 80% lactose. Generally, DPW powder contains 2–7% protein, 3–4% moisture, and 8–11% ash. DPW is widely used as a replacer for sweet whey powder or lactose in bakery and confectionary applications, drink mixes, snack foods, and in certain ice-cream formulations. DPW powders may undergo chemical and physical changes such as caking, Maillard browning, and oxidation during storage. Amaltheys analyzer (Spectralys Innovation, Romainville, France) is a compact and portable fluorometer designed with 2 excitation light-emitting diodes at 280 and 340 nm. It is a rugged optical design with a low noise and enhanced UV sensitivity linear charge-coupled device. The objective of the present study was to use Amaltheys analyzer for monitoring Maillard changes during storage of DPW powder. For this purpose, 30 DPW samples were collected from a commercial manufacturer from different lots of production and storage periods. The FAST index (fluorescence of advanced Maillard products and soluble tryptophan) and the whey protein nitrogen index (WPNI) for DPW powders were measured by fluorescence-based Amaltheys analyzer. Additionally, colorimetric L*, a*, and b* values and water activity (a_W) were also determined. The changes in terms of color and a_W of DPW powder effected by storage time exhibited definite correlations. The L* values of DPW powders ranged from 85.86–92.02 and a_W values ranged from 0.307–0.418. It was observed that lightness (L*) was negatively correlated ($R = -0.71$; $P < 0.01$) with a_W of DPW powders. On the other hand, redness (a*) value was positively correlated ($R = 0.82$; $P < 0.01$) with a_W of DPW powders. From the Amaltheys analyzer, the highest FAST index was observed as 362.24 for the powder with a_W of 0.394. On the other hand, the lowest FAST index observed was 87.16 at a_W of 0.381. It was also observed that FAST index was positively correlated ($R = 0.46$; $P < 0.05$) with redness (a*) value of DPW powders. A negative correlation ($R = -0.89$; $P < 0.01$) between FAST index and WPNI was observed. The FAST index and WPNI obtained using Amaltheys analyzer method is a simple, rapid, and low-cost method for the detection of Maillard changes in stored DPW powders.

Key Words: deproteinized whey powder, Maillard changes, FAST index

0509 Evaluation of mineral compositions in commercial Mongolian dried yogurts (Aaruul) marketed at retail stores in Mongolia. Y. W. Park[1], B. I. Davis[*1], J. H. Ko[2], K. P. Bastola[3], A. Siddique[1], and J. O. Jones[1], *[1]Fort Valley State University, GA, [2]Mongloia Huree University of ICT, Ulaanbaatar, Mongolia, [3]Fort Valley State University, GA.*

Dried yogurt products (DYPs: Aaruul) have traditionally been produced and consumed in Mongolia in various product shapes and packages. However, information on nutrients and mineral compositions of Mongolian DYPs are almost nonexistent. The objective of this study was to determine mineral compositions of commercial Mongolian DYPs. Five varieties (MD, KA, AC, AA, HU) of Mongolian DYPs were purchased at local retail outlets at Ulaanbaatar, Mongolia. Concentrations of 20 major and trace minerals were quantified by an Inductively Coupled Plasma Optical Emissions Spectrometer (Thermo Jarrel Ash Enviro 36, Worchester, MA) using argon as carrier gas and the USEPA Method 6010 at different wavelengths for each different minerals. The respective wavelengths used for the analysis of 20 elements were: Al, 396.2; B, 249.7; Ba, 233.5; Ca, 317.9; Cd, 228.8; Co, 228.6; Cr, 267.7; Cu, 327.4; Fe, 238.2; K, 766.5; Mg, 285.2; Mn, 257.6; Mo, 202.0; Na, 589.6; Ni, 231.6; P, 213.6; Pb, 220.4; Si, 251.6; Sr, 421.6; Zn, 206.2 nm. The ranges of dry matter (DM) and ash contents of DYPs were 67.7 to 96.6 and 1.3 to 4.1%, respectively, indicating the Mongolian Aaruul products contained very high DM and ash contents. The respective mean mineral concentrations (ppm, wet basis) of the highest (AC) and lowest (MD) brands were: Ca 5183, 1236; P 8934, 2419; K 6989, 1350; Na 1523, 233; Mg 440, 123; Fe 17.3, 5.20; Mn 0.787, 0.704; Cu 8.40, 7.53; Zn 34.1, 15.6. These data indicate that the AC brand contained significantly ($P < 0.01$) higher all macro and trace minerals than those of other four brands, which were apparently due to the higher levels of DM and ash in the AC compared with the other brands. The AC product contained much higher levels of P and K than those of the other brands, where the P and K contents were even greater than that of Ca in the products. Heavy metal (Pb, Cd and Ni) contents of all experimental Aarrul products appeared to be in normal ranges. It was concluded that most of the 20 mineral concentrations in Mongolian DYPs were very high, which were greater than those in powdered cow milk products reported previously.

Key Words: Mongolian dry yogurt, minerals, composition

0510 Potential protective effect of camel milk and yogurt with chromium on alloxan induced hyperglycemia in rats. M. M. Motawee[*1] and A. M. Badawi[2], *[1]National Organization for Drug Control and Research, Giza, Egypt, [2]ph.D, Giza, Egypt.*

Insulin and oral hypoglycemic agents are the main ways to treat diabetes mellitus and are effective in controlling hyperglycemia, but these kinds of drugs also have prominent side effects. Camel milk, Yogurt-Camel milk and Chromium have attracted a lot of attention for their potential effects in human health. The aim of this study was to investigate the prophylactic effects of Camel milk (CM), Yogurt-Camel milk (YCM) and Chromium Picolinate (CrPi) on diabetic animals. Oxidative stress and dyslipidemia are associated with diabetes mellitus. The samples of camel milk were collected fresh from Elareesh, Egypt, and were prepared for this study, Forty-eight adult male albino rats were classified into six groups: Group I control negative (-ve), animals of group 2 were rendered to diabetes by alloxan (145 mg/kg body weight, I.P.). Meanwhile, groups 3–6 were fed daily with CM products [(CM)\, (CM-CrPi), (YCM) and (YCM-CrPi)] for 6 wk then induced diabetes by alloxan. The study was assigned for 6 wk. The results revealed that the CM and YCM showed a significant decreases in serum glucose, glycosylated hemoglobin (HbA1C) and lipids level ($p < 0.05$) and improved lipid per-oxidation, serum insulin level, lipid profile and total antioxidant capacity (TAC) in diabetic rats. Both CM and YCM supplementation with CrPi potentially ameliorated effect in glucose, and oxidative stress and also increased serum insulin level in diabetic rats. The histopathological examination confirmed our results. In conclusion, the administration of CM and YCM with CrPi supplementation can lower the side effects of hyperglycemia, hyperlipidemia, improve antioxidant activity and healthy status of diabetes.

Key Words: alloxan, camel milk, chromium, yogurt

0511 Characteristics, composition and sensory properties of butter from cows on pasture versus indoor feeding systems. T. F. O'Callaghan[*1,2], H. Faulkner[2], S. McAuliffe[3], M. G. O'Sullivan[1], D. Hennessy[3], P. Dillon[3], K. N. Kilcawley[2], C. Stanton[1,2], and R. P. Ross[1], *[1]University College Cork, Ireland, [2]Teagasc Food Research Centre, Cork, Ireland, [3]Teagasc Animal and Grassland Research and Innovation Centre, Cork, Ireland.*

This study evaluated the effects of three widely practiced feeding systems of cows on the characteristics, quality and consumer perception of sweet cream butter. Fifty-four multiparous and primiparous Holstein Friesian cows were divided into three groups ($n = 18$) for an entire lactation. Group 1 was housed indoors and fed a total mixed ration diet (TMR), Group 2 was maintained outdoors on perennial ryegrass only pasture

(GRASS), while Group 3 was also maintained outdoors on a perennial ryegrass/white clover pasture (CLOVER).

Mid-lactation butter was manufactured in triplicate with milk from each group in June 2015, and was analyzed over a 6-mo storage period at 4°C for textural and thermal properties, fatty acid composition, volatile analysis and sensory properties.

The nutritional value of butters was improved by pasture feeding; having lower atherogenecity index scores than that of TMR butters. With this, pasture derived milks produced butter with significantly higher concentrations of CLA ($_{c9t11}$) ($P <$ 0.01) and β-carotene ($P < 0.05$). Alterations in the fatty acid composition of butter resulted in significant differences in textural and thermal properties, and spreadability index scores. Volatile analysis of butter by GC/MS identified 25 compounds present in each of the butters, five of which differed significantly ($P < 0.05$) based on feeding regimen including acetone, 2-butanone, 1-pentenol, toluene and β-pinene. Toluene was significantly ($P < 0.00$) correlated with pasture derived butter. Sensory analysis revealed significantly higher scores ($P <$ 0.01) for GRASS derived butter in several attributes including "liking" of appearance, flavor and color. Partial least square regression plots of fatty acid profiles showed clear separation of butter from grazed pasture-based diets from that of a TMR system, offering further insight into the ability of fatty acid profiling to verify pasture derived dairy products.

Key Words: cows diets, butter, conjugated linoleic acid

0512 Identification of protein fractions in ripened American style natural cheese manufactured utilizing recombinant bovine and camel chymosin by capillary electrophoresis.

A. C. Biswas* and L. Metzger, *South Dakota State University, Brookings.*

During ripening, natural cheese undergoes a series of complex proteolytic reactions that are critical for flavor development. The initial phase of proteolysis is caused by the milk clotting enzyme generally known as chymosin. Recently, recombinant camel chymosin (CHY-MAX® M) has been developed, and is commercially available as a milk coagulant for natural cheese manufacture. The objectives of this study were to identify and characterize the various protein fractions by CE in American style natural cheese manufactured utilizing CHY-MAX® Extra (recombinant bovine chymosin) and CHY-MAX® M (recombinant camel chymosin). The electropherograms obtained from CE analysis showed that there was a significantly ($P <$ 0.05) higher degree of hydrolysis of α_{S1}-CN and β-CN which resulted in the formation of smaller α_{S1}-CN f(1–23), α_{S1}-I-CN [α_{S1}-CN f(24/25–199)], and various γ-caseins fractions in the natural cheese manufactured utilizing bovine chymosin as compared with the natural cheese manufactured utilizing camel chymosin. It was also observed that a significantly ($P <$ 0.05) higher percentage of soluble nitrogen at pH 4.6 develop in the natural cheese manufactured utilizing bovine chymosin. These findings suggested that CE is a suitable technique to determine protein fractions in cheese, and CHY-MAX® M could be an appropriate alternative for CHY-MAX® Extra in American style natural cheesemaking to limit proteolysis.

Key Words: proteolysis, recombinant chymosin, capillary electrophoresis

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0513 Effect of γ radiation on physicochemical properties, protein-protein interaction, and microstructure of whey proteins.

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Whey proteins are generally small globular proteins that could be modified by physical, chemical or other means to improve their functional properties. The effect of γ radiation on the physicochemical properties, protein-protein interaction and microstructure of whey proteins were investigated. Whey protein isolate (WPI) solutions (10–36% protein) were treated with different dosages (10–35 KGy) of γ radiation. The viscosity of 27% protein solution treated at 25 KGy was significantly increased from 2.19 (control) to 4.78 mPa.s (p < 0.01). Overall, the increase in viscosity of WPI solutions was most affected by the higher dosage of γ radiation (> 25 KGy) and viscosity also increased during the 6-mo storage after treatment. Effects of γ radiation level and storage time on the viscosity of whey protein solutions were significant (p < 0.05). Turbidity of WPI solutions increased from 0.14 to 0.16 for untreated and treated samples (35 KGy), respectively. Soluble nitrogen content decreased significantly from 100 to 54.7% in WPI solution after treated by radiation at 35 KGy. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) showed that protein cross-linking might occur in the whey protein solutions treated by γ radiation. Transmission Electron Microscopy (TEM) micrographs indicated that protein-protein interactions were induced by γ radiation in the treated WPI solutions, which displayed more uniform whey protein cluster structures compared with control samples. Results indicated that high intensity γ radiation could result in structure damages of whey proteins.

Key Words: whey protein, γ radiation, interaction, microstructure

0514 Effects of sodium polyphosphate on distribution of particle size of polymerized whey protein. M. Guo[*1,2], D. Liu[1], and C. Wang[1], *[1]College of Food Science and Engineering, Jilin University, Changchun, China, [2]University of Vermont, Burlington.*

Protein-based fat replacers have been used in dairy foods for many years. The objective of this study was to develop a novel fat replacer using whey protein concentrate (WPC). WPC was heated with sodium tripolyphosphate (STPP) to prepare polymerized whey protein particles as fat replacer for nonfat dairy product formulation. The effects of STPP concentration (0–1%, wt/wt), protein content (8–10%, wt/vol), pH (7.5–8.5), heating temperature (70–85°C), and time (5–25 min) on the particle size distribution were investigated. Results showed that heating WPC solution (8.0%, wt/vol) with 0.4% STPP at pH 7.5 at 85°C for 5 min resulted in 40% of particles in the range of 1–3 μm, which were as large as fat globules in dairy products. There were no large particles (> 10 μm) yielded when 0.4% STPP was added, but higher STPP levels (> 0.5%) produced larger particles (> 10 μm) at a unimodal distribution. The percentage of particle size between 1 and 3 μm decreased with increasing WPC concentration. A wide distribution or even multi-peaks with more large particles (> 10 μm) were observed when the mix was heated at higher pH values (8–8.5). When heating the mix at 70–85°C for 5 min, 20%-40% of the particles were in the range of 1–3 μm and prolonged heating time also generated large particles (> 10 μm). Results indicated that heating whey protein concentrate with STPP could produce particles/aggregates that might be suitable as fat replacer for non or low fat dairy products.

Key Words: fat replacer, sodium tripolyphosphate, whey protein concentrate

0515 Effects of ultrasound treatment on physicochemical properties of whey protein soluble aggregates. X. Shen[1], T. Fang[1], T. Zhang[1], and M. Guo[*1,2], *[1]Department of Food Science, College of Food Science and Engineering, JiLin University, ChangChun, China, [2]Department of Nutrition and Food Science, College of Agriculture and Life Science, University of Vermont, Burlington.*

Functional properties of whey protein could be improved by heat-induced aggregation. The aim of this study was to determine the effect of high-intensity ultrasound on thermal aggregation of whey proteins. Whey protein solutions were sonicated for 20 min using an ultrasonic probe (frequency: 20 kHz; amplitude: 20%) pre- and post-thermal aggregation (85°C for 30 min). Changes in particle size, zeta-potential, surface hydrophobicity, free sulphydryl group content (-SH), protein-protein interactions, turbidity, thermal denaturation properties and viscosity were studied. Soluble aggregates prepared with ultrasound treated post-thermal aggregation resulted in significantly smaller particle size and broader size distribution compared with those prepared by untreated or ultrasound treated pre-thermal aggregation ($P < 0.05$). It was suggested that the surface hydrophobicity of the soluble aggregates was slightly but significantly increased by ultrasound treated post thermal aggregation ($P < 0.05$). There was a significant reduction in turbidity of whey protein solutions by ultrasound treated post thermal aggregation ($P < 0.05$). The viscosity of WPI dispersions significantly decreased by ultrasound treated post-thermal aggregation ($P < 0.05$). Ultrasound treatment increased denaturation temperature (Td) and decreased DH of soluble aggregates slightly, suggesting that limited improvement of heat stability. There were no significant changes in zeta-potential, free sulphydryl group by ultrasound treatment either pre- or post-thermal aggregation ($P > 0.05$). Results indicated that ultrasound treatment on post thermal aggregation had considerable impact on particle size, surface hydrophobicity, turbidity, and viscosity of whey protein soluble aggregates.

Key Words: whey protein, thermal aggregation, physicochemical property

0516 Crystallization of calcium phosphate in stabilized-paste white mold cheese rinds. G. F. Tansman[*1], P. S. Kindstedt[1], and J. M. Hughes[2], *[1]Department of Nutrition and Food Sciences, University of Vermont, Burlington, [2]Department of Geology, University of Vermont, Burlington.*

Increased pH at the surface of traditional white mold cheese results in calcium phosphate (CaP) crystallization and accumulation of CaP in the rind. At the same time, this phenomenon results in depletion of CaP in the rest of the cheese wheel. An experiment was conducted to identify crystals that form in the rind of stabilized-paste white mold cheese and to correlate the crystallization phenomenon to pH gradients between the center and rind and to the diffusion of dissolved minerals from the center of the cheese to the rind. In this randomized block design, three batches of a Vermont stabilized-paste white mold cheese (batches representing blocks) were sampled throughout the aging process from 1 d post-manufacture to 4 d after packaging. Two wheels were removed from each batch on d 1, 4, 7, 10, 14, and 18, with d 0 representing the day of manufacture and packaging occurring on d 14. Three-millimeter-thick samples were cut from rind and center locations of each cheese and tested for moisture by forced draft oven drying, and the dried samples were tested for calcium and phosphorus by ashing and analyzing with ICP–AES. Rind and center pH measurements were collected from each wheel. Powder X-ray diffraction (PXRD) patterns were generated from cheese collected from the center and rind of each wheel to identify crystal phases. Petrographic microscopy (PM) images were also collected from rind and center samples to observe the size of

crystals. PXRD revealed that brushite ($CaHPO_4 \cdot 2H_2O$) deposited in the rind by d 10 with increasingly stronger PXRD signals for brushite apparent on d 14 and 18. PM revealed that the crystals grew to a maximum of 20 μm in diameter by d 18. The appearance of brushite corresponded to significant increases in rind pH, accumulation of CaP in the rind, and depletion of CaP in the center. Rind pH rose from approximately 5.1 on d 1 to approximately 5.3 by d 10 and to approximately 5.6 by d 18, while the center pH did not rise above 5.1. This was a considerably smaller pH increase than occurs in traditional white mold cheese. Nonetheless, the mechanism of crystallization and diffusion of dissolved CaP in stabilized-paste white mold cheese appears similar to that previously observed in traditional white mold cheese.

Key Words: cheese, crystals, brushite

0517 Effect of buffalo αs1-casein polymorphism on the semi-hard Monterey Jack-type cheese quality.

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The influence of α_{s1}-casein polymorphisms on milk processing properties, and cheese quality of cow milk have been well researched, while the effect of buffalo milk protein polymorphisms on cheese quality is still unclear. The objective of this study was to investigate the effect of buffalo α_{s1}-casein polymorphisms on the quality of semi-hard Monterey Jack-type cheese. Water buffalo milk with different α_{s1}-casein genotype (BB and AB) and the same κ-casein (BB) and β-casein (BB) type was collected from local dairy farm, mixed sample from milk tank was used as control. The protein/fat ratio of buffalo milk was standardized to 0.75(g/g), then fresh Monterey Jack-type cheese was made according to the standard procedure, vacuum-packaged and stored at 4°C, samples were tested at 7 d. The composition (fat, protein, ash, Ca and P), texture and color difference (CD) of cheese samples with manufactured from milk with different α_{s1}-casein (BB, AB and control) type were analyzed. Results showed that cheese made from milk with BB type α_{s1}-casein (BB type cheese) contained significantly lower fat, but higher protein, ash, Ca and P content in DM than AB type ($P < 0.05$). The Ca/protein content of BB type cheese was 3.78g/100g, which was also higher than AB type (3.51g/100g) and control (3.60 g/100g). For the texture, hardness and springiness of BB type cheese were 41.21 N and 6.31 mm, significant higher than AB type (29.45 N, 5.56 mm) and control (38.21 N, 5.25 mm), except that, the gumminess, adhesiveness and chewiness of BB type cheese were also higher than AB type ($P < 0.05$). For the CD, b value of BB type cheese was lower than AB type ($P < 0.05$), which means the cheese color of BB type was more white. In conclusion, the quality of semi-hard Monterey Jack-type buffalo milk cheese was related with α_{s1}-casein polymorphism, BB type cheese has the best texture and color for traditional Monterey Jack-type cheese.

Key Words: α_{s1}-casein polymorphism; buffalo milk; cheese quality

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0518 Membrane fractionation of delactosed permeate to enhance salty taste.

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Delactosed permeate (DLP), commonly referred to as mother liquor, is a byproduct of lactose manufacture and is typically relegated to animal feed use. Previous work has established that compounds other than sodium, such as organic acids and potassium (K), contribute to the salty taste of DLP but that residual lactose suppresses salty taste. The objective of this study was to determine the viability of fractionating DLP into two components, one that would be re-cycled into the lactose manufacturing processing and one that would be used as a salt substitute. Two lots of commercial DLP were obtained from four different lactose manufacturers (totaling eight samples). The composition of these samples ranged from 27.9 to 39.7% total solids. Each DLP sample was diluted to approximately 5% TS using soft tap water and then subjected to nanofiltration (500 Da MWCO, NFW-3B-3838, Synder Filtration) in a batch process. Nanofiltration was performed until the flux rate dropped below 10 Lmh. Subsequently, the NF permeate fraction was concentrated to approximately 8% TS using reverse osmosis (RO) (RO2–3838-BS04, Parker-Hannifin). The initial DLP, NF retentate, and RO retentate were analyzed for total solids (vacuum oven) and ash (muffle furnace). Selected minerals (Ca, Na, Mg, P, S and K) were determined by plasma emission spectroscopy, lactose and organic acids by HPLC, and volatile compounds by GC–MS. A trained panel documented sensory properties of the liquid DLP and fractions at equivalent solids (8% (w/w)). The DLP displayed a variety of aromatic flavors including cardboard, beefy, and potato as well as distinct salty taste, consistent with previous studies. Nanofiltration of DLP followed by RO resulted in a fluid that was higher in salty taste ($p < 0.05$) than the DLP or NF retentate with consistent low, but distinct, bitter taste. Concurrent with increased salty taste, the RO retentate had higher K and Na, higher concentrations of citric, lactic and orotic acids and decreased lactose than the NF retentate ($p < 0.05$). Aromatic flavors present in DLP were detected in both NF and RO retentates suggesting the need to address removal of these flavors. Membrane fractionation of DLP can be applied to enhance its application as a salt substitute.

Key Words: delactosed permeate, nanofiltration, reduced sodium

0519 Characterization of queso fresco made with Na/K salt blends and stored for 12 wk.
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Health-conscious consumers are looking for ways to reduce dietary sodium yet want their cheeses to have the flavor, texture, and shelf-life of full-salt cheese. The objectives of this study were to determine the effects of different Na-K salt blends and storage on the compositional, sensorial, microbial, functional, and rheological properties of Queso Fresco (QF), a fresh cheese with a distinct salty taste. QF was made in triplicate on different days with curds from each vat being divided and salted using 1.0% NaCl and 0.5, 1.0, 1.3, or 1.5% added KCl; a 2.0% NaCl QF control and a 0.75%:0.75% Na:K QF were also made. The QF were then stored at 4C for up to 12 wk.

Although the variation in salt treatments were in a fairly narrow range, 1.5 to 2.5% total salt, differences ($P < 0.05$) in some of the QF characteristics were noted. Moisture and ash levels were influenced by salt content while storage impacted moisture and salt levels, water activity, and pH. Only QFs with 1.0% NaCl and 1.3 or 1.5% KCl had sensory saltiness scores similar to the 2.0% NaCl QF control. Loss of free serum from the cheese matrix significantly increased up to 7.5% over the 12 wk of the study with the samples at the higher levels of salt retaining more of the serum in the cheese matrix. Aerobic microbial counts decreased slightly after 2 wk for QF containing > 1.5% salt, and all samples increased 1 to 2.7 logs by wk 10. The variation in the salt content did not alter the non-melt characteristic of the QF samples, while the 2% NaCl QF control had the lowest change in color when baked (130°C for 30 min) and the QF containing 1.0 to 1.5% KCl had the lowest color change when broiled (232°C for 5 min). No significant differences were noted in texture hardness, springiness, or chewiness or in the viscoelastic properties among the treatments or over time.

The minor differences in quality traits that resulted in aging QF made with 1% NaCl and 0.5 to 1.5% added KCl showed that KCl substitution was a viable route for reducing sodium in QF. The best overall Na-K blend for QFs were made using 1% NaCl and 1.3 or 1.5% KCl. Findings from this study will help in developing a reduced sodium QF that meets the demand of health-conscious consumers.

Key Words: cheese, queso fresco, reduced sodium

0520 Effect of micro-encapsulated iron salts on Cheddar cheese divalent cation balance and composition.
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Milk is a considered an important source of macro- and micronutrients but naturally low in iron content. Cheese and other dairy products had been fortified with iron with low success due to negative changes in composition and organoleptic attributes. There is limited information about using micro-encapsulation of iron compounds in dairy products. Minerals have the ability to displace one another in any system; consequently, it is expected that encapsulation will avoid divalent cation displacement within the cheese matrix. The objective of this study was to analyze divalent cation balance in fortified Cheddar cheese with micro-encapsulated ferrous sulfate. Furthermore, proximate analysis was done to provide more information about any compositional changes after fortification.

Cheddar cheese was manufactured using standard Cheddar cheese procedures a total of three times. Cheddar cheese was either fortified with large micro-encapsulated ferrous sulfate (LMFS; 0.9536 g micro-encapsulated ferrous sulfate/Kg cheese, 700–1000 μm diameter) or small micro-encapsulated ferrous sulfate (SMFS; 1.7801 g microencapsulated ferrous sulfate/Kg cheese, 220–422 μm diameter). Iron treatment was incorporated to Cheddar cheese processing in the salting step but omitted for the control. After 90-d aging, calcium, iron, magnesium and zinc content were analyzed using Atomic Absorption Spectroscopy and percent recoveries were calculated. Moisture, ash, fat, and protein analysis were done using AOAC methods. All collected data was analyzed using one-way ANOVA and Tukey's HSD Test ($p = 0.05$).

Iron content for all treatments were significantly different ($P < 0.05$); approximately 0.03 mg Fe/g cheese for the control, 0.134 mg Fe/g cheese for LMFS, and 0.174 mg Fe/g cheese for SMFS. Results showed 81.3% iron recovery for LMFS and 90% iron recovery for SMFS. Proximate analysis, and magnesium, zinc and calcium content were not significantly different when comparing fortified cheeses with the control. Overall, micro-encapsulated ferrous sulfate caused no major changes in terms of Cheddar cheese composition and successfully increased iron content. Micro-encapsulated ferrous sulfate with smaller diameter showed slightly better results for iron retention in Cheddar cheese. The proposed fortified Cheddar cheese can help increase total iron intake for children, pregnant women, vegetarians and those whose diets are likely to be deficient in iron by providing at least 5 mg Fe (30% RDA) per serving.

Key Words: cheese, minerals, fortification

0521 Chemical characteristics and enhanced hepatoprotective activities of Maillard-reaction products derived from milk protein-sugar system.
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The objective of this study was to investigate the characteristics, antioxidative properties, and hepatoprotective effects of Maillard reaction products (MRP) from milk protein reacted with sugars. The MRP were obtained from milk protein, whey protein concentrates and sodium caseinate, using 2 types of

sugars, lactose and glucose, by heating the mixture at 55°C for 7 d in a sodium phosphate buffer (pH 7.4). Changes in the chemical modification of the milk protein were monitored by measuring the protein-bound carbonyls and PAGE protein profiles. The results showed that the amount of protein-bound carbonyls increased after Maillard reaction (MR). In addition, sodium dodecyl sulfate-PAGE analysis indicated a formation of high-molecular weight complexes through MR. The modification sites induced by MR of milk protein were monitored by matrix assisted laser desorption/ionization time-of-flight mass spectrometry analysis of tryptic-digested gel spots of MRP. As a result, modification and their localization in AA sequence of MRP was identified. Also, the MRP showed higher antioxidant activities than the intact milk protein, and they reduced intracellular reactive oxygen species production and inhibited the depletion of the reduced glutathione concentrations in the HepG2 cells. In particular, glucose-sodium caseinate MRP showed the highest biological activities among all MRP. Therefore, these results suggest that the MRP from milk protein reacting with sugars possess effective antioxidant activity and have a protective ability against oxidative damage.

Key Words: Maillard-reaction, milk protein, hepatoprotective effect

DAIRY FOODS DIVISION: DAIRY CHEMISTRY II

0522 Prediction of intact casein in cheese by using amaltheys: A front-face fluorescence analyzer.

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During cheese ripening, proteolysis is an important biochemical event which leads to texture and functionality changes over time. The intact casein content of cheese decreases during aging due to the enzymatic hydrolysis. However, because of the difference in storage history and compositional variability, it is difficult to rapidly estimate the amount of intact casein of different batches of cheese. In this study, the feasibility of using front-face fluorescence spectroscopy (FFFS) to predict the amount of intact casein in different cheese samples was evaluated by using fluorescence-based Amaltheys analyzer (Spectralys Innovation, Romainville, France). Twenty cheese samples from different manufacturers and with different storage time were used for this study. The intact casein was measured by fractionation of cheese proteins using Sharp's solution (pH = 4.6) and followed by nitrogen analysis using Kjeldahl method (6.38 conversion factor). Cheese was cut into the size which can fit the cuvette for fluorescence measurement using Amaltheys, and 5 fluorescence scans from 5 different locations on each cheese sample were analyzed. 3D fluorescence spectra were collected on each cheese sample at room temperature and processed using parallel factor analysis (PARAFAC) algorithms. PARAFAC scores were then used to build a calibration model against the reference intact casein values. Practical utility of the model was evaluated using the range error ratio (RER) and the ratio of prediction error to deviation (RPD). The RPD was found to be over 2 and RER was over 10, indicting a good practical utility of the model. Hence, FFFS can be used as an analysis technique to predict intact casein in cheese and the results indicate that Amaltheys analyzer can be a rapid and accurate device to analyze intact casein in cheese samples.

Key Words: front-face fluorescence spectroscopy, intact casein, cheese ripening

0523 Changes of the state of calcium and protein in low-fat and full-fat processed cheese during cheesemaking.

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"Creaming" is an increase in the viscosity of hot molten cheese during processed cheese cooking, and it is important for cheese manufacturers to control the viscosity during the production process. The objective of this study was to understand the interactions between protein, calcium, and fat in full-fat (FF)/low-fat (LF) processed cheese. Processed cheeses were made from 4-mo-old 9% fat Cheddar cheese and 2.3% tetrasodium pyrophosphate (TSPP). Anhydrous milk fat was added for FF cheese. A steam-jacketed kettle was used to heat 7 kg of the ingredients up to 80°C, and approximately 200 g of hot molten cheese was extracted during the holding process (80°C with shear) at certain points (0–40 min). It was poured into plastic bags, and rolled to a thickness of 4 mm, and cooled in chilled water. Both FF and LF cheeses had the same pH (5.6) and protein (24%) content. No moisture loss was observed during cooking. The viscosities of molten cheese were measured during holding time. The functional properties were assessed by hardness using a creepmeter, and degree of flow (DOF) values were measured using a modified UW-Melt profiler. The precipitate compositions of cheese dispersion after centrifugation were analyzed, and the serum phase of the cheese was extracted from the dispersion by ultrafiltration and the casein-bound calcium content was assessed. Creaming was observed in LF and FF cheeses. In LF cheese, the viscosity was drastically increased at 30 min holding time. Over-creaming was observed in FF cheese at 40 min holding time. As the holding time increased, the hardness of both cheeses increased, whereas the DOF of both cheeses decreased. LF cheese initially

showed much higher DOF values than the FF cheese; however, the value drastically decreased at ≥ 30 min holding time and indicated no significant difference ($P > 0.05$) with that of FF cheese, which showed a limited flow. Casein-bound calcium content initially decreased from 0 to 20 min and increased from 20 to 40 min for both cheeses. TSPP initially may have sequestered calcium, and casein–calcium pyrophosphate cross-links may have been formed during cooking. The protein content in the dry matter in the precipitate from FF cheese increased with the holding time. This may be due to the interaction between homogenized fat droplets and proteins. Currently, the types of protein interactions in the insoluble phase are being investigated and will be reported.

Key Words: processed cheese, calcium, creaming

0524 Effect of selenium fortification on mozzarella cheese quality. K. L. Peng[1], J. X. Liu[2], and D. X. Ren[*3], *[1]Institute of Dairy Science, College of Animal Science, Zhejiang University, Hangzhou, China, [2]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [3]Institute of Dairy Science, College of Animal Sciences, Zhejiang University, Hangzhou, China.*

Selenium (Se) is an important trace element that has significant impacts on human and animal health. The objective of this study is to investigate the effect of Se fortification on mozzarella cheese quality. The mozzarella cheese was made following the manufacturing procedures until hand-stretched and cooled in cold water. The made-up cheese was divided into five pieces of 1 kg each, and put into 2% salt water without (control) or with Se yeast (1.25, 2.5, 5, and 10 mg Se/L, respectively) overnight. The cheese was then cut, vacuum packaged and stored at 4°C for 3, 30, and 60 d until analysis. On d 3 after adding Se yeast at 1.25, 2.5, 5, and 10 mg Se/L, the Se content of the outside or center of cheese was at 27.6, 35.7, 42.3, and 45.1 μg/kg or 20.4, 22.7, 23.4, and 23.9 μg/kg, respectively, significantly higher than that in control (15.4 for outside and 15.7 for center). After storage for 60 d, the Se concentration of the outside reduced to 24.1, 31.6, 34.1 and 36.4 μg/kg, while that of cheese center increased to 22.3, 27.8, 30.1, and 31.9 μg/kg, respectively. No significant differences were found in the cheese composition and texture between the control and Se fortified cheeses. However, compared with the control, the functional properties (meltability, flowability and stretchability) were improved, while the pH and water activity were lower in the Se-fortified cheese (5 and 10 mg/L) after 60 d storage. For the total bacteria count, the 5 and 10 mg/L Se fortified cheese were significantly lower ($P < 0.05$), but the 1.25 and 2.5 mg/L Se fortified cheese were higher than the control. The results of this study indicated that the Se content in mozzarella cheese can be increased by dipped into Se fortified solution without affecting the cheese quality, and that Se could migrate from the outside into center of the cheese during the storage.

Key Words: mozzarella cheese, Se fortification, functional property

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0525 Relationship between the yield of mozzarella cheese of buffalo's milk, milk quality and the recovery of constituents in whey. D. C. Sales[1], A. H. N. Rangel[1], J. G. B. Galvão Júnior[*2], L. H. F. Borba[1], A. R. Freitas[3], and E. O. Moura[1], *[1]Federal University of Rio Grande do Norte, Natal, Brazil, [2]University of New Hampshire, Durham, [3]Brazilian Agricultural Research Corp. (Embrapa), São Paulo, Brazil.*

The dairy industry measures the efficiency of its processes by the quality and yield of the final product, which are influenced by the quality of the milk. The aim of this study was to investigate the relationship between the yield of mozzarella cheese (MY) with the composition of buffalo milk and the recovery of constituents in whey (RW). The study involved tracking the processing of 30 lots of buffalo mozzarella in a dairy operation in northeast Brazil. For each batch a sample of raw milk and whey was collected to analyze the fat (F), total protein (TP), casein (C), lactose (L) and total solids (TS) via infrared spectroscopy. The somatic cell count (SCC/ml) of the milk was estimated by SOMATICEL®, and transformed by $\log_2$ (SCS). The MY is the relation between the cheese and milk mass (%); RW is the ratio between the constituent of whey versus that in milk (%). The MY relation to the level of the constituents in milk and RW was verified by the Pearson correlation (r) at a 5% level of significance, obtained by the SAS 2000 CORR procedure. Significant r between MY and other variables was not found ($p > 0.05$). There was a negative correlation between MY with F (−0.26), and a positive correlation with C (0.28), TP (0.27), L (0.11) and TS (0.01), demonstrating that the protein/fat ratio and casein content are factors directly related to efficiency in manufacturing mozzarella. The SCS has a weak and negative correlation with MY (−0.12), indicating that its increase in milk can result in lower manufacturing efficiency. The MY showed a negative correlation with RWTP (−0.19) and a positive correlation with RWF (0.17), RWL (0.17) and RWTS (0.29), indicating that TP (casein) should be used in the curd to promote MY and to reduce its losses in whey. The variables, C, TP, F, RWTS and RWTP have a greater influence on MY.

Key Words: dairy food, efficiency, losses in whey

0526 Transmission Electron Microscopy (TEM) identifies major microstructural changes in soft feta cheese. A. H. Vollmer*[1], D. J. McMahon[1], J. C. Grande[2], and N. N. Youssef[1], *[1]Western Dairy Center, Utah State University, Logan, [2]Analytical Sciences Laboratory, GE Global Research, Niskayuna, NY.*

Feta is a low-pH, rennet-set, brined cheese with a crumbly texture. If the cheese pH during manufacture is higher than ~4.8 at the point of brining, textural changes can be seen with the Feta cheese becoming softer as it ages. Our objective was to find the structural basis for this change in texture utilizing high-resolution transmission electron microscopy. Feta cheese was made using 136 kg standardized and pasteurized whole cow's milk (P/F = 0.72). The make procedure was modified by storing the packed curd overnight at 35°C (control; A), 20°C (B), and 3°C (C), respectively, before storage in brine at 3°C for up to 4 mo. This produced feta cheeses with the desired range of pH values (4.80, 4.88, and 5.17, respectively). Samples were taken during the make procedure (after renneting, before draining, and after the fourth turn), as well as during ripening (after 1, 7, and 90 d of brining), and immediately chemically fixed for transmission electron microscopy (TEM). A change of texture was macroscopically observed particularly during later stages of aging. To quantify these changes, texture profile analyses of samples taken at 120 d of brining were performed and demonstrated significant differences in hardness as indicated by a decrease in shear and compression force with higher cheese pH (B and C). TEM analysis revealed a major change in the formation of the protein network, which had formed a continuous matrix in the highest-pH feta cheese (C) after 90 d of brining, whereas it had remained largely open in the control feta cheese (A). Furthermore, high-magnification TEM analysis indicated a fundamental change in the protein matrix itself as it appeared to have dissolved into areas with less compact morphology. These changes were observed as early as 1 d after brining but were most pronounced after 90 d of brining. To quantitate texture differences in the protein matrix, morphometric image analysis was performed and corroborated the interpretation of the TEM data. Concluding, electron microscopy identified major microstructural changes that explain the softer texture of aged feta cheese as influenced by relatively small changes in cheese pH during production.

Key Words: microstructure, texture, morphometrics

0527 Performance shelf life extension of LMPS mozzarella using high-pressure treatment and low-temperature storage. L. A. Jiménez-Maroto*[1], S. Govindasamy-Lucey[2], J. J. Jaeggi[2], M. E. Johnson[2], and J. A. Lucey[1,2], *[1]University of Wisconsin, Madison, [2]Wisconsin Center for Dairy Research, Madison.*

Low moisture part skim (LMPS) mozzarella has a performance shelf life of approximately 3 mo (or less) at refrigeration temperatures. As an alternative to freezing to further extend the performance shelf life of reduced Na LMPS mozzarella, we tested the potential of high-pressure processing (HPP) and very low storage temperatures. Five replicate batches of reduced Na LMPS mozzarella were manufactured using Chymax M as coagulant. Mean composition of the reduced Na (1.0 ± 0.1% salt) LMPS mozzarella cheeses was 46.4 ± 0.4% moisture, 23.5 ± 0.3% fat, and 25.5 ± 0.2% protein. After ripening the cheese for 2 wk at 5°C, each batch was separated into two groups; one group was HPP treated (600 MPa for 3 min), the other was non-pressurized (control treatment). Each cheese group was further divided into three storage temperature treatments (+4, 0, and −20°C). The pH, rheological, textural, sensorial, and functional properties were determined after the HPP treatment, and after 3 and 5 mo of storage. Samples that were stored at −20°C were first thawed at 4°C for 7 d before analysis. Cheese functionality was monitored using texture profile analysis and dynamic low-amplitude oscillatory rheology. Changes in flavor, texture, shred properties, and pizza performance were evaluated using a 10-member panel trained in Quantitative Descriptive Analysis. HPP treatment caused an increase in pH from 5.2 to 5.3, but decreased cheese hardness, and decreased the melting point and shred straightness. HPP treatment did not affect cheese flavor or pizza functionality. At 3 mo, pH was unaffected by storage temperature, but was higher in HPP (5.3) than control (5.25) samples, cheese hardness was lower in HPP samples regardless of storage conditions, pizzas made with HPP samples and stored at 0 or −20°C presented reduced blister quantity and increased strand thickness, and cheese flavor and melting properties were unaffected by the treatments. At 5 mo, pH was lower in −20°C samples, HPP treatments, at all temperatures, showed higher maximum loss tangent; indicating higher flow of melted cheese, shred straightness was higher in HPP treated samples stored at 0°C and −20°C, and samples stored at 4°C presented difficulties when shredding. Cheeses will be monitored for 7, 9, and 12 mo. HPP and very low storage temperature could be used as an alternative to freezing to extend the performance shelf life of mozzarella cheese to more than 6 mo.

Key Words: high-pressure processing, freezing, mozzarella cheese functionality

0528 Hydrolysis of phosphates with a different chain length in water, milk and calcium caseinate.
W. H. Viotto*[1], and D. Maus[2], [1]*University of Campinas, Brazil,* [2] *University of Campinas, Brazil.*

Sodium phosphates, with different chain lengths, are widely used as emulsifiers in the manufacture of processed cheese for the stabilization of casein. The production of processed cheese involves heating and cooling steps, which can influence the phosphate chain length due to hydrolysis reactions that occur due to the heat treatment, pH and ionic environment. The objective of this work was to investigate the hydrolysis rate of phosphates with different chain sizes in water, milk and calcium caseinate during heat treatment. The salts used were sodium tripolyphosphate (TPS) (n = 3), sodium hexametaphosphate (HMPS) (n > 10) and a commercial salt SELF B4 (n = 30). Nuclear Magnetic Resonance ^{31}P was used to evaluate the phosphates hydrolysis products. Dual probe resonance was used, equipped with field gradient in the Z direction, coupled with spectrometer Bruker AVANCE III®. Analyses were performed using temperature ramp to mimic the steps of heating and cooling process of spreadable processed cheese manufacture. The heating was performed from 25°C to 90°C, followed by cooling to 5°C. The pH of salts in different matrices was determined. In water, the hydrolysis of the phosphates was started from 70°C. The higher the phosphate chain size, the lower the pH (SELF B4 = 3.61; HPMS = 6.60; TPS = 8.90) and higher the rate of hydrolysis (SELF B4 = 32.9%; HMPS = 13.6%; TPS = 9.0%). For milk, the onset of hydrolysis was at 50°C, with TPS showing a higher percentage of hydrolysis (23.3%, pH 8.00), followed by self B4 (20.5%, pH 6.20), and HMPS (12.1%, pH 6.80). In calcium caseinate, TPS hydrolysis was started from 40°C while hydrolysis of the HMSP and SELF B4 only occurred at 60°C. The hydrolysis of phosphates in caseinate (TPS = 6.7%; HMPS = 7.5%; SELF B4 = 7.2%) was less intense when compared with water and milk. The pH is close to neutral in calcium caseinate (TPS = 7,6; HPMS = 6.80; SELF B4 = 6.53) due to the high buffering capacity of the protein. The results indicate that hydrolysis of phosphates depended on the phosphate chain length; the matrix used and heat treatment but was mostly governed by pH. Therefore, the initial pH control in the manufacture of processed cheese is essential to control the rate of hydrolysis. Acknowledgment: São Paulo Research Foundation (FAPESP), grant no. 14/07291–3

Key Words: phosphates, hydrolysis, heat treatment

0529 Water mobility, texture and composition of requeijão cremoso manufactured with polyphosphates of different chain lengths.
W. H. Viotto* and V. R. Dias*, University of Campinas, Brazil.*

Requeijão cremoso is a Brazilian spreadable processed cheese made by heating a fresh curd (pH~5.5), in the presence of sodium polyphosphates with different chain lengths, under partial vacuum and stirring. The salts disrupt the casein micelle, by chelating the calcium, resulting in a more open and homogeneous protein matrix with superior water-binding and emulsifying properties. Differences in chain length of polyphosphates change the salt properties as their sequestering ability, buffering capacity, ability to hydrate and disperse caseins, and effectiveness in promoting emulsification. The study evaluated the effect of four commercial sodium phosphates with different chain sizes (n) on composition, water mobility and texture of requeijão cremoso. The following commercial emulsifying salts with different chain lengths (n) were applied: A (n = 2–10), B (n = 10–25), C (n = 25–30) e D (n > 50). The processed cheeses were formulated according to the legal requirements for requeijão cremoso: moisture content–maximum 65%; and fat content–minimum 55% on a dry weight basis. Emulsifying salt (1.8%), NaCl (1%) and water were added to the blend and the processed cheese was made in a Stephan-Geiger homogenizer-grinder. There was a difference in the kinetics and amount of immobilized water during the manufacture and storage of cheeses depending on the type of salt used. The use of the salt A, which presents a high proportion of tetrasodium pyrophosphate, resulted in cheeses with a greater content of calcium bound to casein, higher pH, and lower firmness when compared with cheeses produced with larger chain size phosphates (n > 10). These results can be explained by the presence of tetrasodium pyrophosphate (salt A), which favors interactions water-protein, resulting in a less firm texture cheese. Acknowledgment: São Paulo Research Foundation (FAPESP), grant no. 14/07291–3

Key Words: sodium phosphates, processed cheese, emulsifying salts

0530 Effect of carbon dioxide injection on protein interaction to reduce viscosity of high solids skim milk concentrates.
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Viscosity of skim milk concentrates (SMC) is an important property that constraints the extent of concentration obtained during evaporation and leads to problems like increased tube fouling, reduced heat transfer, and shorter run time. The objective of the present study was to investigate the effect of carbon

dioxide (CO_2) injection as an intermediate processing step to lower the pH of skim milk concentrate and decrease the viscosity of higher solids SMC. SMC with total solids (TS) 30% (w/w) pH 6.5 was warmed to 55°C and CO_2 was injected using a sparger fitted in-line, forming a closed loop with a positive displacement pump. CO_2 was injected at an injection pressure of 5.5×10^5 N/m^2 maintaining a flow rate of 1.4×10^{-3} m^3/sec until the pH was lowered to 6.05. Following this treatment SMC was concentrated to 55% (w/w) TS using a rotary evaporator under vacuum at 70°C. Apparent viscosity of the final concentrate was measured using an ATS Stresstech Rheometer at 55°C with shear rates from 50 s^{-1} to 1050 s^{-1} with 50 s^{-1} ramp. Concentrate was analyzed for particle size using Malvern Zetasizer Nano-ZS and for heat stability by measuring heat coagulation time using an oil bath maintained at 140°C. A sample from the same lot of SMC without the CO_2 injection treatment, concentrated and analyzed similarly, served as the control. The experiments were repeated at least twice and all results were analyzed for statistical significance (at $p < 0.05$) using SAS software. Significant difference ($p < 0.05$) in apparent viscosity was observed between CO_2 treated and control SMC samples. Concentrate obtained from CO_2 treated SMC sample had significantly ($p < 0.05$) lower viscosity compared with that obtained from untreated control sample. The dispersed particle size analysis revealed that concentrate from CO_2 treated SMC sample had lower particle size compared with the control. The changes in dispersed particle size and the resulting change in viscosity of skim milk concentrate can be explained by differences in casein and whey protein interaction between two samples as indicated by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). In conclusion CO_2 injection can be used as a clean label treatment to control viscosity of highly concentrated SMC to eventually improve efficiency of drying process.

Key Words: skim milk concentrate, viscosity, CO_2 injection

0531 Hauling and receiving practices at dairy processing facilities. E. Kuhn*, J. Waite-Cusic, and L. Goddik, *Oregon State University, Corvallis.*

Milk hauling is an overlooked portion of the dairy industry and its impact on raw milk quality is not well characterized. Practices are mandated by the Pasteurized Milk Ordinance; however, gaps exist in the specifics of practices that could impact downstream milk and milk product quality. Description and classification of hauling and receiving practices and their relative impact could allow for the prioritization of improved practices that could improve quality throughout the dairy industry. The objective of this study was to identify current practices that could negatively impact the microbiological quality of raw milk during hauling and receiving. This objective was approached from two angles: (1) An industry survey was conducted to characterize milk hauling and receiving practices, and (2) a database that represented 2-yr of differences in raw (IBC) and PI (PIC) counts between receivers and producers (n = 23,285 tanker loads) was analyzed to identify and quantify hauling situations that have a negative impact on milk quality. Dairy processing facilities (n = 14) were asked to participate in the survey, of which 10 responded (78% response rate). The majority of facilities (10/14) utilized repeated tanker use per 24 h; however, facilities that only receive a few tankers a day washed after each load (n = 4). Frequency of CIP system validation greatly varied among facilities (daily to annually). This suggests that facilities that do not frequently validate could potentially have underlying CIP issues that could have a negative impact on tanker cleaning efficacy. For the database analysis, negative impact was defined as the top 2.5% of instances (n = 583) where the tanker and producer load average difference was ³ 7.67 IBC/mL and ³ 61.5 PIC/mL. Negative impact was more pronounced in PI counts. There was not an identifiable trend in seasonality. The analysis demonstrated that in instances of negative impact, the load typically included milk from a producer with historically high counts. This study suggests that CIP validation frequency and route management may need increased attention to minimize the impact hauling and receiving practices have on raw and downstream product quality.

Key Words: raw milk, quality

0532 Comparing fluorescent and light-emitting diode (LED) retail lighting effects on consumer acceptability of fluid milk. S. Duncan*, H. Potts, and K. N. Amin*, Virginia Tech, Blacksburg.*

The objective was to assess the effect of fluorescent and light-emitting diode (LED) lighting under retail storage conditions on consumer acceptability of milk. Little is known about the effect of retail light exposure on consumer acceptability of milk, especially for LED light. Packaging materials designed to interfere with light wavelengths may be needed to maintain milk quality and consumer acceptability. Consumer acceptability (two studies; *n* = 150+ in each) was assessed using a 9-point hedonic scale (1 = dislike extremely; 9 = like extremely) for overall milk acceptability and acceptability of attributes (appearance, aroma, flavor, mouthfeel, aftertaste, freshness). Just-about-right (JAR) scale (5-point scale; 3 = just about right) characterized the influence of flavor and mouthfeel on consumer acceptability. Analytical measures of milk oxidation included dissolved oxygen content and riboflavin retention. Study 1 evaluated milk stored in high density polyethylene (HDPE) packages for 4 h under LED (about 960 lux). HDPE package treatments included white (low titanium dioxide (TiO_2,), yellow, designed (high TiO_2) and controls: natural HDPE (0% TiO_2) with a light-blocking foil overwrap and without foil (both LED and fluorescent light exposure). Study 2 evaluated polyethylene terephthalate (PET) packages for 4 h under fluorescent and LED (about 1460 lux) light. PET package treatments included two experimental treatments (medium

TiO_2; high TiO_2) and four controls: light-exposed HDPE (fluorescent), light-exposed PET (fluorescent and LED), and light-protected control. Acceptability (overall, attributes) and JAR attributes were analyzed by Fisher's LSD and Penalty Analysis function, respectively, using XLSTAT (a = 0.05). Analytical measures were analyzed by ANOVA and Tukey's HSD (a = 0.05) for mean separation as appropriate. Overall mean acceptability of milk ranged from 5.7 to 6.7 (< like moderately to < like very much), with a significantly lower acceptability for milk exposed to fluorescent light in natural HDPE and clear PET packages. All PET and HDPE packages protected milk flavor from LED lighting; packages with higher TiO_2 had the most optimum performance as indicated by overall acceptability and attributes. JAR flavor evaluation illustrated penalties to overall acceptability for all HDPE packages except the designed package. Only the fluorescent light condition (both PET and HDPE in fluorescent lighting) diminished overall acceptability in study 2 based on JAR flavor evaluation. Changes in dissolved oxygen content, as an indication of oxidation, supported the observed differences in consumer acceptability in fluorescent and LED light. Acceptability in milk quality decreases over short (4 h) light exposure, especially under fluorescent lighting, without appropriate packaging.

Key Words: milk, oxidation, sensory

0533 Effect of various storage conditions on the stability of Sulphonamides in raw milk. M. Chen[1,2], F. Wen[1,3], H. Wang[4], N. Zheng[1,3], and J. Q. Wang[*1,2], *[1]Ministry of Agriculture Laboratory of Quality and Safety Risk Assessment for Dairy Products, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, [4]College of Animal Science and Technology, Yangzhou University, China.*

Sulphonamides (SAs) are synthetic compounds that are widely used in veterinary field to treat bacterial and protozoan infections in dairy cattle, due to its low cost and broad spectrum against common bacterial infections. However, improper use of SAs may lead to SAs residues in milk. Therefore, maximum level limits (MRLs) are established and raw milk is compulsory to be detected for antibiotics, including sulphonamides, by many countries and authorities. Before confirmation experiments are performed, raw milk may be preserved under different conditions. To guarantee the scientific risk assessment of SAs in raw milk and find the optimal storage condition for analytical method, this study was performed to investigate the stability of 8 SAs, including sulfaguanidine (SGD), sulfapyridine (SPD), sulfadiazine (SDZ), sulfamonomethoxine (SMM), sulfamethoxazole (SMX), sulfadimethazine (SMZ), sulfachlorpyridazine (SPDZ) and trimethoprim (TMP), in raw milk under various conditions. Storage conditions included different storage temperature/time (4°C for 4, 8, 24, and 48 h; −20°C for 1, 7, and 30 d; −80°C for 1, 7, and 30 d), thawing temperature (25°C, 40°C and 60°C), freeze–thaw cycle times (once, twice and three times), and addition of different preservatives (odium thiocyanate, sodium azide, potassium dichromate, bronopol and methanal). Raw milk collected from a local farm in Beijing was transported to our lab immediately, spiked with SAs at the MRLs level, kept under the above conditions and then analyzed by UHPLC-MS. Results showed that most SAs were quite stable (recovery = 90% ~ 120%) under 4°C, −20°C, −80°C within 48 h, 30 d, 30 d respectively, thawed at 25°C, 40°C and 60°C, and thawed at 40°C for 1 and 3 times. But most SAs of interest degraded when raw milk was thawed 5 times and preserved with preservatives added. What's more, sulfachlorpyridazine (SPDZ) seemed to be the most labile sulphonamide under these storage conditions. Preservatives seemed to be the most influential factor that affected the stability of sulphonamides in raw milk.

Key Words: raw milk, storage stability, sulphonamides

0534 Effect if pH on the hydrolysis of sodium polyphosphates in different dairy matrices. W. H. Viotto* and A. P. Barth, *University of Campinas, Brazil.*

Sodium polyphosphates are essential ingredients in processed cheese production. These salts are mainly used for their calcium-binding ability and also to control pH, which further aids in protein dispersion and hydration. Hydrolysis of polyphosphates may occur as a function of pH, temperature and chemical environment, altering the composition of salts and their action on cheese. The objective of this work was to investigate the effect of pH (5.2, 5.6, 6.0, 6.4, 6.8) on the hydrolysis of a commercial polyphosphate salt in water, milk and calcium caseinate. Aqueous solutions of polyphosphate were prepared by dissolving the commercial sodium polyphosphate blend in distilled water at 2.3% (w/w). Milk and calcium caseinate were prepared by dissolving skim milk powder (10%, w/w) and calcium caseinate powder (10.5%, w/w), respectively, in distilled water. The same concentration of polyphosphate was used for all the dairy matrices. The hydrolysis of samples was obtained by integration and normalization of the ^{31}P nuclear magnetic resonance spectra (NMR). Dual probe resonance was used, equipped with field gradient in the Z direction, coupled with spectrometer Bruker AVANCE III®. Spectra were obtained at 25°C, 90°C and 10°C to mimic the thermal processing to which the cheeses are subjected. In water, the hydrolysis rate increased as the pH decreased (4.2% for pH 6.8 to 7.59% for pH 5.2), increasing orthophosphate concentration. The same trend was observed in milk, but the rate of hydrolysis was higher (7.85% for pH 6.8 to 17.02% for pH 5.2), probably due to the presence of calcium ions. Calcium

caseinate hydrolysis was similar to that observed in water and milk, except at pH 5.2, where the hydrolysis rate was lower (8.19%) than that observed in milk. This can be explained by the lower mobility of the particles since the protein matrix is more aggregate at this pH. Small variations in pH influenced the hydrolysis of polyphosphate which could result in changes of processed cheese properties. Acknowledgment: São Paulo Research Foundation (FAPESP), grant no. 14/07291–3

Key Words: ^{31}P NMR, hydrolysis, sodium polyphosphate, process cheese

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0535 NIR technology as a process analytical tool for cheese inspection. W. H. Viotto*, D. F. Barbin, and C. Karaziack, *University of Campinas, Brazil.*

The chemical composition of cheese is significantly related to quality, as it is responsible for its shelf life, yield and texture. However, conventional methods for determination of chemical composition are laborious and time-consuming. Fast assessment tools such as NIR spectroscopy and spectral imaging could be used for the quality control of cheeses. The advantage of this technique is that it allows several constituents to be measured simultaneously in a quick and nondestructive way. The objective of this work was to investigate spectral imaging combined with principal component analysis (PCA) for assessment of cheese samples. Spectral information of six varieties of cheese (Cheddar, coalho, Minas, mozzarella, prato and block processed cheese) were obtained using a spectral imaging system, between 928 and 2524 nm, with 6 nm intervals, resulting in 256 analyzed wavelengths. The first two principal components were responsible for 98.2% of the variation among samples, and the score plot presented good separation among samples of coalho cheese, mozzarella and Minas cheese. Loadings show that some peaks are strongly influenced by wavebands, associated to chemical bonds related to protein and fat. Spectral imaging combined with multivariate analysis can be a potential tool for fast cheese quality assessment.

Key Words: PCA, quality control, spectral imaging

0536 Extraction of phospholipids from procream using supercritical carbon dioxide and ethanol as a modifier. B. Li*[1], Z. Linghu[1], F. Hussain[1], S. J. Smith[2], and J. K. Amamcharla[1], *[1]Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan, [2]Kansas State University, Manhattan.*

Procream is a co-product obtained during manufacture of whey protein isolate. It mainly contains whey proteins (63%–72%), fat (12–20%), and approximately 20% of phospholipids (PLs) in total fat. The interest in PLs as functional ingredients is increasing in recent years. PLs affect several cell functions, such as growth, molecular transport system, memory processing, stress responses, and central nervous system myelination. Neutral lipids can be successfully extracted using supercritical carbon dioxide (SCO_2). However, the solubility of PLs is limited in SCO_2 and therefore a modifier such as ethanol is often needed to increase the solubility of PLs. The objective of present study was to use SCO_2 and ethanol as a modifier to extract PLs from procream. For this purpose, the central composite rotatable design based on response surface methodology was used to optimize extraction conditions. The pH of procream (4-8) and extraction pressure (300–550 bar) were used as independent factors. The CO_2 flow rate (5 mL/min), extraction time (1 h), and ethanol flow rate (0.033 mL/min) were kept constant. The extractions were performed in a supercritical extraction system supplied by Applied Separations Inc., PA. Procream was procured from a commercial manufacturer and stored at −20°C until use. A two-step extraction process was followed. In the first step, 10 g of procream was mixed with glass beads in the ratio 1:1 (v:v) and placed in the extraction vessel. Neat supercritical CO_2 was allowed to pass through the extraction vessel to remove all the neutral lipids. In the second step, SCO_2 and ethanol as a modifier was used to extract phospholipids. The remaining lipids from spent solids after the second extraction were extracted using the solvent extraction method. All the lipid fractions were analyzed by high performance lipid chromatography (HPLC) with kinetex™ HILIC (150 × 4.6mm, 5 µm) column. The amount of lipids extracted from after the second stage was significantly ($P < 0.05$) affected by pH of procream. However, pressure was found be not significant ($P > 0.05$). Only Sphingomyelin was found in the lipid fractions obtained after the second extraction step and it was found to be at higher concentrations at pH 7.4. On the other hand, phosphatidylcholine and phosphatidylethanolamine were not detected in lipids obtained after second extraction. Ethanol as a modifier was not able to improve the solubility of phospholipids in SCO2.

Key Words: supercritical fluid extraction, procream, ethanol as a modifier

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0537 Evaluation of Sol-Gel non-stick surface modification in dairy thermal processing. Z. Liu*[1], J. K. Amamcharla[1], and L. Metzger[2], *[1]Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan, [2]South Dakota State University, Brookings.*

Fouling is a common problem in the dairy industry across many types of processing equipment. It necessitates regular and frequent cleaning, which leads to increased down-time and reduced operating efficiency. One way to achieve a reduction in milk fouling is to modify the surface characteristics of stainless steel (SS) surfaces. This study examines the potential viability of Thermolon™, an environmental friendly and food safe surface modification on SS, in dairy thermal processing. SS 316 L coupons (1 inch × 1 inch) with 2 B finished surface (cold rolled, annealed, and pickled) were used in

this study. Sol-gel (Thermolon™) surface modification of SS coupons were provided by Porcelain Industries Inc. (Dickson, TN). The surface properties of the modified and control coupons were characterized by contact angle measurement. The measurements showed that the modified surface gave a higher contact angle at 105.5 ± 0.5°, while the control stainless steel had 82.9 ± 2°, indicating a more hydrophobic surface after modification. Control stainless steel coupons and Thermolon™ modified coupons were then inserted into a benchtop plate heat exchanger (bPHE) and raw milk was pumped through the bPHE to an average temperature of 85°C for 8 h to create milk fouling. Triplicate tests were conducted and significant reductions of milk deposit on modified surfaces was observed ($P < 0.05$). An average of 0.1231 ± 0.0145g of fouling was observed on the control coupons, while 0.0017 ± 0.0018 g of deposit on the modified surfaces. Fouling was reduced by over 90% on the modified surfaces under the same fouling condition. Overall, the Thermolon™ modified surface which has a non-stick property showed fouling resistance and potential to be used in thermal processing of milk.

Key Words: milk fouling, surface modification, Sol-gel

0538 Foaming and baking properties of MPC and egg white protein mixtures. V. Hor* and B. Vardhanabhuti, *University of Missouri, Columbia.*

Egg white protein is the major foaming ingredient used in baked goods. With the Avian flu outbreak that caused a shortage in eggs and an increase in egg prices, egg alternatives have been explored for baking applications. Milk protein concentrate (MPC) is a primary ingredient in many food products due to its functional and nutritional properties; however, its foaming properties are still underutilized. This goal of this study was to determine the effects of MPC to egg white protein isolate (EWI) ratio on foaming properties and baking properties of angel food cake.

Foam of EWI and preheated (55°C) MPC solutions were prepared by beating protein solutions for 20 min in a KitchenAid mixer. Foaming properties were observed by measuring overrun and drainage 1/5 life. Baking properties were determined by measuring the volume of angel food cakes using rapeseed displacement method, textural properties using TA-XT2 Texture Analyzer, and color using a Hunter Colorimeter. Yield stress of cake batter was measured using a Kinexus Pro rheometer.

Results showed that foam overrun and drainage significantly decreased with 20% EWI replacement. No change in overrun was observed with increasing MPC ratio ($P > 0.05$) while drainage increased. Similar trend was observed with yield stress of cake batter. When used in angel food cake, replacing 20% EWI did not significantly affect cake volume, chewiness or gumminess ($P > 0.05$) though hardness decreased by 12% and springiness increased by 14%. At 40% replacement cake volume significantly decreased and continued to decrease at higher %MPC. Largest changes in TPA attributes were observed at 40% replacement. At higher MPC ratios, the cakes were too dense such that hardness and gumminess started to increase. Replacing EWI with MPC did not affect cake color.

In conclusion, using 20% replacement yields the closest results to the traditional angel food cake especially in terms of baking properties. Modification of protein properties or addition of other ingredients to improve foaming properties are needed to improve foaming and baking properties of MPC.

Key Words: angel food cake, milk protein concentrate, egg white protein, texture, volume, foam, overrun, drainage, rheology

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0539 The effect of emulsifying salts on the turbidity of a diluted milk system with varying pH and protein concentration. M. Culler*, Y. Saricay, and F. M. Harte, *Pennsylvania State University, University Park.*

Casein micelles' stability has been shown to be dependent on the surrounding environmental conditions. In the dairy industry, salts are frequently used as functional additives to tailor stability and melting properties for various applications. Thus, there is a clear need to understand the role that salts can have on the milk system, particularly their effect on the casein micelles. The aim of this study was to examine the effect of various salt types and concentrations on the turbidity of a diluted milk system at different pH's and protein concentrations to draw conclusions about the aggregation and dissociation of the casein micelles.

Solutions of 10 commonly used emulsifying salts listed in the Code of Federal Regulations for pasteurized process cheese were made by mixing the salts in a 1-in-20 dilution of water in skim milk ultrafiltrate (3 kDa MWCO) to obtain salt concentrations from 0 to 248 mM. The effect of the salts at different pH's was also examined by using salt solutions buffered to 4.8, 5.8, 6.8, 7.8 or 8.8. The turbidity of diluted skim milk (40 uL) in a given salt concentration and pH (1960 uL) was measured by UV-Vis spectroscopy at 400 nm at t = 0, t = 30 s and t = 30 m. Measurements were completed in duplicate. For experiments with varying protein contents, ultrafiltration retentate and permeate were used in differing ratios to obtain concentrations of 1.4, 2.8, 4.2, and 5.6% casein.

At pH values 5.8 and above, an increasing salt concentration resulted in a decrease in the turbidity of the diluted milk system, however salts at pH 4.8 exhibited upward trends as concentration increased. Each salt's effect on the turbidity of the system changed with varying pH and salt concentration. At pH 6.8 and t = 0, 1 mM of sodium hexametaphosphate caused a decrease in absorbance from 0.597 absorption units (AU), while 100 mM of monosodium phosphate caused only a 0.116 AU decrease for the same pH and time. Absorbance decreased slightly (> 2 AU) between t = 0 and t = 30s, however a larger decrease (1- 4 AU) was observed for t = 30 m at

pH 6.8. When the effect of varying protein concentration was tested on trisodium phosphate, the slope of the turbidity curve did not change with increasing protein concentration, but the extent of the decrease in turbidity was more pronounced at higher protein concentrations.

Key Words: casein, salt, turbidity

0540 Effect of high pressure jet processing on the rheological properties of ice cream mix. M. Tran*, D. R. Roberts, and F. M. Harte, *Pennsylvania State University, University Park.*

Homogenization is a general term that describes a process that reduces the heterogeneity of a system. In the dairy industry, two-stage valve homogenization (< 20 MPa) is used to prevent milk creaming by reducing the fat globule particle size and to homogenize ice cream mix before freezing. Advances in material science and engineering enabled high pressure jet technology (HPJ) to achieve processing pressures up to 600 MPa. The HPJ contains a diamond nozzle (75 to 400 μm diameter) which forces liquid into a jet stream, differing from high pressure homogenization that uses a valve (HPH). The HPJ is able to induce higher shear stress, temperature, cavitation, turbulence, and friction as compared with conventional homogenization. The objective of this study was to evaluate the rheological properties of conventionally processed ice cream mix processed through HPJ at 0 to 500 MPa (125 MPa increments) to understand the impacts of this technology on the physical properties of mix. The mix was evaluated for changes in density and rheological behavior. Density of the mix decreased with increasing pressure, from 1.045 g/mL at 0 MPa (control) to 0.785 g/mL at 500 MPa. All samples exhibited shear thinning behavior consistent with the Power Law model. Consistency index (k) of mixes dramatically increased to 0.788 at 500 MPa, compared with mix processed at 250 MPa (k = 0.117). The flow behavior index (n) dropped from 0.643 to 0.425 for control samples vs. ice cream mix processed at 500 MPa. Rheological properties of ice cream mix are highly affected by HPJ processing with increasing pressures, indicating structural changes within the mix. The results from this study will provide further information on the implications of HPJ processing on ice cream mix, as well as other dairy systems.

Key Words: pressure, ice cream, rheology

0541 Fat reduction in ice cream and its effect on physical structure and consumer acceptability. M. L. Rolon*, A. J. Bakke, J. N. Coupland, J. E. Hayes, and R. F. Roberts, *Pennsylvania State University, University Park.*

Fat reduction is often pursued as a way to reduce the overall energy density of food products. Ice cream is a complex food where removal of one ingredient may affect not only physical properties but also multiple sensory characteristics that are important to consumers. Fat, in particular, plays a role in structuring ice cream, contributing to the characteristic smoothness, dryness and melting rate. Removal of fat from ice cream without replacement of solids has been shown to decrease sensory quality indicators. Previous work evaluating fat removal strategies has focused on changes in key sensory descriptors, with surprisingly little information being collected on consumer acceptability of reduced-fat products. Here, we evaluated the effect of replacing fat with maltodextrin (MD) on consumer acceptability and on selected physical properties of ice cream simultaneously. Vanilla ice creams were formulated with 6, 8, 10, 12, and 14% fat and 8, 6, 4, 2, and 0% maltodextrin, respectively. A series of sensory tests were conducted in the Sensory Evaluation Center at Penn State, each with ~100 participants, to measure liking and intensity of various attributes. Physical measures included fat particle size, fat destabilization, hardness and melting rate. The experiment was replicated three times. Data were analyzed using mixed model ANOVA and correlation to assess relationships between consumer acceptability, physical variables and sensory attributes. Additional sensory testing was conducted after 19 wk of storage at −18°C. Fat particle size and fat destabilization significantly decreased with fat reduction, but consumer acceptability did not significantly differ with fat content for fresh or stored ice cream. Overall liking was correlated with slower melting rate in fresh ice cream. Following storage, ice creams with 6, 12, and 14% fat did not change in consumer acceptability compared with fresh ice cream. However, ice creams with 8 and 10% fat (and 6 and 4% MD) each showed a significant drop in liking score following storage. Collectively, the changes on the physical structure of ice cream caused by the reduction in fat from 14 to 6% did not show evidence of gross changes in consumer acceptability for either fresh or aged ice cream, although storage altered liking for some formulations but not others.

Key Words: ice cream, consumer acceptability, fat reduction

0542 Inactivation of *Listeria innocua* on cheddar cheese by supercritical fluid CO_2. S. Padilla Antunez*[1], and R. Jimenez-Flores[2], [1]*California Polytechnic State University, San Luis Obispo,* [2]*Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

Hard cheeses contaminated with *L. monocytogenes* and potential illness in consumers are unacceptable risks in today's commercial environment. Novel methods, such as supercritical fluid extraction with CO_2 (SFE), could potentially reduce the risk of microbial contamination and increase the safety of cheeses. The aim of this study was to evaluate the efficacy of SFE in reducing the population of *Listeria innocua* (a surrogate for *L. monocytogenes*) on the surface of cheddar cheese.

The effects of SFE on the pH, water activity, and appearance of cheddar cheese were also evaluated. Cheddar cheeses were inoculated with *L. innocua* (10^6 log CFU/g) and incubated overnight at 4°C to emulate post pasteurization contamination. The treatment with SFE was measured at two pressure and temperature combinations (120 bar at 40°C and 150 bar at 50°C) for 30 min. Treated and untreated samples were analyzed for *L. innocua*, coliforms, pH, and water activity immediately after treatment. Counts results were analyzed and compared using ANOVA. *Listeria innocua* in cheddar cheese decreased approximately 2.0 and 4.0 log CFU/g after SFE treatment at 120 bar and 40°C and SFE treatment at 150 bar and 50°C for 30 min, respectively. The water activities and pH were 0.9640 and 5.35 for treated and untreated cheddar cheeses. Cheddar cheeses showed some signs of deformation, such as some openings and splits in the surface after SFE treatment, because treatment was done in unrestrained cubes. These data suggest that SFE could potentially be used to reduce *L. monocytogenes* in cheese products.

Key Words: supercritical fluid extraction with CO_2, *Listeria innocua*, *L. monocytogenes*, hard cheeses, cheddar cheese

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0543 Evaluation of the effect of cavitation on biofilm forming ability of sporeformers. T. Almalki*[1], and S. Anand[2], [1]*Midwest Dairy Foods Research Center, Dairy Science Department, South Dakota State University, Brookings,* [2]*South Dakota State University, Brookings.*

Thermoduric sporeformers survive heat treatment and lead to the formation of contact surface biofilms. These biofilms are difficult to clean and cause cross-contamination of milk and dairy products during milk processing. To inactivate the thermoduric sporeformers, a novel technique based on the cavitation effect is being studied in our lab. In addition to inactivating sporeformers, the cavitation may also lead to surface modifications of any surviving cells and their endospores. It is hypothesized that cavitation would result in their reduced ability to attach to contact surfaces and form less biofilms on their recovery. The present study is thus focused on the effect of cavitation on the biofilm-forming ability of three dairy related sporeformers: *Geobacillus stearothermophilus*, *Bacillus licheniformis*, and *Bacillus sporothermodurans*. Individual organisms were spiked in to sterile skim milk samples at a rate of 6.0 log CFU/mL. For the cavitation effect, the spiked samples were treated by ultrasonicator processor (VC 505; Sonics and Materials Inc., CT) at 20 kHz frequency, 500 W power, and 80% amplitudes for 10 min each. The pre- and post-ultrasonicated spiked samples were used to develop biofilms on stainless steel (SS) coupons under static conditions. The respective biofilm counts were taken after 72 h of incubation by standard microbiological techniques. Scanning electron micrographs were also taken to visually observe the developed biofilms. The replicate data from 3 trials for each organism were statistically analyzed and means were compared using the Student *t* test. The pretreatment counts in spiked milk samples were 7.2, 8.0, and 7.7 logs, respectively, for the three sporeformers. After the cavitation treatment, the counts got reduced significantly to 3.4, 4.2, and 3.7 logs, respectively. Further studies indicated that within biofilm matrices on SS coupons, the pretreatment counts for the three sporeformers were 5.35, 6.42, and 6.5 logs, respectively, while the biofilms of cavitated cells revealed significantly ($P < 0.05$) lower counts of 4.39, 5.44, and 5.82 logs, respectively, for the three organisms. Of the three organisms tested, *Geobacillus stearothermophilus* formed the least biofilms after cavitation. The results obtained in the study thus support the hypothesis that the cavitated sporeformers would form lower biofilms.

Key Words: cavitation, sporeformers, biofilm

0544 The effect of *Lactobacillus brevis* and fibrolytic enzymes on fermentation of switchgrass silages. L. Jingjing*, *State Key Laboratory of Animal Nutrition, Engineering Technology Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

The objective of this study was to determine the effect of *Lactobacillus*, enzymes, and a *Lactobacillus* + enzymes mixture on fermentation characteristics, nutritive value, and microbial diversity of switchgrass silage. Switchgrass (*Panicum virgatum* L.) was harvested at vegetable stage and treated with distilled water (control), *Lactobacillus brevis*, fibrolytic enzymes, and *Lactobacillus brevis* + fibrolytic enzymes (denoted C, LB, E, and LB+E, respectively) before ensiling. Treated switchgrass was ensiled in sealed 1.0-L plastic jars. Jars of each treatment were opened after 3, 10, 20, and 30 d for chemical and microbial analyses. Inoculation accelerated the decline of silage pH. Compared to other treatments, LB+E had the most rapid decline ($P < 0.05$) in pH during the first 3 d of ensiling. After 30 d, for C, LB, E, and LB + E, pH declined to 5.3, 4.6, 4.8, and 3.7, respectively. There was no butyric acid detected in LB and LB+E. The lactic acid concentration of LB and LB+E increased by 5.53 times and 21.75 times compared to that of C, respectively. Acetic acid concentrations of LB and LB+E decreased by 36.34% and 9.40%, respectively. NH_3–N concentrations of LB, LB+E, and E decreased by 67.7%, 74.55%, and 69.88%, respectively. Treatments with enzymes (E, LB+E) effectively ($P < 0.05$) decreased neutral detergent fiber (NDF) and acid detergent fiber (ADF) concentrations. NDF concentrations in E and LB+E decreased by 8.09% and 8.43%, respectively. ADF concentrations in E and LB+E decreased by 3.03% and 10.88%, respectively. Crude protein (CP) content of C, LB, E, and LB+E was 77.6, 96.2, 88.0, and 97.0 g/kg DM, respectively, suggesting that inoculation increased the CP content of switchgrass silage significantly ($P < 0.05$). The

16S rRNA gene-based pyrosequencing was used to analyze the community of the 30-d silage, and results indicated that the diversity of microorganisms differed among treatments significantly ($P < 0.05$). Microbial diversity was lower in treated switchgrass silages than that in the control switchgrass silage. *Enterobacter* was the dominant species in C, and the relative abundance of *Enterobacter* was 53.60%. *Enterobacter* was the dominant species in E, although the relative abundance of *Enterobacter* decreased to 40.67%, and that of *Lactobacillus* increased to 26.13% in E. In LB and LB+E, *Lactobacillus* was the advantageous species (91.19% and 96.89%, respectively), and *Enterobacter* was inhibited effectively. In conclusion, the addition of bacterial and enzymatic additives can improve switchgrass silage fermentation quality to different extents. Adding a mixture of *Lactobacillus brevis* and fibrolytic enzymes worked more effectively than either adding *Lactobacillus brevis* or fibrolytic enzymes, respectively.

Key Words: switchgrass silage, fermentation characteristics, nutritive value, microbial diversity, *Lactobacillus brevis*, fibrolytic enzymes

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0545 Influence of flax seed on the bile tolerances of *Lactobacillus acidophilus*, *Lactobacillus bulgaricus*, and *Streptococcus thermophilus*.

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Consumption of flax seed provides health benefits such as lowering blood glucose and cholesterol levels. Bile tolerance is an important probiotic characteristic allowing survival of probiotics in the intestinal tract. This experiment was conducted to determine whether or not flax seed enhances the bile tolerance of *Lactobacillus acidophilus, Lactobacillus bulgaricus*, and *Streptococcus thermophilus*. Control (no flax seed) and experimental (62 g flax seed/L) broths were prepared for each culture. The broths were sterilized, cooled, inoculated, and plated for 8 h. The MRS broth contained 0.3% oxgall for *Lactobacillus acidophilus* LA-K and 0.3% oxgall with 0.2% sodium thioglycolate for *Lactobacillus bulgaricus* LB-12. The M17 broth contained 0.3% oxgall and 5% lactose for *Streptococcus thermophilus* ST-M5. MRS agar, MRS agar pH 5.2, and M17 agar containing 5% lactose were used for plating *Lactobacillus acidophilus* LA-K, *Lactobacillus bulgaricus* LB-12, and *Streptococcus thermophilus* ST-M5, respectively. *Lactobacillus acidophilus* LA-K plates and *Lactobacillus bulgaricus* LB-12 plates were incubated anaerobically at 37°C for 48 h and for 72 h, respectively. *Streptococcus thermophilus* ST-M5 plates were incubated aerobically at 37°C for 24 h. For *Lactobacillus acidophilus* and *Lactobacillus bulgaricus*, the log counts in the absence of flax seed significantly decreased from 0 to 8 h while no significant difference was observed in the presence of flax seed. However, no significant difference in log counts of *Streptococcus thermophilus* between 0 and 8 h for the broth either with or without flax seed was observed. Therefore, flax seed improved the bile tolerance of *Lactobacillus acidophilus* and *Lactobacillus bulgaricus* but not of *Streptococcus thermophilus*.

Key Words: flax seed, bile tolerance, dairy cultures

0546 Characterization of *Lactobacillus wasatchensis* from aged cheeses showing late-gas defects.

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Lactobacillus wasatchensis WDC04, a nonstarter lactic acid bacterium, was isolated from aged cheddar cheese that had late gas formation. Subsequent studies have demonstrated that *Lb. wasatchensis* can produce gas in culture and in experimental cheeses. This organism has also been isolated from five other geographically distant production facilities (UT, WI, WA) in cheese samples with late gas defects. It has not been found in normal cheeses that exhibit no late gassy defect. The objective of this study was to characterize and compare *Lb. wasatchensis* strains isolated from the different cheese samples. Strains from each cheese were compared using 16S rRNA gene sequencing, rep-PCR, and the API® 50CH carbohydrate metabolic assay. The strains have 100% sequence identity to WDC04 based on the alignment of approximately 1200 bp of the 16S rRNA gene. However, rep-PCR analysis indicates that the strains are related but not identical. This might suggest multiple geographical sources for contamination. In addition, several primer sets specific for *Lb. wasatchensis* have been designed and tested for specificity against other *Lactobacillus* and NSLAB species. A specific primer set will allow more rapid, and possibly quantitative, detection of *Lb. wasatchensis* in cheese. Further, these primers will help to identify sources of the contaminant in the environment and to monitor critical steps in the production process, such as the incoming milk and pasteurization effluent, as possible sources of *Lb. wasatchensis*.

Key Words: lactobacilli, gassy defect, cheese

0547 Determination of antagonism between NSLAB strains and *Lactobacillus wasatchensis* WDC04 using the agar-flip method. C. J. Oberg*[1], M. Walker[2], M. D. Culumber[1], and D. J. McMahon[3], [1]*Department of Microbiology, Weber State University, Ogden, UT,* [2]*Weber State University, Ogden, UT,* [3]*Western Dairy Center, Utah State University, Logan.*

Lactobacillus wasatchensis WDC04, a new obligatory heterofermentative nonstarter lactic acid bacteria (NSLAB), was recently isolated from "gassy" cheddar cheese. Evidence indicates WDC04 may be an important cause of late gassy defect in aged cheese. One way to control WDC04 may be to incorporate other NSLAB strains into cheese that inhibit its growth. Experiments were performed to determine if inhibition occurs between common NSLABs and WDC04 utilizing the agar-flip method. A lawn of WDC04 was swabbed on MRS agar with 1.5% ribose (MRS-R) and incubated anaerobically at 25°C for 2 d or 4 d. Agar was then aseptically flipped over and individual NSLAB challenge cultures swabbed on the exposed surface. Plates were incubated anaerobically at 30°C or 37°C (for *Lb. helveticus*) for 5 d. Growth of NSLAB cultures was compared to their growth on MRS-R plates without a WDC04 lawn (controls). In a second experiment, the same procedure was utilized, except the media contained 4% NaCl and pH 5.2 to mimic the cheese environment. In a third experiment, MRS-R (4% NaCl, pH 5.2) was also used, but the NSLAB cultures were initially swabbed as the lawn, incubated, and then WDC04 was streaked on the opposite side of the agar. In the first and second experiments, *Lb. curvatus* WSU1 showed the greatest inhibition by WDC04 while *Lb. paracasei* Lila and *Lb. rhamnosus* 7469 were the least inhibited. All challenge NSLAB strains showed decreased levels of growth compared to their control plates. In both experiments, most NSLAB cultures showed more inhibition by WDC04 grown for 4 d compared to 2 d before the culture challenge. Results from the third experiment suggest that some NSLAB strains can affect growth of WCD04 under cheese-like conditions with *Lb. casei* F19, *Lb. paracasei* Lila, and *Lb. rhamnosus* 7469 exhibiting inhibition. Since there was no direct contact between WDC04 and each NSLAB challenge strain, any inhibition was due to secretion of inhibitory compounds. Examining the antagonism between NSLABs and WDC04 allows for the selection of NSLAB strains that could inhibit this problematic bacterium during cheese ripening.

Key Words: *Lactobacillus wasatchensis*, nonstarter lactic acid bacteria, late gas defect

0548 Determination of treatments to reduce late gassy defect in cheese due to *Lactobacillus wasatchensis* WDC04 contamination. C. J. Oberg*[1], I. Bowen[2], M. D. Culumber[1], and D. J. McMahon[3], [1]*Department of Microbiology, Weber State University, Ogden, UT,* [2]*Weber State University, Ogden, UT,* [3]*Western Dairy Center, Utah State University, Logan.*

Lactobacillus wasatchensis WDC04 is a recently discovered lactic acid bacterium isolated from gassy cheddar cheese. Previous research associated WDC04 with late gassy defect in aged cheese, which results in serious commercial losses. Experiments were performed to determine its salt tolerance at pH 5.2 and 6.5, resistance to HTST pasteurization, and pH tolerance. Understanding these characteristics of WDC04 could allow manipulation of the cheese environment to control it. MRS with 1.5% ribose (MRS-R) was prepared at either pH 5.2 or 6.5 with salt concentrations ranging from 0.0% to 10.0%. Two mL of each MRS-R media was added to wells in a 24 micro-well plate and an absorbance reading taken (600 nm). Immediately, 100 mL of WDC04 was inoculated into each well, and the plate incubated at 25°C for 3 d (pH 6.5) or 2 d (pH 5.2). Plates were then placed in a Teacon Infinite 2000 with absorbance readings (A_{600}) taken every 4 h for 24 h. Results showed that WDC04 grew best at 3.0% salt (pH 6.5) and 2.0% salt (pH 5.2) but showed some growth up to 6% at either pH. Further testing was performed using a narrower salt range (5.25%–6.75%) to determine if a salt concentration used in cheese could suppress WDC04 growth. Above 6.0% salt, WDC04 was inhibited. Using this methodology, the pH range (2–8) for WDC04 was also determined. Results confirmed WDC04 grows best at pH 5–6 (cheese pH) but not below pH 4 or above pH 7. To model HTST pasteurization, WDC04 was grown in MRS-R broth for 2 d, diluted, then heat shocked at 72°C for 15 sec and plated. With an initial count of 10^8 CFU/ml, results showed a decrease of 10^5 CFU/ml in survival of WDC04, indicating WDC04 could be contaminating cheese by surviving pasteurization if it is at high levels in the raw milk. Results suggest that using a higher salt/moisture ratio in cheese and increasing pre-pasteurization sanitation to remove biofilms would decrease the likelihood of *Lb. wasatchensis* WDC04 in ripening cheese, thus, reducing the possibility of late gassy defect.

Key Words: lactobacilli, cheese, gas

0549 Regional milk sourcing impact on non-starter lactic acid bacteria (NSLAB) in raw milk and cheddar cheese during aging. L. Goddik*, C. Baird, and J. Waite-Cusic, *Oregon State University, Corvallis.*

Non-starter lactic acid bacteria (NSLAB), which include lactobacilli, are found at low levels in fresh raw milk. Lactobacilli are important to the dairy industry because of their potential impact on the flavor and texture of yogurt, sour cream,

and cheese. The objective of this study was to investigate the contribution of lactobacilli from raw milk on the microbiological profile of cheddar cheese during aging (0–6 mos). Using a standardized recipe, cheddar cheeses were made with raw milk sourced from dairies on the Oregon Coast (n = 4) and in the Willamette Valley (n = 2) and aged up to 6.5 mos at 53°C. Lactic acid bacteria counts (LAB) were determined in raw milk and cheese samples using standard serial dilution and spread plating techniques on Lactobacilli MRS Agar with anaerobic incubation at 30°C for 48 h. Isolates (n = 5–10/sample) were selected for preliminary speciation using high resolution melt analysis (HRM) PCR assay targeting the V1 region of the 16S rDNA. Strains were further subtyped using a second HRM repetitive sequence-based PCR (rep-PCR). *Lactobacillus curvatus* and *L. paracasei* were identified in raw milk sourced from the Oregon Coast. *Lactobacillus paracasei* was also identified in the Willamette Valley cheeses. Species diversity decreased throughout aging in all cheeses with the exception of cheese made from milk sourced from a single dairy on the southern Oregon Coast. After 6.5 mos of aging, the predominant species across all cheeses was *L. paracasei* (40.8% of the identified isolates). Strain diversity was highest in milk sourced from the northern Oregon Coast, with six unique strains of *L. paracasei*. Evidence suggests that milk sourcing impacts the strain diversity of NSLAB present in raw milk and cheddar cheese.

Key Words: lactobacilli, rep-PCR, HRM-PCR

0550 Effect of rate of cooling and ripening temperatures on non-starter lactic acid bacteria in cheese. D. I. Khan*, and S. Anand, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Non-starter lactic acid bacteria (NSLAB) play a major role in influencing cheese flavor and quality. These bacteria increase during the ripening process, and many of the heterofermentative lactic acid bacteria could lead to some typical cheese defects. Rate of cooling to different temperatures and the corresponding ripening temperatures could also affect their counts. To study this, a set of cheese samples was fast cooled to 3°C and compared with another set that was slow cooled to 10°C. These two treatment sets were each ripened at 3°C and 10°C for a period of 2 mo. Samples drawn were microbiologically analyzed using standard techniques. The selective media used included Rogosa selective *Lactobacillus* agar for NSLAB, deMan Rogosa and Sharpe (MRS) agar for specific *Lactobacillus* sp., MRS-V agar with 20 µg/ml of vancomycin for *Leuconostoc* spp., and MRS-VR agar with 2 µg/ml vancomycin and 1.5% ribose for *Lactobacillus wasatchensis*. Isolated colonies on the selective media were further identified using matrix assisted laser desorption ionization mass spectrometry-time of flight. The data were statistically analyzed, and the means were compared by a t test. Significance was declared at $P < 0.05$. At the start of the study, the NSLAB were lower ($P < 0.0001$) in samples cooled to 3°C (5.87 logs) as compared to 10°C (6.19 logs). This trend of lower NSLAB counts was maintained in samples cooled to 3°C, on further ripening at 3°C, and reached an average count of 6.00 logs at the end of 2 mo. While under similar ripening duration, the counts were 6.21 logs in the samples cooled to 3°C but ripened at 10°C. In comparison, the samples cooled to 10°C and ripened at 3°C for 2 mo showed higher counts of 6.58 logs. Similar higher counts (6.49 logs) were observed in 10°C cooled samples, which were ripened at 10°C. The predominant heterofermentative isolates included *Lactobacillus paracasei* and *Lactobacillus rhamnosus* in addition to others such as *Pediococcus acidilactici*, *Streptococcus salivarius* ssp. *thermophilus,* and *Lactococcus lactis*. None of the samples, however, showed the presence of *Lactobacillus wasatchensis* and *Leuconostoc* spp. In conclusion, fast cooling treatments to 3°C, followed by aging at 3°C would lead to lower NSLAB counts and is likely to result in a better cheese quality. This information would help cheese manufactures to choose the appropriate rate of cooling and ripening temperatures.

Key Words: cheese, ripening, NSLAB, heterofermenters

0551 Efficient removal of spores from skim milk using microfiltration: spore size and surface property considerations. E. R. Griep*, Y. Cheng, and C. I. Moraru, *Cornell University, Ithaca, NY.*

The presence of spores in milk can cause numerous quality and shelf life issues for dairy products. Microfiltration (MF) using a 1.4 µm pore size can effectively remove vegetative bacterial cells from milk and is used in commercial applications. However, this pore size may not be equally effective in spore removal. The objective of this study was to determine the effectiveness of MF using a 1.4 µm and a 1.2 µm pore size for removing spores of *Bacillus licheniformis* (BL) and *Geobacillus spp.* (GEO) from skim milk. Cell sizes of both spores and vegetative cells were evaluated by scanning electron microscopy (SEM), surface charge by zeta potential analysis, and surface hydrophobicity by contact angle measurements, in triplicate. Commercially pasteurized skim milk was inoculated in a sterilized feed tank with a spore suspension at about 10^6 spores/mL and was then treated by MF (in triplicate) using ceramic Isoflux membranes at 6°C, cross-flow velocity of 4.1 m/s, and transmembrane pressure between 69 and 74 kPa. Total aerobic plate count and spore count of the permeate were conducted. An unpaired t test was used to determine significant differences between samples at the $P < 0.05$ significance level. Vegetative cell length ranged between 2.40 and 3.82 µm and the width between 0.39 and 0.64 µm. Spores were shorter and wider, averaging 1.39–1.58 µm in length and 0.63–0.88 µm in width, thus having a higher probability to pass through a 1.4 µm membrane. Indeed, for BL (1.39 µm length by 0.63

μm width), an average spore reduction of only 2.17 log was achieved by 1.4 μm pore size. For the 1.2 μm membrane, a 4.57 log reduction was achieved. For GEO spores, their larger spore size (1.58 μm length by 0.81 μm width) allowed a practically complete removal using both pore sizes (spore counts in permeate below the detection limit). The surface properties of BL and GEO indicated that they may interact differently with the membrane. Both spore species and the ceramic membrane had negative surface charge at the milk pH, indicating slight electrostatic repulsion between them. GEO spores were hydrophilic, while BL spores were slightly hydrophobic; the ceramic membrane surface changes from hydrophilic (in unfouled state) to hydrophobic after adsorption of caseins during MF. Consequently, BL spores may experience slight attractive force to the membrane through hydrophobic interactions, which will facilitate their passage through the membrane. A good understanding of all factors that affect the removal of spores using MF can lead to the production of milk with lower spore count, higher quality, and increased shelf life.

Key Words: microfiltration, spore removal, skim milk

0552 Evaluation of microbial enzymes for degradation of exopolymeric substances (EPS) within biofilm matrices for more effective cleaning. N. Garcia-Fernandez[*1,2], A. Hassan[3], and S. Anand[2,4], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Midwest Dairy Foods Research Center, Brookings, SD, [3]Daisy Brand, Garland, TX, [4]South Dakota State University, Brookings.*

This study was conducted to determine whether biofilms on reverse osmosis (RO) membranes could be disrupted by natural crude enzymes (CE) obtained from microorganisms with the ability to degrade exopolymeric substances (EPS). The first enzyme extract (termed CE1) was obtained from a bacteriophage with infectivity for the EPS producing *Lactococcus lactis* ssp. *cremoris* strain JFR. The phage was isolated from a dairy plant environment and propagated overnight in liquid cultures of its host. The pH was then neutralized (pH 7.0) and phage particles were removed by centrifugation (75,600 × *g* for 60 min). The second extract (CE2) was obtained from supernatants of JFR cultures in 10% whey protein concentrate (WPC35), showing a reduction in its viscosity after 72 h incubation (suspected to produce hydrolases to degrade its own EPS). The third extract (CE3) was derived from supernatants of overnight tryptic soy broth (TSB) cultures of *Bacillus mojavensis* strain Bc, which hydrolyzed amylopectin and reduced viscosity of milk fermented with ropy yogurt cultures. All supernatants were microfiltered (0.22 μm) and then concentrated by ultrafiltration (10 KDa). Standard static biofilm assays were conducted by developing biofilms on 2 by 2 cm pieces of RO polyamide membrane for 24 h. The CE1 preparation was applied to JFR biofilms that were formed using M17 as the suspension medium. The CE2 was applied to biofilms formed on membranes by slime producing *Bacillus* cultures (*B. mojavensis* strain Bc and *B. licheniformis* strain K1) using TSB. The CE3 was applied to biofilms formed by a ropy strain of *Streptococcus thermophilus* (ST3534) with M17. The biofilms were treated with CE at 1% (v/v) in phosphate buffer saline (PBS) or just PBS as control at 37°C for 30 min under agitation. The viable cell counts were determined by standard culture techniques after detaching cells with stomacher. All experiments were repeated 3 times. The CE extracts obtained from the bacteriophage (CE1), JFR (CE2), and Bc (CE3) cultures reduced the counts of the respective single species biofilms by 0.5 log CFU/cm^2 (JFR), 0.3 and 0.7 log CFU/cm^2 (Bc or K1), and 0.2 log CFU/cm^2 (ST3534), respectively. These results provide an early indication that natural crude enzymes from microbial sources have the potential to selectively degrade the resistant biofilms matrices. This work also suggests that cleaning applications must contain a diverse mixture of hydrolytic enzymes to degrade the complex matrix of multiple species biofilms of dairy separation membranes.

Key Words: biofilms, enzymes, membranes

0553 Comparison of biofilm formation on stainless steel and modified surface milk plate heat exchangers. S. Jindal[*1], S. Anand[1], J. K. Amamcharla[2], and L. Metzger[1], *[1]South Dakota State University, Brookings, [2]Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan.*

Flow of milk through the plate heat exchanger (PHE) results in denaturation of proteins, resulting in fouling. This also accelerates bacterial adhesion on the PHE surface, eventually leading to the development of biofilms. In the case that milk is processed further through the fouled plates, it would result in shedding of bacteria cross-contaminated from biofilms into the product, which ultimately limits the duration of production runs. Altering surface properties, such as surface energy and hydrophobicity of the pasteurizer plates, could be an effective approach to solve this issue. This study was conducted to evaluate and compare the extent of biofouling on native stainless steel (SS) and modified surface PHEs. Raw milk was pasteurized through both the PHEs for 17 h. For microbial studies, raw and pasteurized milk samples were aseptically collected from inlets and outlets of both PHEs at various time intervals to examine the shedding of bacteria in the milk. The 3M quick swabs and ATP swabs were used for sampling from all sections of the pasteurizers (regeneration, heating, and cooling) at the end of the run, with the latter being effectively used to estimate the efficiency of Cleaning in Place. The data was statistically analyzed for analysis of variance, and means were compared. Modified PHE experienced lower mesophilic and thermophilic attachment and biofilm formation (average 1.0 and 0.99 log CFU/cm^2) in the regenerative section of the pasteurizer than those of SS PHE (average 1.49 and 1.47 logs). Higher relative light units (RLUs) were also observed

for SS PHE, as compared to the modified PHE, illustrating the presence of more organic matter on the surface of the SS PHE. In addition, at the 17th hour, milk collected from the outlet of the SS PHE experienced a sudden increase in the plate counts (5.44 log CFU/cm^2). These counts were significantly higher than those for pasteurized milk collected from modified PHE (4.12 log CFU/cm^2). This also provided evidence in favor of the modified PHE in achieving better microbial quality of pasteurized milk in long process runs. Moreover, since cleaning the SS PHE involves an acid treatment step, while only an alkali treatment step is sufficient for the modified PHE, use of the latter is both cost and time effective, making it a more ideal surface for milk processing.

Key Words: biofilms, stainless steel, modified

0554 Improved functionality of fermented milk is mediated by the symbiotic interaction between *Cudrania tricuspidata* leaf extract and *Lactobacillus gasseri* strains. N. S. Oh*, J. Y. Lee, J. Y. Joung, S. G. Kim, and Y. K. Shin, *R&D Center, Seoul Dairy Cooperative, Ansan, South Korea.*

This study was designed to investigate the cooperative effect of selected *Lactobacillus gasseri* strains and *Cudrania tricuspidata* leaf extract (CT) in enhancing the health-promoting activities of fermented milk. Addition of CT increased total bacterial counts and proteolysis during fermentation of milk with *L. gasseri* strains. Antioxidant capacities were determined by measuring the ABTS, DPPH, and peroxyl radical scavenging activities and ferric reducing power. The antioxidant capacity of CT-supplemented milk was greater than that of milk without supplementation; moreover, the antioxidant activity of CT-supplemented milk was synergistically improved by fermentation with *L. gasseri* strains. In particular, CT-supplemented milk fermented by *L. gasseri* 505 showed the highest antioxidant activity. The phenolic compounds in CT, such as neo-chlorogenic, chlorogenic, and caffeic acid, were metabolized during fermentation with *L. gasseri* strains, and 3,4-dihydroxy-hydrocinnamic acid was produced as a fermentation metabolite. Moreover, the liberation of bioactive peptides of fermented milk was increased by the proteolytic activity of *L. gasseri* strains. In particular, six peptides, which were mainly derived from β-casein, were newly identified in this study. These findings suggest that *L. gasseri* strains metabolize the phenolic acids in the CT and the bioactive peptides released through this interaction improve the antioxidant activity of fermented milk.

Key Words: *Lactobacillus gasseri*, *Cudrania tricuspidata*, milk peptide

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0555 Influence of proteolytic *Bacillus* spp. on sour cream characteristics. D. Mehta*[1], L. Metzger[1], A. Hassan[2], and B. Nelson[2], [1]*South Dakota State University, Brookings,* [2]*Daisy Brand, Garland, TX.*

Bacillus spp. are frequently found as spoilage-causing microorganisms in milk and dairy products due to their heat resistant enzymes and spore formation. Hydrolysis of protein by *Bacillus* spp. has been reported in various milk and dairy products. However, limited information is available on the impact of such microorganisms on fermented dairy products. The objective of the current study was to evaluate the influence of proteolytic *Bacillus* spp. isolated from the dairy environment on physicochemical, rheological, and textural properties of sour cream during storage. *Bacillus subtilis* and *Bacillus licheniformis* were inoculated at 10^{3}cells/mL separately or together in the sour cream mix before fermentation, while mix without added *Bacillus* served as a control. The sour cream mix was fermented at 26°C using a commercial sour cream starter culture to a pH value of 4.6, followed by storage at 4°C for up to 30 d. The pH and bacterial count were monitored during fermentation and storage. Water holding capacity, rheological characteristics, and proteolysis were measured at 0, 15, and 30 d of storage. The *Bacillus* count increased by about one log during fermentation until pH 5.2, followed by a reduction in the count with a decrease in pH toward the end of fermentation. The sour cream containing *Bacillus* showed significantly ($P < 0.05$) higher viscoelastic moduli, hysteresis loop, viscosity, firmness, and proteolysis while water holding capacity and flow behavior index were lower than the control. In conclusion, this study shows that proteolysis caused by *Bacillus* during the fermentation of cultured dairy products can impact their rheological and textural properties.

Key Words: sour cream, *Bacillus*, proteolytic, texture

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556 Heat tolerance of *Leuconostoc mesenteroides* as influenced by prior subjection to mild heat. I. Osorio*, and K. J. Aryana, *Louisiana State University Agricultural Center, Baton Rouge.*

Leuconostoc mesenteroides is recognized for its contribution to flavor and aroma of some cultured dairy products. Among its therapeutic benefits, it has proved to be an extremely potent cytokine producer. The anti-inflammatory effects could aid in the treatment of inflammatory conditions such as irritable bowel syndrome. In the manufacture of health beneficial new dairy products, such as probiotic cheese dips, survival of this mesophile *L. mesenteroides* would depend on its ability to tolerate high processing temperatures. The hypothesis was whether prior exposure to mild heat would enhance the heat tolerance of *L. mesenteroides.* The objective was to evaluate the effect of prior exposure to various mild temperatures for various times on the growth of *L. mesenteroides*. *Leuconostoc mesenteroides* subspp. *cremoris* Vivolac Cremosa CIT/

FPC samples were subjected to mild heat of 25°C, 35°C, or 45°C for 10 or 20 min. Samples were subsequently incubated for 24 h at 30°C followed by subjecting them to 60°C for 20 min. MRS Agar was used for plating in duplicate. Plates were incubated aerobically at 30°C for 48 h. Each experiment was conducted in triplicate. Results were analyzed using analysis of variance and Tukey mean separation. Average counts observed after subjecting mild-heat treated *L. mesenteroides* to 60°C for 20 min were 7.6 Log at 25°C for 10 min, 8.7 Log at 25°C for 20 min, 7.9 Log at 35°C for 10 min, 8.3 Log at 35°C for 20 min, 7.9 Log at 45°C for 10 min, and 8.3 Log at 45°C for 20 min. No growth was obtained when culture was not subjected to prior mild heat. Exposure of *L. mesenteroides* to mild heat enhanced its tolerance to subsequent higher heat.

Key Words: mesophile, heat tolerance

0557 *Lactobacillus plantarum* ameliorates inflammation in LPS-induced RAW 264.7 cells and DSS-induced colitis animal model.

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The purpose of this study was to screen lactic acid bacteria (LAB) for anti-inflammatory activities using RAW 264.7 cells and a dextran sulfate sodium (DSS)-induced colitis animal model. Among 150 lactic acid bacteria strains isolated from healthy human feces, eight LAB strains showing excellent nitric oxide (NO) inhibitory activities were selected for further study. Peptidoglycan extracts of these strains were conducted in NO assay, western blot, and enzyme-linked immunosorbent assay (ELISA). Peptidoglycan extracts of four LAB strains significantly inhibited the production of NO related enzyme activities, such as inducible nitric oxide synthase (iNOS) and cyclooxygenase 2 (COX-2), and key cytokine levels, such as tumor necrosis factor-α (TNF-α) and interleukin 6 (IL-6), in RAW 264.7 cells. These four isolates were identified as *Lactobacillus plantarum* based on biochemical and molecular biological characterization. Additionally, the oral administration of the four LAB strains inhibited dextran sulfate sodium (DSS)-induced loss of body weight, colon shortening, and damage of colon tissue in ICR mice. Important protein level in their colon tissue, including iNOS, COX-2, TNF-α, and IL-6, were significantly reduced in the *L. plantarum* treated group. Therefore, these isolates could be used as candidate probiotic strains for the prevention and treatment of inflammatory bowel disease (IBD). We need to further investigate the mechanisms of interaction between peptidoglycans of the *L. plantarum* strain and the upstream cellular signaling mediators.

Key Words: *Lactobacillus plantarum*, anti-inflammatory, RAW 264.7 cells, dextran sulfate sodium

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0558 Composition and antioxidant activity of full-fat cheese fortified with (+)-catechin, and recovery of (+)-catechin after simulated in vitro digestion.

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(+)-Catechin, the principal catechin in green tea, was incorporated into a full-fat hard cheese at concentrations from 125 to 500 ppm to determine the extent of retention in the cheese matrix, the total cheese antioxidant activity, and recovery of catechin after in vitro digestion. Cheeses were ripened for 90 d at 8°C and digested in a gastrointestinal simulated digestion model. Measurement of pH, proximate composition, total phenolic content (TPC), and antioxidant activity after manufacture and ripening showed that the addition of (+)-catechin significantly ($P \leq 0.05$) decreased the pH of both whey and curd during cheese manufacture and ripening, but there were no significant ($P > 0.05$) differences found for moisture, protein, and fat content between the cheeses. (+)-Catechin increased TPC and antioxidant activity (measured by ferric reducing antioxidant power and oxygen radical absorbance capacity assays), although the increase was not proportional with an increasing concentration of added (+)-catechin. The retention coefficient of (+)-catechin in the curd and recovery from the mature cheese after digestion were determined by HPLC. Between 57 and 69% of (+)-catechin was retained in the cheese curd, and 19–39% (depending on the concentration) was recovered from the cheese digesta. Transmission electron micrographs showed that the ripened control cheese had a homogeneous pattern of milk fat globules with regular spacing entrapped in a homogenous structure of casein proteins, whereas the presence of (+)-catechin disrupted this homogenous structure. Evidence for interaction between (+)-catechin and cheese fat globules was provided by Fourier transform infrared spectroscopy. Association between catechin and fat globules should be taken into account when incorporating polyphenolic compounds, such as (+)-catechin, into functional cheese products to maximally retain catechin and maintain the required level of antioxidant activity without disrupting the microstructure of the cheese.

Key Words: catechin, antioxidant, digestion

0559 Prediction of fat globule particle size in homogenized milk using mid-FTIR.

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Our objectives were to develop partial least squares (PLS) prediction models using data from Fourier transform MIR (mid-FTIR) spectra to predict the particle size distributions

d(0.5) and d(0.9), surface volume mean diameter D[3,2], and volume moment mean diameter D[4,3] of milk fat globules and to validate the models. Five in-line IR homogenizers with different homogenization efficiencies were used to homogenize pasteurized modified unhomogenized milks and farm raw bulk tank milks. Homogenized milks were collected from the homogenizer outlet and then run through a mid-FTIR milk analyzer without an in-line homogenizer to collect infrared spectra of the homogenized milks for modeling. A separate portion of each homogenized milk was analyzed with a laser light scattering particle size analyzer to obtain particle size reference values. The study was replicated 3 times with 3 independent sets of modified milks and farm raw bulk tank milks. Validation of the models was done with a set of 34 milks that were not used in the model development. The PLS model factors, standard error of cross validation (SECV), and R-square for d(0.5), d(0.9), D[3,2], and D[4,3] were factors (12, 10, 12, 10), SECV (0.03, 0.12, 0.02, 0.09), and R-square (0.93, 0.88, 0.92, 0.68), respectively. The validation mean difference (MD), standard deviation of the difference (SDD), and relative standard deviation (RSD) for d(0.5), d(0.9), D[3,2], and D[4,3] were MD (−0.024, 0.019, −0.012, −0.029 μm), SDD (0.036, 0.148, 0.022, 0.110 μm), and RSD (5.47, 9.10, 4.32, 12.67%). The basis for the ability to model particle size distribution of milk fat emulsions was hypothesized to be the result of the PLS modeling detecting absorbance shifts caused by light scattering in mid-FTIR spectra of milk fat due to the Christiansen effect. The independent sample validation of particle size prediction models found that there was more variation in d(0.9) and D[4,3] predictions than the d(0.5) and D[3,2] predictions relative to laser light scattering reference values, and this may be due to variation in particle size among different pump strokes. The accuracy of the d(0.9) prediction would be fit-for-purpose for routine quality assurance to determine if the homogenizer within a mid-FTIR milk analyzer was near the failure level (i.e., d(0.9) > 1.7 μm) and needed to be replaced. This could be done as a monitoring for the daily average of the particle size performance (i.e., d(0.9)) of a homogenizer based on the mean for the day.

Key Words: particle size, homogenization, mid-FTIR

0560 Impact of mid-FTIR homogenizer performance on repeatability and predicted values for major milk components. D. M. Barbano, and L. di Marzo*, *Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

Our objective was to determine the impact of Fourier transform mid-infrared (mid-FTIR) in-line homogenizer efficiency on the repeatability and accuracy of mid-FTIR predicted fat, true protein, and anhydrous lactose determination given by traditional filter and partial least squares (PLS) prediction models. Before the experiment, the slopes and intercepts for fat, true protein, and anhydrous lactose were adjusted by running modified milk calibration samples through a mid-FTIR milk analyzer with an in-line homogenizer that produced homogenized milk with about 1.4 μm for a d(0.9). Five two-stage in-line homogenizers with different homogenization efficiencies (i.e., produced d(0.9) from 1.35 to 3 μm on unhomogenized milk) were used to homogenize unpreserved, pasteurized, externally homogenized whole milk and unhomogenized whole milk. Homogenizer selection was based on performance determined in advance using laser light scattering particle size analysis. Milk that was externally homogenized and unhomogenized milk were each tested 18 times in sequence, producing predicted values for fat B, fat A, fat PLS, true protein, true protein PLS, anhydrous lactose, and anhydrous lactose PLS. Repeatability and accuracy of fat, true protein, and anhydrous lactose determination using traditional filter models and PLS models were determined. Component predictions on externally homogenized milks (d(0.9) = about 1.0 μm) had excellent repeatability and accuracy on all components when pumped through both efficient and inefficient homogenizers. Variation in homogenizer performance on unhomogenized milks had a much larger impact on accuracy of component testing than on repeatability. The largest absolute impact was on fat measurements, producing a lower fat B test by about 0.16% at a d(0.9) of 3 μm. The fat A and fat PLS predictions were low by 0.08 and 0.07% fat, respectively, at a d(0.9) of 3 μm. Variation in homogenization had very little impact on true protein measured using the traditional filter approach but did have a larger impact on true protein predicted with a PLS model (low by 0.1% at a d(0.9) of 3 μm). Effects of variation in homogenization on anhydrous lactose predictions were small. The USDA Federal Milk Market laboratories use a d(0.9) value of 1.7 μm as a criteria to make the decision to replace the homogenizer in an IR milk analyzer. In our study, a d(0.9) of 1.8 μm produced a change in reading of < 0.04% fat and < 0.02% true protein. Both traditional filter and PLS mid-FTIR component prediction models were influenced by homogenizer performance.

Key Words: component accuracy, homogenization, mid-FTIR

0561 Lipolysis effect on milk fat and protein analysis by infrared spectroscopy using filter and Fourier transform infrared (FTIR) methods. R. M. Longo[1], L. F. Ferreira[1], F. D. A. C. Feijo[1], R. S. Conrrado[2], M. E. R. Costa[1], M. M. O. P. Cerqueira[1,2], M. O. Leite[1,2], and L. M. Fonseca[*1,2,3], *[1]Universidade Federal de Minas Gerais (School of Veterinary Medicine), Belo Horizonte, Brazil, [2]Laboratory of Milk Quality/UFMG/FUNDEP, Belo Horizonte, Brazil, [3]CNPq-Produtividade em Pesquisa, Brasilia, Brazil.*

Normal composition is an important aspect of milk quality. Infrared spectroscopy (IR) is used by most laboratories

worldwide to determine milk composition. However, the results obtained by this method may be affected if reactions, such as lipolysis, occur in milk. The objective of this work was to quantify the effect of lipolysis on milk fat and protein measurement by IR spectroscopy using filter and FTIR (Fourier transform infrared) methods. Ten liters of high quality raw milk was collected and immediately pasteurized (LTLT). This volume was aliquoted into 40-mL samples containing bronopol as a preservative. Lipolysis was induced using *Pseudomonas fluorescens* Lipase (Sigma Aldrich®; 20.000 U/g; EC number 232-619-9) added at three concentrations (100 U, 300 U, 600 U) and was followed by incubation at 7°C, 20°C, 30°C, and 40°C. Samples without enzyme addition were used as a control. Incubation periods were 0, 3, 6, 24, 48, and 96 h. IR spectroscopy methods included filter (Bentley® 2000 CombiSystem) and FTIR (CombiScope® FTIR) equipment. The experiment was a split plot design, with treatments as factorial 4 × 4 × 6 × 2 (enzyme concentrations, temperatures, incubation periods, and IR methods). ANOVA with the Duncan test (P = 0.05) were used to detect differences among treatments. There was a significant effect of milk lipolysis on milk components measured by both IR spectroscopy methods, with reduction of up 27% (2.87 g/100g to 2.08 g/100g) of fat, and increase of up to 15% (3.40g/100g to 3.92 g/100g) of protein readings for the treatments with the highest enzyme concentration and incubation at temperatures of 20°C, 30°C, and 40°C. Although component analysis in both infrared methods was affected by milk lipolysis, FTIR spectroscopy was more robust than the filter method for fat measurement ($P < 0.05$). It is concluded that lipolysis can have a significant effect on fat and protein contents measured by both IR spectroscopy methods. This is of particular concern in dairy herd improvement programs in tropical regions, where samples are usually transported and stored for long periods without refrigeration before arriving to the official laboratories. These results indicate the need for better sample management to obtain compositional results like the original samples of milk.

Key Words: lipolysis, infrared spectroscopy, milk quality, lipase

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0562 Complimentary calcium fractionation techniques to increase coproduct solids value and utilization.

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Soluble and precipitated calcium can be fractionated from other solids by utilizing complimentary techniques. Our research is focused on combinations of cross flow filtration together with mechanical separation via a sanitary hydrocyclone. We hypothesize that larger CaP particles are more abrasive for dairy equipment than the smaller particles. Hydrocyclones can remove large (> 50 µm) particles of CaP precipitate, before utilizing high temperature compatible, large MWCO ultrafiltration and microfiltration elements to purify and concentrate the smaller sized CaP precipitate from acid whey coproducts. Deproteinized acid whey (UF permeate) was subjected to nanofiltration (NF) to reduce the volume and impurities (lactic acid, simple sugars, and monovalent ions), which increased the calcium and phosphate concentrations. Optimal conditions for the precipitation of calcium phosphate by a combined heating/neutralization step were established as temperature 60–70°C and pH 7.0. CaP precipitates were fractionated on the basis of particle size using a sanitary hydrocyclone. We studied the impact of hydrodynamic conditions (vessel shape, agitation) on CaP precipitate size range and separation efficiency of hydrocyclone. It was observed that when neutralization/heating was done in vessels with less turbulence, the CaP particle size was bigger, which increased the hydrocyclone separation efficiency. Another significant finding was that hydrocyclone overflows from both low turbulence and high turbulence tanks have very similar particle size profiles. Apex nozzle size of the hydrocyclone did not impact separation efficiency. The small CaP particles classified into the hydrocyclone overflow were purified and concentrated using various wide pore membrane sizes of high-temperature-compatible UF and MF elements (Microdyn DS-UV200-3838 (200 kDa), DS-MP005-3838 (0.050 µm), and DSMP020-3838(0.20 µm)) membranes. It was found that the separation efficiency of CaP by either UF or MF was much better than centrifugation, as the total Ca contents in the centrifugal supernatant and MF permeate were 47.9 and 16.7 mg/100 g, respectively. Milk mineral concentrate with a small, and relatively narrow, particle size range and high CaP purity was obtained using this process (composition: 76.7% ash, 30.2% calcium, and 16.1% phosphorus (solids basis)). Study of the abrasiveness of CaP precipitate in relation to its particle size is currently in progress.

Key Words: coproducts, hydrocyclone, milk minerals, acid whey

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0563 Impact of controlling the lactose to casein ratio of concentrated milks on the properties of cheddar cheese.

R. A. Ibáñez[*1], S. Govindasamy Lucey[2], J. J. Jaeggi[2], M. E. Johnson[2], and J. A. Lucey[2], *[1]University of Wisconsin-Madison, Madison, [2]Wisconsin Center for Dairy Research, Madison.*

Final pH value in cheese is determined by the amount of lactic acid in the curd as well as its buffering properties, which are determined by the concentration of casein and residual insoluble calcium phosphate. The use of concentrated milks requires the adjustment of cheesemaking parameters to achieve similar cheese composition and pH values compared with unconcentrated milks. We believe that the final pH value of cheese made from concentrated milk could be better controlled by maintaining a constant lactose-to-casein (L:CN) ratio in the milk. The objective of this study was to investigate

the effect of three casein concentrations (2.3, 2.9, and 3.2%) in milks that were standardized to a constant L:CN ratio of 1.3, on the composition, texture, functionality, and sensory properties of milled-curd cheddar cheese through 9 mo of ripening. Whole milk was concentrated by ultrafiltration, and the composition was standardized by combining retentate, permeate, and/or water to obtain appropriate CN levels while maintaining a constant L:CN ratio. Preliminary work demonstrated that increasing the CN content of milk resulted in cheeses with lower moisture content ($P < 0.05$). To keep the moisture contents similar between all CN levels, modifications to cheese manufacturing procedure (such as increasing curd particle size, depth of the milled-curd, and the salting regimen) were necessary for the milks containing higher CN levels. Cheese functionality during ripening was assessed using texture profile analysis and dynamic low-amplitude oscillatory rheology. Sensory Spectrum® and quantitative descriptive analysis were conducted with 9 trained panelists to evaluate texture and flavor attributes using a 15-point scale. Increasing the CN content of milks resulted in cheeses with lower pH, higher buffering capacity, and higher residual lactose and lactic acid concentrations ($P < 0.05$). Hardness obtained from texture profile analysis showed no differences between treatments; however, treatments made from milks with higher CN contents exhibited lower maximum loss tangent (meltability). Sensory results indicated that acidity was higher in cheeses made with increased CN ($P < 0.05$). This study suggested that to maintain similar pH values in cheeses made from concentrated milks, the L:CN ratio would need to be varied. Adjustment of the L:CN ratio of milk is a promising technique to improve the control of the final pH in cheeses made from concentrated milks.

Key Words: higher casein milk, lactose, cheddar cheese functionality

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0564 Enhanced dairy membrane operations through control of deposit formation on membrane surfaces. U. Kulozik*, *Technical University of Munich, Freising-Weihenstephan, Germany.*

The objective is to present recent developments and insights on novel ways to operate dairy membrane operations at higher levels of efficiency and predictability. Boundary layer phenomena at the surfaces of membranes, in particular, adsorption, retention, and deposit formation are still not fully understood. Hence, adverse effects reducing flux and unpredictable permeation of components cannot reliably be prevented. Deposits reduce flux and in many cases dominate the system's retention characteristics. Deposit formation is dependent on the position along the membrane surface, which is a result of the pressure drop in crossflow situations. These aspects will be discussed with particular regard to whey concentration and milk protein fractionation by means of microfiltration as possibly the most challenging example. The related phenomena were investigated experimentally and theoretically in terms of assessing deposit properties (casein micelle multi-layers, in this case), such as thickness and porosity, as a function of position along the membrane. For this purpose, special membrane prototypes were constructed enabling the measurement of flux and convective transport of material through the membrane pores in four sections along a tubular, industrially sized ceramic membrane. Similarly, the effect of membrane length has been studied for spiral wound modules (SWM), which are the dominating membrane type in dairy installations. Deposit amounts and structures were assessed by means of chemical analysis and synchrotron-based X-ray analysis, using the novel GISAXS technique (grazing incidence small angle X-ray scattering). This way, casein micelle deformation was found to occur as a result of elongational flow of the filtrate stream toward the membrane surface. Further, a method for improved whey ultrafiltration performance as a result of a pre-microfiltration step is presented. The removal of protein aggregates in whey increases flux levels considerably, and a reduction of the microbial load is achieved. Novel cascade-like combinations of UF and RO/NF are discussed as a means to achieve high levels of concentration for whey and, for comparison, milk. The UF step removes the protein, such that the RO step has only to cope with osmotic pressure and remains unaffected by deposit formation. Thus, higher concentration levels and an increased flux can be achieved as well as concentration in shorter times at reduced energy levels. UF was assessed in the form of various processing concepts, namely conventional polymeric spiral-wound and ceramic crossflow systems as well as dynamic rotating ceramic membranes, which are able to produce and to cope with high protein concentration levels.

Key Words: membrane technology, microfiltration, milk protein fractionation, milk protein concentration

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0565 Constant permeate flux microfiltration of liquid whey protein concentrate for the separation of whey proteins from fat. S. L. Beckman*[1], and L. Metzger[2], [1]*Midwest Dairy Foods Research Center, South Dakota State University, Brookings,* [2]*South Dakota State University, Brookings.*

Value added whey protein concentrates (WPC) are often processed by membrane filtration to fractionate valuable components. One such application is microfiltration (MF) applied to cheese whey to separate proteins from fats before the protein-rich fraction can be further concentrated into products containing > 80% (wt/wt) total nitrogen on a dry basis. The objective of this research was to evaluate protein recovery into permeate during MF of reconstituted WPC 50% protein on a dry basis by using constant permeate flux (CF) operation compared to conventional constant pressure (CP) operation. Typically, MF is started and operated at low (e.g., 27 to 138 kPa) and constant pressures (baseline and differential), which

could affect the long term fouling and throughput of the filter. An alternative is to maintain a constant permeate flux by modulating applied pressure during MF to modify the initial fouling, hopefully increasing protein permeation and recovery. Approximately 400 kg of liquid WPC 50% (10% solids) was made by mixing whey permeate, pure water, and liquid WPC 80%. A 200-kg aliquot was MF (0.5 µm, 6.0× mass concentration factor, 150% water diafiltration [wt/wt on a feed mass basis], 60°F) using either CP or CF operation. This was replicated three times, using different lots of WPC 50% for each replicate. During CF MF, flux (L/m^2 per h) was initially controlled by adjusting a permeate outlet valve to achieve the desired flow. As product in the recirculation loop became concentrated, flux was maintained by opening the permeate valve and then increasing the differential pressure and, thus, the inlet pressure. Pressures during CP MF were maintained at 27.6 kPa baseline and 82.7 kPa differential, giving an inlet of 110.3 kPa. Inlet pressure during CF MF increased to 172.4 kPa when the solids in the recirculation loop increased, whereas baseline pressure remained steady at 27.6 kPa. Protein (total nitrogen) recovery from feed into permeate was 63.2 ± 1.1 and 71.8 ± 4.4% for CP and CF MF, respectively. Average permeate flux during MF was 19.4 ± 3.7 and 17.4 ± 3.2 L/m^2 per h, for CP and CF MF, respectively. These results indicate that CF operation during whey MF can increase the amount of protein recovered without greatly affecting the throughput of the filtration. This research could help whey processors improve the efficiency and value of their products by implementing relatively minor changes to their processes.

Key Words: whey, microfiltration, constant permeate flux

0566 Critical factors for evaluation of cheese yield performance and fat loss in large cheese factories.

D. M. Barbano, and B. Margolies*, *Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

Our objectives were to develop a data analysis system that utilized existing data within a cheese factory to evaluate cheese yield performance and fat loss using yield formulae for cheddar and mozzarella cheese manufacturers, to determine the accuracy of input data, and determine the sensitivity of the performance evaluation results to uncertainty in the accuracy of input data. Daily cheese manufacturing and analysis data on an individual vat basis were collected (for 1 yr) from cheddar and mozzarella cheese factories that each processed about 900,000 kg of milk per day. The source and quality of all input data was identified and evaluated during repeated site visits. Observed outcomes (based on data collected in the cheese plants) for cheese yield and fat recovery were found to be very sensitive to the quality of input data for milk weight, milk fat and protein in the vat, and the moisture, fat, and salt content of the cheese. Different types and the placement of flow meters were evaluated. Milk analysis was done by mid-FTIR and cheese analysis was done with near-IR in both factories. Proficiency evaluations of the accuracy of milk and cheese analysis were conducted in comparison to physical and chemical reference methods. Observed bias differences in analytical results were used to establish ranges for sensitivity analyses. Cheese moisture and fat sensitivity analysis ranges were +0.5% and salt was +0.25% daily based on proficiency test results. This variation in moisture, fat, and salt uncertainty produced a deviation of (+)450 kg cheese/day and 225 kg cheese/day for salt. It was clear that as cheese factories have increased greatly in weight of cheese produced per day, the uncertainty in sampling and analytical accuracy of milk and cheese analysis that was adequate previously has a level of uncertainty that allows a large margin for error in controlling the financial performance of the business. A bias error in moisture with the factory laboratory being high by 0.5% moisture on cheddar was equated to a missed opportunity in 1 yr of 175,000 kg more cheese. It was concluded that given the impact on economic performance of the factory, better cheese sampling approaches and cheese analytical systems are needed to optimize and control the financial performance of the cheese manufacturing process.

Key Words: cheese yield, fat loss, cheese analysis

0567 Kinetics studies of chemical reactions in conjugated linoleic acid (CLA) enriched milk treated with high-pressure sterilization.

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Conjugated linoleic acid (CLA), a bioactive lipid naturally found in milk, is degraded through oxidation during thermal processing. Application of pressure-assisted thermal processing (PATP) reduces the thermal exposure during processing, protecting a variety of bioactive compounds. This study evaluated the impact of PATP on the CLA content at conditions where commercial sterilization has been achieved. In addition, the effect of PATP on some quality indicators was evaluated, including lactulose formation, inactivation of alkaline phosphatase, and retention of CLA during storage. At 600 MPa and 120°C for 15 min, ~78% of the CLA was retained while only ~20% was retained at 0.1 MPa and 120°C. The Weibull model was used to predict the retention kinetics of CLA. Temperature and pressure accelerated the formation of lactulose, with a maximum value of 650 mg L^{-1} at 120°C, 600 MPa, and 15 min. The PATP conditions needed to reduce 7-log of *B. amyloliquefaciens* endospores in inoculated milk were determined as well as the effect of adding nisin (4–64 mg L^{-1} milk). A reduction of 7-log was obtained after 5 min at 600 MPa and 120°C in milk with nisin added. Milk treated at 600 MPa and 120°C for 5 min was selected to evaluate the impact of PATP on the CLA retention and formation of hydroperoxides during storage. Milk with nisin added and

treated with PATP delivered higher CLA retention and a lower hydroperoxide concentration compared with the UHT equivalent process. The kinetic information obtained was used to build pressure-temperature diagrams for CLA retention and lactulose formation. The outcomes of this study are considered a step further for the development of shelf-stable milk processed by PATP.

Key Words: conjugated linoleic acid, kinetics, modeling,

0568 Impact of shear, heat and pH on the conformation, digestibility and antigenicity of lactoglobulin.
M. T. Rahaman, L. Ramchandran, and T. Vasiljevic*, *Victoria University, Melbourne, Australia.*

Processing-induced conformational changes can modulate the digestibility of food allergens and their antigenicity. Effects of pH (3, 5, 7), temperature (80, 100, 120°C), and shear (100, 500, and 1000 s^{-1}) on conformational changes (monitored by surface hydrophobicity, total thiol content, FTIR, and gel electrophoresis) and their relation to antigenicity (determined by indirect enzyme-linked immunosorbent assay) of β-lactoglobulin (β-lg) were investigated. Overall, heating at low pH (3) caused the unfolding of proteins and fragmentation by partial acid hydrolysis and thereby exposed β strands that contributed to the appearance of some hidden epitopes resulting in higher antigenicity. Heating at pH 5 and 7 decreased allergenic response due to covalently bonded molecular polymerization and aggregation, which destroyed and/or masked some epitopes. Shear alone had no effect on the antigenic response of β-lg but could have an influence in combination with pH and/or temperature. Overall, heating β-lg solutions to 120°C at pH 5 with shearing (100–1000 s^{-1}) resulted in minimal antigenicity. Structural modifications of β-lg via denaturation or SS/SH-mediated interactions can either enhance or decrease its antigenicity. Based on these results, effects of different pH (3, 5, or 7), temperature (room temperature or 120°C), and shear (0 s^{-1} or 1000 s^{-1}) on the gastrointestinal digestibility of β-lg and post digestion antigenic characteristics were further studied. Regardless of pH, unheated β-lg showed resistance to peptic digestion with high antigenic value while it was fairly susceptible to pancreatin with moderate reduction in antigenicity. Heating at 120°C significantly improved both peptic and pancreatic digestion attributed to structural alterations and resulted in much lower antigenicity; the level of reduction was pH dependent and the lowest antigenicity was recorded at pH 5. High shear (1000 s^{-1}) slightly reduced digestibility and, thereby, enhanced antigenicity of unheated β-lg at pH 5 and 7 but reduced at 120°C irrespective of the pH. Thus, treatment at pH 5, 120°C, and 1000 s^{-1} could potentially reduce post digestion antigenicity of β-lg.

Key Words: processing, shear, heat, pH, β-lactoglobulin, digestibility, antigenicity

DAIRY FOODS DIVISION SYMPOSIUM: ADVANCES IN SUSTAINABILITY WITHIN THE DAIRY PROCESSING INDUSTRY

0569 New packaging and strategies to enhance your sustainability plan.
E. Comere*, *Tetra Pak Inc., Denton, TX.*

Tetra Pak is the world's leading food processing and packaging solutions company. Working closely with our customers and suppliers, we provide safe, innovative, and environmentally sound products that each day meet the needs of hundreds of millions of people in more than 170 countries around the world. With more than 23,000 employees based in over 80 countries, we believe in responsible industry leadership and a sustainable approach to business. Technical development in the packaging industry is intense today, and everyone is trying to crack the code of sustainable packaging introducing new base materials (e.g., renewable, plant based, biodegradable, etc.), processes, and strategies. Driving innovations that address environmental impacts and designing products with the environment in mind will deliver a new competitive edge that can't be ignored. We have already seen multiple innovations in packaging over the last few years. After light weighting and recycling, the next stage of evolution and innovation is around raw material selection, with companies acknowledging our natural resource challenges and rethinking what their packaging is made of. At the same time, new packages have to meet stakeholder demands and offer good convenience while winning environmental arguments in an increasingly competitive business environment and circular economy context. It also highlights how predominant the role of packaging is in the food and drink supply chains (beyond ensuring food contents are delivered safely to consumers, it helps reduce food waste). This session will focus on packaging trends and new sustainable material options, sustainable sourcing, i.e., expanding focus from the end of life of the package (reuse/recycling) to the beginning of a package's life cycle and increasing use of renewable materials responsibly sourced, and understanding the nature of consumer knowledge (including gaps) surrounding sustainable packaging practices

Key Words: sustainable, environment, renewable

0570 Life cycle environmental assessment of yogurt production and consumption in the USA.
Y. Wang*[1], G. Thoma[2], D. Kim[2], and J. Burek[2], *[1]Innovation Center for U.S. Dairy, Rosemont, IL, [2]University of Arkansas, Fayetteville.*

The innovation Center for U.S. Dairy commissioned and jointly conducted a life cycle assessment (LCA) of the yogurt supply chain focused on defining potential environmental

impacts with the University of Arkansas. The system boundaries for this study include milk production, yogurt processing, filling and packaging, retail, and finally consumption of the yogurt including disposal of the packaging material. Estimated impacts in various unit processes (milk production, processing, packaging, transport, retail, and consumption) including product losses at each stage are reported and discussed. The functional unit is 1 kg of yogurt products consumed by U.S. consumer as sold at retail, for the year 2013. LCA data were analyzed using stochastic methods (Monte Carlo simulation) to quantify and characterize uncertainty. The impact categories used in the evaluation include climate change, photochemical oxidant formation, cumulative energy demand, freshwater eutrophication, freshwater depletion, water eutrophication, human toxicity, and marine eutrophication, ecosystems, and ecotoxicity. Here, the environmental profile is defined as the comprehensive set of inventory and impact assessment results. The report also provides interpretation and evaluation of the results to help identify the potential risks and opportunities in the yogurt production value chain. The overall cradle-to-grave GHG emissions for set, stirred, and nontraditional Greek yogurt as sold at retail were found to be 6.03, 4.98, and 7.65 kg CO_2e per kg of yogurt consumed, respectively. Using a simulated traditional Greek yogurt plant for production LCI, the cradle-to-grave greenhouse gas emissions were estimated to be 8.92 kg CO_2e per kilogram consumed. In the cradle-to-grave assessment, production of milk is the dominant contributor to most environmental impacts, and thus ongoing industry efforts to improve milk production will lead to improvements in the yogurt manufacturing sector as well. In the farm-gate-to-retail-gate analysis, yogurt transport was the single largest GHG emission contributor followed by ingredients, electricity, and packaging materials. The results suggest that careful optimization of the transport distances and the selection of transport refrigeration system using low-GWP refrigerants could reduce environmental impacts.

Key Words: yogurt, LCA, environmental impact

0571 Using big data to drive sustainable CIP. J. Curran*, *Ecolab, St. Paul, MN.*

The promise of big data as a means to drive process consistency and conformity is alluring to many industries; however, the execution often falls short of the desired outcome due to a lack of analytical resources or an inability to capture the key metrics that help drive decisions. In food and beverage processing, much of this data is already captured using existing plant instrumentation. Further, the trend has been toward recording this information electronically to allow for more data points and faster analysis; however, this data is rarely used to its fullest potential. It is stored as required, and reviewed as necessary. In the development of a new platform, Ecolab has created a method of transforming this data into actionable information, allowing customers to utilize their own data around Clean in Place, coupled with new devices to more accurately measure chemical concentration. This data is captured and utilized in process-specific algorithms to drive sustainability, profitability, and product quality. The result has been a dramatic reduction in water, energy, chemistry, and time consumed for CIP, while at the same time achieving a quantifiable increase in product quality. This is often achieved simply due to the increased process visibility, enhanced analysis, and the increased consistency and conformity that results from the analytical process and does not require large capital investment. Using big data in food and beverage processing facilities to drive sustainability has proven itself as a concept. It does, however, require process understanding and a focus on the drivers within each facility to ensure that change is made in a way that positively impacts both sustainability and product quality, food safety, and brand protection.

Key Words: CIP, analytics, sustainability

0572 Processing sustainability: ideas to create a comprehensive effort. D. Skidmore*, *Hilmar Cheese Company, Inc., Hilmar, CA.*

Hilmar Cheese Company, Inc. was recognized with the 2015 Outstanding Dairy Processing & Manufacturing Sustainability award by the U.S. Dairy Sustainability Awards. The company's Headquarters & Innovation Center was designated LEED Platinum® (Leadership in Energy and Environmental Design) in 2014. The company has produced an annual commitment to sustainability report since 2010 documenting progress and improvements and sharing this information with customers and consumers. The publicized report follows the Stewardship and Sustainability Guide for U.S. dairy, a voluntary framework for tracking and communicating progress. It also incorporates some of the methodologies outlined in the Global Reporting Initiative. The company tracks and improves in four key areas: environment, employees, economic value, and community engagement. The conference presentation will highlight activities in each key area, including water recycling and reuse, solid waste reduction, employee engagement, and community education.

Key Words: corporate responsibility, environmental stewardship, economic value, social responsibility, water reclamation

DAIRY FOODS DIVISION SYMPOSIUM: INCREASING UTILIZATION OF DAIRY CO-PRODUCTS

0573 Consumer demand, innovation, and opportunity for co-products. B. Graves*, and R. Kapoor, *Dairy Management Inc., Rosemont, IL.*

Due to their superior nutritional quality, dairy ingredients and co-products can play a key role to meet the unmet consumer demand for production of healthy, convenient, and great tasting dairy and dairy-based products that fit the way people live today. The successful introduction of new dairy products, such as Greek yogurt, as well as the increasing production of milk and whey protein concentrates has driven the creation of new co-products like Greek yogurt whey, milk and whey permeates, delactosed-whey, and milk minerals. These co-products need to have value-added utilization to increase the value of farmer's milk, improve sustainable nutrition, and decrease the carbon footprint of dairy products. There are opportunities to develop novel technologies to enhance the utilization co-products to advance our Nation's ability to produce dairy ingredients that cannot only be used in applications such as food aid, nutritional beverages, meal replacers, infant formula, and medical foods but also help food companies fulfill the current consumer trends related to high protein, clean label, and health and wellbeing.

Key Words: whey, permeate, co-products

0574 Permeate use as a sodium replacer/flavor implications. M. Drake*, *Southeast Dairy Foods Research Center, North Carolina State University, Raleigh.*

Whey and milk permeates are co-products of high-protein powder manufacture. Permeates are comprised of minerals, lactose, and organic acids. Permeates contain sodium, but potassium and organic acids contribute salty taste enhancement. As such, permeates provide value added opportunities for solids as well as sodium replacement in many foods. Sensory and chemical properties of permeates from different whey and milk sources and ingredient applications will be addressed.

Key Words: permeate, sodium reduction, dairy foods

0575 Fractionating acid whey into value-added ingredients. K. E. Smith*, *University of Wisconsin-Madison, Madison.*

There has been a huge expansion in acid whey production due to the rapid growth in Greek yogurt manufacture. Acid whey is difficult to process for many reasons, and whey from Greek yogurt manufacture is no exception. Traditionally, recovery of the whey protein has provided an economic incentive to process whey; however, Greek yogurt whey is especially low in protein as compared to other sources of acid whey, and therefore, it is more difficult to justify the expense of converting the whey into dairy ingredients as opposed to disposal. The objective of our research is to find economical methods to recover/convert the nonprotein components in Greek yogurt acid whey into value added ingredients. Membrane filtration has been used for many decades in the dairy industry to fractionate components. Our focus is on reducing the calcium content of the UF permeate from Greek yogurt acid whey through the use of novel nanofiltration membranes. Calcium can interfere with the production of ingredients, such as crystalline lactose and hydrolyzed lactose syrups. Excessive calcium incorporation into the lactose crystal results in crystalline lactose that does not meet specifications for U.S. food grade lactose, and hydrolyzed lactose syrups with high mineral contents may taste salty. Nanofiltration membranes traditionally are able to permeate monovalent ions like chloride, while retaining divalent ions such as calcium. The membranes evaluated in our study had been modified such that calcium could also permeate. Our results indicated lactose and calcium permeated the novel NF membranes to differing degrees as compared to the control NF membrane that did not permeate either component. Varying temperature, pressure, and concentration of the starting permeate during NF resulted in changes in the relative permeation of lactose and calcium. Using a modified NF membrane, we were able to concentrate permeate from Greek yogurt acid whey to approximately 25% total solids. A lactase enzyme with an acidic pH optimum was then added to produce a dairy syrup with enhanced sweetness and a reduced salty flavor as compared to a control made with a traditional NF membrane. The ability to economically remove calcium from the UF permeate should enable processors to recover value from the permeate of products like Greek yogurt acid whey.

Key Words: acid whey, membrane processing, nanofiltration

0576 Demineralization of delactosed permeate and acid whey. J. K. Amamcharla*, *Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan.*

The dairy industry is continuously working on novel technologies for producing value added products or ingredients with superior functional and nutritional qualities. Consequently, a coproduct that is relatively low in value is also being produced. It is equally important to look for new ways to increase the market for these coproducts. For example, delactosed permeate (DLP), a coproduct, is obtained after recovering milk proteins and most of the lactose from milk or whey permeate. Milk proteins are removed by using ultrafiltration processes, and lactose is separated by crystallization processes. DLP does not have a standard of identity or a defined composition. The

high moisture content (60 to 75%) and presence of organic acids poses a challenge to use it as a food ingredient without further processing. Researchers have studied the thermodynamics of moisture migration in DLP. Greek yogurt whey is compositionally different from cheese whey and, thus, poses economic and environmental challenges to the dairy industry. Greek style yogurt in the United States is one of the largest growing sectors in the dairy industry. Greek yogurt is produced by removing a part of water and water-soluble components from yogurt. Consequently, a large quantity of Greek yogurt whey (GYW) is being produced as a co-product. The objective of the present work was to present a review of newer knowledge on the manufacture and utilization of dairy co-products. It includes evaluations of the use of magnetic fluid treatment (MFT) and addition of clay minerals as alternative methods for separating valuable DLP and GYW components.

Key Words: demineralization, delactosed permeate, Greek yogurt whey

0577 Advancements in drying lactose and acid whey.
J. G. Ronckers*, *Relco, Willmar, MN.*

Aspects involved in the drying of whey and its lactose containing co-products will be highlighted, including lactose crystallization and its influences on lactose crystallization rates and drying efficiency. Glass transition, thermo plasticity, and the sticky line will be defined and discussed in relation to post crystallization in the dryer. Challenges with the Maillard reactions (nonenzymatic browning) and caking of the powder will be discussed. Drying of crystallized lactose, for instance, and the application of the "CrystaLac," a lactose crystallizing evaporator that helps increase yields, will be discussed. Methods of crystal separation and refining will be covered. Details will be shared about how lactose drying is conducted in 2 stages, using a primary attrition dryer with built in powder moisture and size classifier and a secondary stage for after drying and cooling with a fluid bed. Drying of permeate and sweet whey will be covered, including the "HiCon," a high concentration evaporator, the "CCC" Cooling, Concentration, and Crystallizing unit, and the dryer. The influences of lactose crystal sizes on drying efficiency will be covered. Finally, challenges of drying acid whey will be discussed. We will also discuss the crystallization of lactose and sticky components in acid whey and the challenges that we face when drying acid whey. The history of drying acid whey will be summarized. Future possible solutions will be proposed, such as increased crystallization by higher solids, small crystal sizes, membranes to filter out sticky components, humidity control of dryer exhaust air to prevent sticky powder, and the use of a desiccator for decreasing and controlling drying air humidity to be able to dry at lower temperatures.

Key Words: lactose, whey, crystallization, drying, co-products

0578 Lactose derivatives and GOS as prebiotic fibers.
T. C. Schoenfuss*, *University of Minnesota, Department of Food Science and Nutrition, St. Paul.*

Lactose is a disaccharide in dairy ingredients and co-products that can be polymerized by both chemical and enzymatic reactions into soluble dietary fiber. Products of each of these manufacturing processes can also be prebiotics if they have demonstrated benefits such as the positive modulation of gut microbiota and improvements in other indicators of digestive health. The enzymatic reaction involves incubating the enzyme β-galactosidase with lactose under specific concentration and temperature conditions to favor the polymerization reaction over hydrolysis. The polymerized product of this reaction is called galactooligosaccharides (GOS). The source of the β-galactosidase enzyme greatly affects the temperature requirements for polymerization, the products of the reaction (the amounts of branching and degree of polymerization), and temperature stability of the enzyme. Polymerization of lactose can also be achieved through reacting acid with lactose during heating. This can be achieved under vacuum or pressure during heating either in batch or continuous processes. The degree of polymerization and branching can vary greatly depending on the reaction conditions. The products of this reaction are called polylactose. This seminar will provide an overview of the production of both types of products and an evaluation of these fibers for prebiotic activity.

Key Words: fiber, polymerization, GOS

EXTENSION EDUCATION

0579 S survey of serum trace mineral concentrations in weaned Montana ram lambs.
C. M. Page*[1], M. Van Emon[1], S. Spear[1], T. W. Murphy[2], J. G. P. Bowman[1], and W. C. Stewart[1], *[1]Montana State University, Bozeman, [2]University of Wisconsin-Madison, Department of Animal Sciences, Madison.*

Clinical and subclinical trace mineral deficiencies can limit productivity in western sheep production systems. The objective of the study was to quantify trace mineral status among Montana ram lambs post weaning. Based on prior research investigating forage trace mineral concentrations and trace mineral status in cattle, we hypothesized that clinical and subclinical deficiencies would be most prominent with Zn and Se. To test this hypothesis, serum samples (n = 201) were collected from ram lambs 8 to 10 mo of age (BW 52.8 ± 16 kg) at 21 locations throughout Montana and analyzed for Co, Cu, Fe, Mn, Mo, Se, and Zn. The average concentration and range for each trace mineral analyzed in the serum samples were Co (1.00 ± 0.079 ng/mL, 0.09–6.22 ng/mL), Cu (0.84 ± 0.016 µg/mL, 0.3–1.61 µg/mL), Fe (154.85 ± 3.682 µg/dL, 26–350 µg/

dL), Mn (2.56 ± 0.225 ng/mL, 0.7–31.3 ng/mL), Mo (40.14 ± 5.001 ng/mL, 2.8–456.5 ng/mL), Se (111.42 ± 3.31 ng/mL, 16–197 ng/mL), and Zn (0.73 ± 0.015 µg/mL, 0.3–1.74 µg/mL). The two most deficient and marginally deficient minerals across Montana were Se (19% of ranches deficient and 24% of ranches marginally deficient) and Zn (14% of ranches deficient and 52% of ranches marginally deficient). All Se deficient samples were obtained from western Montana. There was considerable variation in serum trace mineral concentrations within individual flocks. Descriptive statistics were analyzed using SAS. Given that Se and Zn play major roles in growth, fertility, and immunity, results suggest opportunities for more effective supplementation strategies. Producers and nutritionists alike can use these results to identify mineral deficient areas and develop cost effective mineral supplementation management practices.

Key Words: trace minerals, zinc, selenium, Montana, sheep, ram lambs

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0580 Breakfast on the farm event is an effective learning activity and improves consumer perceptions of dairy production.

J. M. Smith[*1], and T. A. Ferris[2], *[1]University of Vermont, Burlington, [2]Michigan State University, East Lansing.*

Educational farm tours, such as Breakfast on the Farm, provide the public an opportunity to learn firsthand, ask questions of farmers and other professionals, and give feedback about modern food production. Vermont held its first Breakfast on the Farm event on a dairy farm in August 2015. Patterned after the Breakfast on the Farm events in Michigan, the event was designed to educate consumers on key areas of concern: animal care, environmental protection, and food safety. Educational stations, coordinated by UVM Extension, were placed along a walking tour of the farm facilities allowing visitors to see cow and calf housing, milking facilities, and how feed is produced and fed. An exit survey instrument consisting of pre-post questions evaluated what participants learned and their change in perceptions of several agricultural practices. Of 550 visitors, 227 who were at least 18 yr old completed the questionnaire. Almost half of respondents had visited a working dairy farm fewer than 3 times before this event. On a 5-point scale from very little to very much, respondents indicated how much was learned about how cows are housed (4.08), what cows eat (3.91), how cows receive health care (3.38), how antibiotics are kept out of the food supply (2.87), how technology is used in dairy production (4.33), how farmers protect water quality (3.34), how calves are cared for (3.76), and how crops are grown and stored (3.60). First-time visitors gained the greatest knowledge about how technology is being used and how cows are being housed. On a 5-point scale where 1 is strongly disagree and 5 is strongly agree, first-time visitors had an average score increase of 0.56 between their before and after tour ratings of their agreement with statements that dairy farmers are treating animals humanely, protecting water quality, using pesticides responsibly, and using antibiotics responsibly. The greatest change in beliefs was about dairy farmers treating animals humanely with a mean increase of 0.74 and 0.51, respectively, among first-time visitors and all respondents. The percentage of first-time visitors agreeing or strongly agreeing that farmers treat animals humanely increased from 61% to 91% after touring the farm. Before and after differences were significant at $P < 0.005$ (paired t test) for all questions. This event improved consumer knowledge and impressions about modern dairy farms and management practices.

Key Words: educational farm tour, consumer perception, modern dairy production

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0581 Breakfast on the farm, an educational farm tour, improves consumer trust in animal care, food safety, and modern conventional dairy production.

T. A. Ferris[*1], J. M. Smith[2], E. M. Richer[3], M. Welker[3], J. Stechschulte[3], M. A. Dunckel[4], and A. E. Kuschel[5], *[1]Michigan State University, East Lansing, [2]University of Vermont, Burlington, [3]Ohio State University Extension, Wauseon, [4]Michigan State University Extension, Alpena, [5]Michigan State University Extension, Clinton Twp.*

In 2015, five Breakfast on the Farm (BOTF) educational dairy tours were held in Michigan (MI) with 12,068 participants, one in Ohio (OH) with 3009 participants, and one in Vermont (VT) with 550 participants. Exit surveys were collected from 1406, 578, and 220 participants from MI, OH, and VT, respectively, to determine the impact of educational farm tours on consumer trust in animal care, food safety, and modern food production. Thirty-seven, 60, and 25% of participants from MI, OH, and VT, respectively, had not visited a working dairy farm in the past 20 yr (first-time visitors). Upon exiting the tour, participants were asked about their level of trust on topics "before" and "after" the tour on a 5-point scale from 1 being very low to 5 being very high trust. The mean (± SD) for before, after, and change (after–before) for first-time visitors' level of trust in modern food production were, respectively, 3.60 (± 1.14), 4.50 (± 0.75), and 0.90 (± 0.94) for MI; 3.68 (± 1.13), 4.44 (± 0.89), and 0.76 (± 0.86) for OH; and 3.96 (± 1.02), 4.59 (± 0.80), and 0.63 (± 0.89) for VT. First-time visitors' level of trust that dairy farmers will do the right thing in caring for food-producing animals for before, after, and change, respectively, were 3.94 (± 1.07), 4.69 (± 0.59), and 0.75 (± 0.93) for MI; 4.00 (± 1.04), 4.64 (± 0.68), and 0.64 (± 0.89) for OH; and 3.88 (± 1.03), 4.57 (± 0.73), and 0.69 (± 0.88) for VT. First-time visitors' level of trust that dairy farmers will do the right thing to safe-guard milk for before, after, and change, respectively, were 4.02 (± 1.03), 4.75 (± 0.53), and 0.73 (± 0.95) for MI; 4.11 (± 1.01), 4.71 (± 0.58), and 0.60 (± 0.91) for OH; and 4.24 (± 0.82), 4.73 (± 0.53), and 0.49 (± 0.64) for VT. All mean increases (after–before)

were significant at $P < 0.005$ using a paired-*t* test. Forty-five, 44, and 41% of MI, OH, and VT participants, respectively, rated farmers' efforts to prevent milk from cows treated with antibiotics from being sold to the consumer as a major factor for increasing their trust, and 42, 44, and 65% of MI, OH, and VT participants, respectively, rated their comfort with how animals are housed and managed as a major factor. Exit surveys show educational farm tours increase the level of trust consumers have for animal care and housing, food safety, and modern dairy farms.

Key Words: educational farm tours, consumer trust, modern food production

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0582 Creation, delivery, and assessment of the livestock education and certification for agricultural law enforcement extension program. C. Wickens*[1], M. J. Hersom[2], R. G. Easterly III[1], E. Jennings[1], B. Myers[1], J. Shuffitt[1], B. Stice[1], and J. Weir[1], [1]*University of Florida, Gainesville,* [2]*Department of Animal Sciences, University of Florida, Gainesville.*

Many law enforcement and government agencies have dedicated law enforcement officers (LEOs) who respond to agricultural crime, agricultural inspection, urban/rural interface issues, and potential livestock neglect cases. These LEOs are potential Extension clients with educational needs. We partnered with Farm Bureau and Florida Department of Agriculture and Consumer Services to develop and implement a training and certification program for Florida LEOs in the field of animal science. The accompanying certification program adds credibility to this clientele group when they present testimony in court and make difficult decisions in cases. Using backward design methodology, a curriculum relevant to the needs of LEOs was developed and delivered by subject matter experts. A pilot program was delivered to a group of veteran LEOs in July 2014. Survey and focus group data obtained from pilot participants were used to modify program content. Three classes were offered to 52 individuals in March and December 2015 and in March 2016. Instruction used a combination of classroom and experiential learning sessions utilizing applicable equipment and live animals. Daily homework assignments and quizzes were administered to enhance retention. Final assessment to achieve certification included six hands-on exercises to demonstrate proficiency and a written, multiple-choice examination. Statistical analysis of survey data was performed using the UNIVARIATE procedure in SAS (v9.2). 94% of the participants passed the certification requirements of the program, and overall subject matter knowledge increased by 36%. Likert scale responses (1 = very little, 2 = little, 3 = some, 4 = much, 5 = very much) regarding knowledge of 14 subject matter topics before (2.89 ± 0.11) and after (3.83 ± 0.07) indicated a mean increase of 0.91 ± 0.09 units. Subject matter knowledge with a > 1 unit increase included cattle (1.40 ± 0.15) and equine (1.43 ± 0.14) body condition scoring, equine behavior (1.00 ± 0.15) and learning lab (1.07 ± 0.12), and animal nutrition (1.13 ± 0.11). Likert scale responses (1 strongly disagree, 2 disagree, 3 neutral, 4 agree, 5 strongly agree) indicated the usefulness of information to participants when working in the field (4.20 ± 0.10), whether participants feel better prepared to respond (4.20 ± 0.08), and whether instructors presented the material clearly (4.34 ± 0.07). The LECALE program addresses specific core curriculum to improve LEOs knowledge and skills. Utilization of the LECALE program by Florida LEOs could result in a savings of nearly $2,500 per client compared to other national certifying services.

Key Words: law enforcement, livestock, training

0583 Benchmark demographics of the Mississippi feeder calf board sale program. E. A. Caldwell*[1], B. B. Karisch[1], J. M. Riley[2], and J. A. Parish[3], [1]*Mississippi State University, Mississippi State,* [2]*Oklahoma State University, Stillwater,* [3]*Mississippi State University, Prairie.*

The semi-annual Mississippi feeder calf board sale program serves as an opportunity for beef cattle producers to build a more successful marketing strategy in the feeder cattle sector. The board sales encourage more uniform load-lots in addition to reduced shrink, handling, and comingling before shipping due to the off-site marketing of calves. Established in 2008, the program has recorded 309 total lots sold consisting of nearly 25,000 heads of cattle, with the receipts from these sales exceeding $19 million. To examine benchmark values of the board sale program, lot demographics of each sale were analyzed using the Proc Means procedure of SAS. Frequencies of hide color characteristics reveal that 92.6% of all lots sold advertised some percentage of black-hided cattle, followed by 47.2% of lots with smoke color, 43% with red, and 18.1% with white color. Specifically, 64% of all lots consisted of at least 75% black cattle, 36.6% of lots contained less than 25% red cattle, and 34% contained less than 25% cattle with smoke hide color. Lots marketed with Brahman influence represent 14.2% of lots sold. The mean weighted average lot body weight per calf across all years was 315.3 ± 4.4 kg. Results show that 0.3% of lots had a weighted average body weight per calf of less than 226.8 kg, 5.9% weighed 226.8 to 271.2 kg, 47.6% weighed 272.2 to 317.1 kg, 30.6% weighed 317.5 to 362.4 kg, 15.3% weighed 362.9 to 407.8 kg, and 0.3% weighed more than 408.2 kg. Mixed gender lots comprised 45.3% of all lots sold, followed by steer-only lots at 33.7% and heifer-only lots at 21%. Use of growth-promoting implants was advertised for 12.6% of total lots, whereas 20.4% of lots marketed cattle produced without growth promotants. Participation results indicate fewer lots per sale since 2008 accompanied by a slight increase in number of heads per sale due to increased number of heads per lot sold. Furthermore, price trends of the board sale program indicate a steady increase in selling price

throughout its history. In summary, the Mississippi feeder calf board sale program continues to provide producers a viable alternative marketing strategy. The specific attributes of each lot are central to its selling value, as consistent and industry-recognizable lot characteristics may bring premiums at sale.

Key Words: board sale, feeder calf, marketing

0584 The show-me-select replacement heifer program: adding value to beef herds in Missouri.

J. W. C. Locke*, J. M. Thomas, B. E. Bishop, J. M. Abel, S. E. Poock, D. S. Brown, J. E. Decker, and D. J. Patterson, *University of Missouri, Columbia.*

The Missouri Show-Me-Select Replacement Heifer Program was designed to improve reproductive efficiency of beef herds in Missouri and increase individual farm income. During the past 18 yr, 822 farms enrolled 122,970 heifers in the program. Regional extension livestock specialists work closely with the 243 veterinarians involved with the program state wide. State specialists provide program support to regional extension field staff and participating veterinarians. The marketing component of the program facilitated the sale of 30,539 heifers in 141 sales from 1997 through sales in 2015. These sales generated interest from 9484 prospective buyers that formally registered to buy heifers and 3366 individuals that purchased heifers from the various sales. Heifers from the program have now sold to farms in 19 states. Collectively, 141 sales have generated $42,984,650 in gross sales. A Tier Two classification was created recently that distinguishes heifers from genetically superior high accuracy sires. Using data from the Fall 2015 sales, in which Tier Two heifers sold, we may consider opportunities for producers to add value to their heifers as a result of improvements in genetic merit. Using the average sales price of Show-Me-Select qualified heifers carrying a natural-service sired pregnancy as a baseline sale average, we can make the following comparisons to determine the relative added value that resulted from improvements in genetics of the heifer and/or the pregnancy the heifer was carrying: Show-Me-Select heifers carrying natural-service sired pregnancies sold for an average sale price per heifer of $2,242; Show-Me-Select heifers carrying AI-sired pregnancies sold for an average sale price per heifer of $2,437, adding $195 per heifer; Tier Two Show-Me-Select heifers carrying natural-service sired pregnancies sold for an average sale price per heifer of $2,371, adding $129 per heifer; and Tier Two Show-Me-Select heifers carrying AI-sired pregnancies sold for an average sale price per heifer of $2,664, adding $422 per heifer. The Missouri Show-Me-Select Replacement Heifer Program is the first statewide on-farm beef heifer development and marketing program of its kind in the U.S. Impact on Missouri's economy that resulted from the past 18 yr of the Show-Me-Select program now exceeds $110M.

Key Words: added value, beef heifer, extension program

0585 Perceived mastitis costs and milk quality management practices among Southeastern United States dairy producers.

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Researchers from four universities in the southeastern United States completed 175-question surveys on 282 farms in TN (n = 83), KY (n = 96), VA (n = 96), and MS (n = 7) from June 22, 2014 to June 21, 2015 as a part of the Southeast Quality Milk Initiative project. The objective of this study was to analyze questions focusing on the costs associated with milk quality management and to quantify dairy producer estimates of mastitis costs. The MEANS procedure in SAS 9.3 (SAS Institute, Cary, NC) was used to summarize costs of pre- and post-milking teat disinfectants, intramammary antibiotics for mastitis treatment, vaccinations, and producer estimates of subclinical and clinical mastitis costs. The average costs associated with specific management practices and producer estimates of mastitis costs are presented in Table 1. One hundred twenty-four and 126 producers provided enough information to allow the researchers to calculate the costs of pre- and post-milking teat disinfectants per cow per day, respectively. Two hundred seventeen producers provided the researchers enough information to determine the cost of intramammary antibiotics per mastitis case. Only 52 and 3 producers provided enough information to calculate the costs of environmental and contagious mastitis vaccines per cow, respectively. When estimating the cost of clinical and subclinical mastitis, 241 and 208 producers provided a numerical estimate, respectively. Remaining producers either did not know or did not provide an estimate. These results provide new insights into producer perception of mastitis and milk quality economics.

Key Words: costs, mastitis, milk quality, SQMI

0586 Development of a web-based calendar tool f or scheduling beef cow management activities.

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Extension efforts often remind producers of timely management practices and their value. Recommendations must

revolve around presumed average time of activities, such as calving and weaning. The objective of the current project was to develop a web-based cow/calf management tool to create a customizable yearly production calendar. The Management Minder (MM) was designed for beef cattle producers to facilitate the timely implementation of routine management steps to optimize health, nutrition, reproduction, and general management. The MM helps beef producers schedule routine activities based on default intervals from the appropriate date category (calving/breeding, weaning, grass turnout, and receiving cattle), and communicate these events to other members of the management team. An automatic portion adds all of the activities in a particular category and a check box is used to eliminate those not needed. Activities can also be added one at a time in a manual build portion. The program emails an ics file of user selections that can be imported by OUTLOOK™, GOOGLE™, and YAHOO™ calendar systems. Thus automatic reminders are put in place so that adequate time is allowed for cow weight gain in the third trimester, AI breeding programs can be planned, or all needed supplies can be obtained in advance of processing days. Users register on the website http://cowweb.exnet.iastate.edu/CowWeb/faces/ with a unique farm/ranch name. The application provides an option to register multiple users under the same operation. Other family/team members, consultants, or veterinarians can be given access to add events to the same farm/ranch calendar. Veterinarians can set up health programs in a calendar form for individual clients. The calendar showing the upcoming activities can be used for planning and to improve communication among team members. A dynamic database stores events for each particular farm/ranch so they can be automatically advanced to the next year, minimizing the time needed for set-up in subsequent years. Supporting information or references regarding best management practices for the selected activities are provided as web links and can be easily updated. Since the program was first made available in January 2016, user suggestions have been incorporated to improve the tool. The concept is applicable to many areas of plant and animal management that function in biological and environmental cycles. Users of this free tool have the opportunity to improve the timeliness of management activities, improve communication with partners, and reduce costs associated with forgotten or delayed management.

Key Words: calendar, cow/calf, extension

0587 Comparing the Penn State and NRC 2001 heifer ration programs. L. K. Mitchell*, and A. J. Heinrichs, *Pennsylvania State University, University Park.*

Formulating dairy heifer rations is an often overlooked aspect of farm feeding programs. The Penn State dairy heifer diet formulator (PSU-HDF) was originally developed to design and evaluate diets used in heifer research. The current objective was to evaluate differences between the PSU-HDF and the 2001 NRC program. Drawing from fundamental heifer studies at Penn State, the basis for diet formulation in PSU-HDF is N intake (g/kg of metabolic body weight) with a target of 1.67 g of N/kg $BW^{0.75}$. In contrast, the NRC emphasizes the intake of crude protein (CP) and its fractions. Furthermore, the NRC recommends dairy heifer diets to meet certain dry matter intakes (DMI) in addition to meeting metabolizable energy (ME) requirements. Research at Penn State has demonstrated that varying DMI can produce similar average daily gains (ADG) provided the diet precisely meets the ME requirements. Therefore, PSU-HDF places more emphasis on meeting ME needs and adjusts DMI as necessary. For a heifer at 6 mo weighing 200 kg targeting an ADG of 800 g, the NRC recommends a diet with 14.2% CP, 11.9 Mcal/d ME, and 5.2 kg/d DMI. Using PSU-HDF, the same heifer had her needs met by a diet with 13.6% CP, 11.7 Mcal/d ME, and 4.3 kg/d DMI. A heifer at 14 mo weighing 400 kg targeting an ADG of 800 g was recommended by the NRC to receive a diet with 11.3% CP, 20.1 Mcal/d ME, and 8.8 kg/d DMI. The diet for the same heifer using PSU-HDF was 13.1% CP, 19.7 Mcal/d ME, and 7.1 kg/d DMI. Comparing the output of these two models, we find that the NRC model often predicts 20% more DMI and 60 to 155 more g CP intake. The NRC recommends 0.2238, 0.2247, and 0.2247 Mcal/kg $BW^{0.75}$ of ME for heifers at 200, 300, and 400 kg, respectively, when targeting an ADG of 800 g. These values are consistently higher than PSU-HDF recommendations of 0.2199, 0.22, and 0.22 Mcal/kg $BW^{0.75}$ of ME for heifers with the same parameters. These results show consistent overestimation of nutrient requirements by the NRC program. According to our research trials using precision and ad libitum formulation, the PSU-HDF model will allow nutritionists to formulate diets to meet dairy heifer needs and reduce feed cost by feeding less protein and dry matter.

Key Words: dairy heifer, diet formulation

0588 Motivations of calf care workers for sick calf identification and treatment decisions. C. Crudo[1], D. A. Moore*[2], J. A. Afema[1], and W. M. Sischo[1], *[1]Washington State University, Pullman, [2]Department of Veterinary Clinical Sciences, Washington State University, Pullman, WA.*

On large dairy farm operations and calf rearing facilities, identification and treatment of sick pre-weaned calves is in the hands of employees. Understanding the motivation behind why and how calf care workers make treatment decisions could help Extension educators and dairy advisors create more tailored messages about judicious antimicrobial use. The purpose of this project was to better understand decision making on these operations by assessing employee motivation using a standardized survey tool. Western United States dairy farms and calf ranches with > 200 pre-weaned calves were contacted through their veterinarian to participate in the study. A sample

Table 0585.

Table 1: Average cost estimates among dairy producers for mastitis control practices and perceived costs of mastitis cases.

	Mean	Standard Deviation	Median
Pre-dip cost/cow/d	$0.04	$0.04	$0.03
Post-dip cost /cow/d	$0.06	$0.05	$0.04
Intramammary antibiotic cost/mastitis case	$14.85	$10.84	$12.67
Environmental vaccine cost/cow/lactation	$3.43	$4.60	$3.00
Contagious vaccine cost/cow/lactation	$3.30	$1.98	$3.60
Cost estimate of clinical mastitis[1]	$288.00	$520.25	$175.00
Cost estimate of subclinical mastitis[2]	$301.00	$746.83	$150.00

[1]Cost estimate made by producer for a clinical case of mastitis

[2]Cost estimate made by producer for a subclinical case of mastitis

size of 96 individuals was estimated based on a prevalence of 0.5 for the dominant motivation type with a precision of 0.1 and 95% confidence. The survey tool was adapted from the Motivations Sources Inventory and included 10 questions on motivation for specific aspects of calf care with response categories referring to the five motivation types: 1. External, motivated by recognition from supervisor or coworkers; 2. Extrinsic, motivated by bonuses or other monetary means; 3. Intrinsic, motivated by one's belief system; 4. Internal, motivated by task enjoyment; and 5. Goal Internal, motivated by a desire to meet the organization's goals. Additional questions included job title, training, communication, and information seeking. One-hundred seven individuals from 28 farms participated in the personal interviews. Most were calf feeders (47%), who had worked in that position for more than 5 yr. The most common motivation type was Intrinsic (41 ± 12%), and there were none of the Extrinsic type (0%). The majority of farms (79%) had calf care workers of a variety of motivation types. Six farms had employees of all the same type. Calf Feeders were predominantly Goal Internal (36 ± 13%). Calf managers and calf treaters were predominantly Intrinsic (40 ± 18% and 44 ± 23%). The dominant motivation type for sick calf identification questions was Intrinsic (32 to 50%). The dominant motivation type for questions dealing with calf treatment was Goal Internal (37 to 51%). There is a great deal of variation in calf care worker motivation types, but overall, messages and training programs to address prudent antimicrobial use could benefit by addressing belief systems for sick calf identification and the reinforcement of goals and protocols when addressing treatment.

Key Words: calf care, motivation, treatment

0589 Developing a feed allocation model to maximize income over feed cost considering farmer risk preferences. D. Liang*, T. F. Rutherford, B. L. Jones, R. D. Shaver, and V. Cabrera, *University of Wisconsin-Madison, Madison.*

We developed a nonlinear programming model that selects the optimal cropping plan and diet formulation to maximize farm income over feed cost (IOFC) in a representative 200-lactating cow, 100-ha south-central Wisconsin farm. Nutrition requirements for 6 cow-groups were formulated according to National Research Council equations. Then, the model selected the group production level toward maximum IOFC, which included milk and surplus feed sale, feed production cost, and feed purchasing cost. Yearly farm-produced feed, forage quality (NDF), and feed production costs were simulated with the integrated farm system model (IFSM, USDA, 2014) using 25-yr daily weather data (1986 to 2010). Farm-produced forage was priced according to its quality. The farm could purchase feed and sell surplus feed at 90% of market price. Feed prices were collected from the Understanding Dairy Market website (http://future.aae.wisc.edu) or predicted using FeedVal v6.0 (http://DairyMGT.info). Purchased feed and milk prices reflected 2015 market conditions, and cost of feed production was calculated aggregating resource inputs according to weather year. The optimal solution maximized the total IOFC across 25 weather years, considering the influences of farmer risk preferences toward decision-making through expected utility theory. Hence, the model also proposed an optimal cropping plan to maximize IOFC. Average IOFC across 25 yr was $8.07/cow per d with the original cropping plan of 57.1 ha of corn and 42.9 ha of alfalfa. The model chose to lower milk production for higher IOFC in some years. The farm's IOFC increased with higher milk production and varied from year-to-year because of crop yield and quality. The difference between the highest and lowest yearly IOFC was 27% on low milk production farms (5 kg per cow per d below Wisconsin average) and decreased to 17% on high milk production farms (5 kg per cow per d above Wisconsin average). Diet formulation and purchasing strategies changed for each weather year to maximize IOFC according to farm-grown feed quantity and quality. Results showed that planting corn and harvesting corn silage were favored. The model would choose to plant alfalfa only if alfalfa production cost was decreased by 8% or corn production cost was increased by 6%. A farmer with higher risk tolerance would prefer to purchase more feed from outside than a farmer with less risk tolerance.

Key Words: income over feed cost, feed allocation, whole-farm optimization

0590 A qualitative assessment of perception and communication barriers that interfere with the transfer of knowledge to dairy farmers.
M. E. Woolpert*[1,2], C. E. Morse[1], and D. M. Barbano[3], [1]*University of Vermont, Burlington,* [2]*William H. Miner Agricultural Research Institute, Chazy, NY,* [3]*Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

Efficient sharing of knowledge between consultants and dairy farmers is critically important to the success of the dairy industry. Awareness of how and where dairy farmers seek expert information when making farm management decisions is essential to understanding the communication network of scientists, agricultural experts, and farmers. This study investigated dairy farmer decision-making and communication networks as part of a larger research project on the relationships between farm management practices and milk fat and protein production on dairy farms in the Northeastern United States. Communication networks and barriers to successful information transfer were described by a subset of the farmers enrolled in the larger study. As managing a dairy farm involves complex decision-making processes across diverse knowledge areas, it was hypothesized that dairy farmers seek information from many sources and that barriers exist that are specific to the source and type of information. This research is framed within the "communication for innovation theory," which acknowledges that a person's experiences influence how he/she perceives and reacts to new information and that information transfer frequently encounters obstacles. Semistructured interviews were conducted with a heterogeneous subsample of farmers (n = 9) to collect detailed, diverse, and in-depth perspectives and experiences on decision-making and information transfer. To investigate the cooperative's role in information transfer, additional interviews were conducted with two cooperative employees. Interviews were audio-recorded, transcribed, and coded to identify common themes expressed by farmers or cooperative employees. Farmers identified the cooperative (which communicates via the internet and field technicians), expert consultants (nutritionist, veterinarian, and agronomists), financial advisors, print publications, and other farmers as principal sources of information. However, barriers to the transfer of information include farm management and family dynamics, lack of access to high speed internet, and difficulties evaluating divergent recommendations from experts. Several farmers expressed an incorrect perception of their farms' fat and protein production compared with cooperative averages, which reduced their motivation to incorporate management changes. Recommendations to overcoming these barriers were suggested by interview participants and include integrating management team meetings and facilitating informal discussion groups between farmers. Knowledge about improving milk fat and protein does not easily find its way to individual dairy farmers due to barriers within their communication network, and the proposed recommendations may aid in overcoming these barriers.

Key Words: decision making, extension education, information networks

EXTENSION EDUCATION SYMPOSIUM: GROWING EXTENSION'S IMPACTS WITH CHANGING BUDGETS AND PERSONNEL

0591 Work-life balance for extension professionals: maybe it should be redefined as 'work-life effectiveness'.
G. P. Lardy*, *North Dakota State University, Fargo.*

The literature is littered with articles related to work-life balance for a variety of professions. Do extension professionals experience work-life balance any differently than other professional or academic careers? Should we redefine work-life balance to instead be referred to as work-life effectiveness as some writers have proposed? Let's start with the first question. One can make the case for both sides of this argument. The case for being different includes the situations where we expect a considerable amount of night and weekend work from extension professionals. Many have split appointments with expectations in research and/or teaching, which tends to increase the expectations of their supervisor(s). However, the case against it includes the fact that many professionals in academia and industry have careers that require travel and many have multiple job duties, similar to split appointments in academia. While there may be some differences, there are likely more similarities. Let's evaluate the second question, should we redefine work-life balance as work-life effectiveness as some writers have proposed? In many cases, I would argue that we should be looking for work-life effectiveness rather than balance. Balance may imply some sort of notion of equal time at work and outside of work. In reality, there are likely few times when that is the case. Effectiveness, however, denotes a system or situation that produces the intended result. So, how does an extension professional (or any other professional) enhance work-life effectiveness? Here are a couple of suggestions. 1. Define what success looks like. What does being an effective extension professional look like? This should be done in concert with your supervisor. As for your personal life, perhaps asking 'What does an effective spouse, mother, father look like?' is an appropriate question to ask. 2. Set boundaries/maintain control. This includes various aspects of your career, including your schedule. If there are important family events that you want to be there for, be sure you get them on the calendar. Schedule time for personal time. Don't schedule every available minute. 3. Find time to ensure that your physical, emotional, and spiritual well-being are nurtured in addition to your professional development. In summary, I believe we should be discussing this topic as work-life effectiveness rather than work-life

balance. In addition, by asking some key questions, extension professionals may be able to better define what that looks like for them as individuals.

Key Words: extension, effectiveness, success

0592 Enhancing your extension program through a strong research program and vice versa.
W. Powers*, *Michigan State University, East Lansing.*

Faculty members with split appointments are successful in conducting joint research and Extension programs. Successful integration of research and Extension responsibilities may appear daunting at first; however, issue relevance provides a strong foundation for both resulting impact and funding alike. Thus, a well-funded research program contributes to impact-driven Extension programming. Similarly, an Extension program that is based on solid needs assessments integrates seamlessly into research support to develop and implement solutions. Perhaps the biggest challenge is finding a balance between research and Extension efforts. Expectations can appear overwhelming in that each responsibility, research, and Extension could be a full-time effort. Without clear goals and objectives, faculty can spend considerable time on Extension activities that don't result in measureable impact at the expense of demonstrating a research trajectory and scholarship needed for promotion. To avoid this pitfall, faculty should carefully and deliberately plan their time and activities such that the research and Extension programs complement each other and build on the other. This begins with an assessment of stakeholder needs and how identified needs tie to fundable research questions that translate into implementable solutions. Through constant and deliberate focus on the interconnectedness of a research and Extension program, faculty can balance a split appointment and achieve intended outcomes and scholarly outputs that lead to promotion in the academic system.

Key Words: impact, outcome, output, scholarship

0593 Culturing and leveraging allied industry support for academic programs.
M. W. Overton*, *Elanco Animal Health, Greenfield, IN.*

The mission of public universities includes undergraduate, graduate, professional, and continuing education, basic and applied research, and dissemination of information via extension programing. State-supported funding for academic positions has eroded, but its reductions usually pale relative to the cuts realized by extension departments. Delivery methods used by extension have changed dramatically in the last 30 yr concurrent with the changing structure of the dairy industry (fewer herds but more cows per herd), educational media, access to information, corporate industry support, and shrinking state economic support. One area of potential support for consideration is allied industry; however, universities are under increasing scrutiny from the public pharmaceutical companies with whom they interact. How does academia experience productive relationships with industry representatives without appearing to "be bought and paid for"? Academic and extension programs should consider the synergistic potential that exists for collaborative efforts with allied industry and pharmaceutical companies. Both industry and academia want to conduct rigorous scientific studies to help improve the level of knowledge and to develop new products or technologies. Unfortunately, many faculty members see their corporate industry allies only as potential cash cows, ready to donate or pay for product promotion. However, this viewpoint is problematic and limited in scope. Consider how many former academics are employed in the corporate world. Many were hired away from universities specifically because of their talents and abilities. Some formerly advised graduate students, taught classes, and ran research programs of their own. There is a wealth of knowledge available to help team-teach portions of courses or to serve as adjunct faculty on graduate committees. Specific collaborative efforts experienced by the authors include the teaching of specialty courses in undergraduate, graduate, and veterinary medicine courses, guest authoring for university publications, serving on Masters or PhD committees as subject matter experts, partnering with faculty members to conduct and publish scientific work unrelated to any specific product or technology, speaking at animal health conferences sponsored by universities, and working with a core faculty group at a university on an annual basis for the purposes of simply brainstorming and sharing potential research ideas. Pre-established boundaries around product highlighting or advertising and an agreement around preserving the ability to publish negative research findings are both key to high integrity collaborative efforts. However, there are many additional opportunities to be experienced through healthy collaborative efforts between academia/extension and their corporate or allied industry.

Key Words: industry support, extension, collaboration

0594 Developing regional and multi-state extension collaborations.
A. J. Young*, *Utah State University, Logan.*

The new norm for extension includes smaller budgets, fewer individuals tasked with greater job duties, and rapidly changing clientele wants and needs. Consequently, historical state boundary- based extension personnel and programs don't make as much sense as they did previously. In many situations, regional and multi-state programs provide a viable alternative to meet the needs of clientele and state universities. Many extension programs recognize this and provide short-term multi-state conferences and workshops, which have been successful in attracting individuals from not only the participating

states but regionally and nationally. However, much less common are regional or multi-state programs where individuals are identified to provide direct support to commodity-based clientele in states other than their own. Utah State University has experience with this type of programming through MOUs developed to provide dairy extension expertise for Montana, Wyoming, and Nevada, which lack dairy specialists but were getting requests from clientele for support. The MOU for each state specified the amount of time spent within the state as well as other activities to be made available. In return, specialist time was bought by the participating state. Our experience provides evidence that these programs can be successful, providing that there is appropriate support from administrators, specialists from the host state, and local county agents. County agent support is critical for achieving the greatest success. Alternatively, there may be opportunities for agreements between states on a county-basis, rather than a state-basis because of proximity of a specialist to localized clientele. Our experience suggests that it works best if money is paid by the state receiving the support to the state that is providing the expertise; it is much cheaper than hiring a new specialist. If a state wants to provide support but doesn't want to provide in-state visits, training workshops via electronic media are an easy option. With the advent of internet audio and video capabilities, extension programming can also be accomplished faster and more economically than physically traveling to that site. Sharing extension expertise across state borders makes sense in many situations, allowing for support of underserved clientele; however, the development of agreements and sharing of a specialist's time requires administrators who are willing to work under a different extension model.

Key Words: extension, multi-state, programs

0595 Extension faculty navigating the tenure and promotion process. N. E. Cockett*, *Utah State University, Logan.*

Decisions of tenure and promotion are a critical mechanism by which a university shapes its future. In addition, each tenure and promotion decision directly affects a faculty member's future in academia. It is imperative that there is clarity in expectations for a faculty position as well as the availability of "best practices" so that a faculty member can be successful in achieving those expectations. Utah State University has developed documents that articulate expectations for Extension faculty (the role statement) and a framework for success (the roadmap). These documents are used not only by faculty members and their direct supervisors to set goals and review performance but also by others, such as the university's central tenure and promotion committee, who are not familiar with the Extension specialist role. The major areas of expectation for Extension faculty include programming and scholarship. Expectations for programming include the identification of needs and issues that lead to the development of programs that disseminate information and address the issues. Extension specialists should emphasize long-term programs with measurable outcomes and impacts and strong working relationships with Extension county agents. The value of Extension programs can be assessed by the number of participants or contacts and the resulting impacts, such as change in behavior, dollars saved, or dollars generated. At Utah State University, specialists demonstrate scholarship through the dissemination of materials, such as journal articles, fact sheets, web sites, curriculum materials, and presentations and abstracts at professional meetings. All materials should be peer reviewed. The value of scholarship can be determined using standard measurements, such as journal impact factors, citations, invitations for presentations or participation on working groups, and recognition through awards. However, the value of Extension scholarship can also be measured by the uptake or adoption by Extension peers. At USU, Extension specialists are tenured within the academic college, whereas Extension county agents are tenured within USU Extension. While the USU Vice President for Extension does not have direct authority over the decisions of tenure and promotion for Extension specialists, there are annual performance review meetings that include the Extension administration, the department head, and the academic dean. This review provides the academic administration with insight on the performance of the specialists in his or her Extension assignment. A single letter is returned to the faculty member so as to avoid mixed messages on performance.

Key Words: extension, faculty, tenure, promotion, expectations

FOOD SAFETY

0596 Monitoring of pesticide residues in animal feeds from the republic of Korea. H. Park*, H. J. Kim, M. S. Jeong, C. R. Kim, E. S. Choe, Y. S. Youn, J. K. Kim, and J. H. Lee, *Experiment and Research Institute, National Agricultural Products Quality Management Service (NAQS), Ministry of Agriculture, Food, and Rural Affairs (MAFRA), Kimcheon, South Korea.*

Animal feeds can be contaminated with pesticides due to the large number of different ingredients from diverse origins. Safe animal feed is important for both animal health and the safety of foods of animal origin. To ensure the safety of animal feeds, the Ministry of Agriculture, Food, and Rural Affairs (MAFRA) regulates the amount of each pesticide that

may remain in and on animal feeds. To strictly control the pesticide residues in animal feeds, the MAFRA expanded the number of the maximum residue limits (MRLs) in a wide variety of animal feeds from 27 pesticides to 121 pesticides in 2015. Therefore, the aim of this study was to investigate the amount of pesticide residues in various complete feeds and feed ingredients (corn, barley, wheat, oat, and roughage) from the Republic of Korea as a part of an official control. A total of 126 samples were collected in 2015 and monitored for 105 pesticides from diversified chemical classes, including organochlorines, organophosphates, carbamates, triazoles, pyrethroids, and others using a validated multi-residue pesticide analysis method. According to the pesticides monitoring results, no residue was found in 84.1% of the samples, whereas 15.9% of samples contained pesticide residues below the MRLs. Pirimiphos-methyl and cyproconazole were the two most frequently found pesticides. The results revealed that all commercial animal feeds monitored in 2015 were safe and below the Korean MRLs. The low levels of residues of pesticides found in animal feeds were not considered to be serious threats to human or animal health. However, continuous monitoring with tighter regulation for pesticide residues in animal feeds is recommended.

Key Words: pesticide residues, monitoring, animal feeds, MRLs, official control

0597 *Bacillus amyloliquefaciens* from UHT organic milk produces biofilm and demonstrates virulence potential. J. L. McKillip*, A. Grutsch, E. R. Wagner, and C. Klug, *Ball State University, Muncie, IN.*

This investigation identified an isolate of biofilm-producing *Bacillus* spp. present in ultra-high temperature (UHT) pasteurized organic whole milk. The overall goal of this project was to genotypically and phenotypically characterize thermoduric *Bacillus* bacteria for virulence potential from a UHT dairy environment. Virulence determinants present in this species were detected, and virulence gene expression over time was quantified in a model food (UHT milk) system compared to *B. cereus* ATCC 14579, a known type strain containing the virulence genes of interest. Pure cultures of UHT organic dairy milk were obtained following nonselective enrichment, were biochemically identified to the species level using the Microgen *Bacillus* ID system (Hardy Diagnostics), and were validated further using fatty acid profiling and 16S rDNA sequencing (MIDI Labs Inc.) as *Bacillus amyloliquefaciens*. To confirm the presence of the virulence and regulator genes, DNA was extracted from TSB-grown pure cultures and used in real-time (SYBR Green-based) PCR with primers specific for each of the target genes. PlcR is a pleiotrophic extracellular virulence factor regulator, CodY is a flagellar repressor, NheA and HblC are well-characterized enterotoxins, and 16S served as the housekeeping gene standard. Results revealed that all gene targets were present in the UHT *B. amyloliquefaciens*. Biofilm production was quantified and determined to be produced in amounts that exceeded levels from the *B. cereus* ATCC type strain control. For virulence gene expression measurements, *B. amyloliquefaciens* was inoculated (10^2 CFU/mL) into sterilized organic milk and incubated at ambient temperature (23°C) for 72 h. Every 2 h, samples were removed for standard plate count (SPC)-based density determination and RNA extractions. mRNA for each gene target noted above were amplified with real-time NASBA and transcript-specific primers, revealing relative levels of expression of hblC, nheA, and plcR to be tightly correlated with density during late-log-to-stationary phase growth in the milk system. Dot-blot assays with anti-PlcR will be used to confirm the presence of this regulator protein in the *B. amyloliquefaciens* during incubation at the same time points used for RNA extractions. These data indicate that *Bacillus* spp. present in UHT milk harbor and express the same virulence determinants that are familiar to microbiologists in their psychrotrophic *Bacillus* counterparts, including biofilm potential. These results necessitate that the guidelines on proper storage and shipment of UHT

Table 0596.

Table 1. Summary of the Animal Feed Samples Analyzed for Pesticides

Pesticide	Use	Total # of Samples	Quantifiable Samples	Feeds	Range (ppm)	Median (ppm)	MRL (ppm)
Azoxystrobin	Fungicide		2	Oat, Roughage	0.66~1.05	0.86	15
Chlorpyrifos-methyl	Insectcide		2	Barley, Oat	0.41~0.84	0.63	6
Cyproconazole	Fungicide		5	Corn	0.58~0.95	0.65	2
Piperonyl butoxide	Insectcide synergist	126	1	Complete feed	0.30	0.30	24
Pirimiphos-methyl	Insectcide		5	Complete feed	0.12~0.30	0.14	5
Propiconazole	Fungicide		3	Roughage	0.10~1.48	0.12	2
Tricyclazole	Fungicide		2	Roughage	0.11~0.32	0.22	5

milk products be revisited to ensure product safety.

Key Words: UHT milk, *Bacillus amyloliquefaciens*, biofilm, enterotoxins

0598 Occurrence of aflatoxin M1 in UHT, pasteurized, and powdered milk marketed in Hubei province (central China). J. L. Xiong[1], H. L. Zhou[2], L. Y. Wu[*1], and F. T. Meng[1], *[1]Hubei Key Laboratory of Animal Nutrition and Feed Science, Wuhan Polytechnic University, Wuhan, China, [2]Xiangyang Engineering Research Center of Animal Medicine, Xiangyang Vocational and Technical College, Xiangyang, China.*

Aflatoxin M1 (AFM1), a strong carcinogenic derivate of aflatoxin B1 (AFB1), occurs in milk from dairy cows fed an AFB1-contaminated diet and subsequently contaminates dairy products. This survey was conducted to evaluate the occurrence of AFM1 in UHT, pasteurized, and powdered milk available in Hubei province (central China) and to compare these milk AFM1 levels with the maximum AFM1 limits of 50 and 500 ng/L set by the European Commission (EU) and China's Ministry of Health, respectively. A total of 271 samples, composed of UHT milk (120 samples), pasteurized milk (121), and powdered student formula (30) from two major dairy brands available in Hubei province were collected from November 2014 to February 2015 (winter season). Milk AFM1 was detected by using a commercial ELISA method (RIDASCREEN® Aflatoxin M1 test kit; R-Biopharm AG, Darmstadt, Germany) with the detection limit of 5 ng/L. Differences in the concentration of milk AFM1 were statistically analyzed by Mann–Whitney comparisons using SPSS version 19.0 software. The results showed that the mean of AFM1 concentration in positive samples of pasteurized milk was significantly higher ($P < 0.05$) than that in UHT milk (133.4 vs. 20.5 ng/L), and there were significant differences ($P < 0.05$) in AFM1 concentration in milk samples among two dairy brands. In addition, AFM1 was detected in 61 samples of UHT milk (50.8%) with concentrations of 5.5–62.3 ng/L and in 115 samples of pasteurized milk (95.0%) with concentrations between 5.2 and 346.2 ng/L. Moreover, 2 samples of UHT milk (3.4%) and 77 samples of pasteurized milk (63.6%) were found to contain AFM1 above the European tolerance limit, but all samples were below China's legal limit. All samples of powdered student formula were negative at the AFM1 detection limit. The findings of the study are as follows: 1) the content of AFM1 in all milk samples was below China's national legal limit though the incidence of AFM1 in UHT and pasteurized milk was high, 2) powdered student formula was free from AFM1 contamination and thus can be considered the safest milk product tested, and 3) the incidence and concentration of AFM1 in pasteurized milk was higher compared to other dairy products. To maintain milk safety, strict monitoring systems are recommended.

Key Words: aflatoxin M1, milk, Hubei province

0599 An aptamer-based biosensor for detection of aflatoxin M1. X. Guo[1,2,3,4], F. Wen[1,3], N. Zheng[1,2,3], S. Li[1,5], M. L. Fauconnier[4], and J. Wang[*1,2,5], *[1]Ministry of Agriculture-Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]Ministry of Agriculture-Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [4]Chimie générale et organique, Gembloux Agro-Bio Tech, Université de Liège, Gembloux, Belgium, [5]Ministry of Agriculture Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Aflatoxin M_1 (AFM_1), one of the most toxic mycotoxins, imposes serious health hazards. AFM_1 had previously been classified as a group 2B carcinogen and has been classified as a group 1 carcinogen by the International Agency for Research on Cancer (IARC) of the World Health Organization (WHO). Determination of AFM_1 thus plays an important role for quality control of food safety. In this work, a sensitive and reliable aptasensor was developed for the detection of AFM_1. The immobilization of aptamer through a strong interaction with biotin-streptavidin was used as a molecular recognition element, and its complementary ssDNA was employed as the template for real-time quantitative polymerase chain reaction (RT-qPCR) amplification. Under optimized assay conditions, a linear relationship (ranging from 1.0×10^{-4} to 1.0 μg L^{-1}) was achieved with a limit of detection (LOD) down to 0.03 ng L^{-1}. In addition, the aptasensor developed here exhibits high selectivity for AFM_1 over other mycotoxins and small effects from cross-reaction with structural analogs. The method proposed here has been successfully applied to quantitative determination of AFM_1 in infant rice cereal and infant milk powder samples. Results demonstrated that the current approach is potentially useful for food safety analysis, and it could be extended to a large number of targets.

Key Words: aflatoxin M_1, aptamer, RT-qPCR.

0600 Individual and combined cytotoxicity assessment of zearalenone and ochratoxin A/α-zearalenol by full factorial design. N. Zheng[1,2,3], Y. Gao[1,2,3], H. Wang[4], and J. Wang[*2,3,5], *[1]Ministry of Agriculture-Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]Ministry of Agriculture-Milk Risk Assessment Laboratory, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China, [5]Ministry of Agriculture Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The co-occurrence of zearalenone (ZEA) and ochratoxin A (OTA) is commonly found in cereals. These mycotoxins can be metabolized after livestock feeding and can then co-occur in later food products in the form of ZEA, α-zearalenol (α-ZOL), and OTA. However, toxicological data concerning the combined effects among these mycotoxins by full factorial analysis design are sparse. In the present study, the combined cytotoxic effects and oxidative damage of ZEA and OTA/α-ZOL on a human hepatoma cell line (Hep G2) were evaluated by 3 × 3 full factorial analysis design and the estimated marginal means plot. Nine groups were adopted to investigate the combined effects of three levels of ZEA (0 μM, 30 μM, and 60 μM), three levels of OTA (0 μM, 6 μM, and 12 μM), and three levels of α-ZOL (0 μM, 15 μM, and 30 μM) after 48 h of exposure. Statistical analysis of the data was performed using the SAS 9.2 statistical software package. For the individual mycotoxin, our results demonstrated that Hep G2 cells were more sensitive to OTA than α-ZOL, and α-ZOL was more cytotoxic than ZEA. For the combined mycotoxins, the cytotoxicity, intracellular superoxide dismutase (SOD), and glutathione peroxidase (GSH-Px) activities as well as malonaldehyde (MDA) and glutathione (GSH) contents showed antagonism in combination of ZEA + OTA, whereas the combination of ZEA + α-ZOL behaved from antagonism to synergism as the concentration of ZEA was increased on the overall interaction. There is a significant correlation between cytotoxicity and oxidative damage in the combinations of ZEA + OTA/α-ZOL ($P < 0.05$), indicating that oxidative damage plays an important role in inducing cytotoxicity.

Key Words: mycotoxins, zearalenone, ochratoxin A, α-zearalenol, combined effect, full factorial design

0601 Distribution and genetic characterization of the top clinically-relevant Shiga toxin-producing *Escherichia coli* in feedlot cattle. J. Hallewell[*1], K. Stanford[2], T. Reuter[2], L. Chui[3], R. Johnson[4], T. A. McAllister[5], E. Topp[6], and T. W. Alexander[1], *[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Alberta Agriculture and Forestry, Lethbridge, AB, Canada, [3]Provincial Laboratory for Public Health, Edmonton, AB, Canada, [4]Public Health Agency of Canada, Ottawa, ON, Canada, [5]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [6]Agriculture and Agri-Food Canada, London, ON, Canada.*

Shiga toxin-producing *Escherichia coli* (STEC) are causative bacterial agents for severe gastrointestinal illness in humans that include the potentially fatal hemolytic uremic syndrome. Cattle shed STEC in their feces, and collectively, seven serogroups of STEC, including O26, O45, O103, O111, O121, O145, and O157, have been implicated as the main serogroups associated with human disease from contaminated beef. Consequently, screening and characterization of these top serogroups is important for mitigating STEC in the human food chain. The objectives of the current study were to characterize the distribution and genetic diversity of clinically-relevant STEC in feedlot cattle. Isolates that were PCR-confirmed as belonging to serogroups O26 ($n = 116$), O103 ($n = 74$), and O111 ($n = 20$) were obtained from the feces of cattle originating in five regions (southwest Alberta, southeast Alberta, central Alberta, Saskatchewan, and British Columbia) in western Canada over a 2-yr period. Isolates were subtyped by pulsed-field gel electrophoresis (PFGE) and compared to human strains from Alberta ($n = 47$) to assess the distribution of potential clinically relevant strains. O26 isolates from cattle were generally diverse, but isolates from southwest Alberta or British Columbia were more closely related ($P < 0.05$) than isolates from other locations and were most uniform in spring and summer seasons ($P < 0.05$). Isolates of O103 ($n = 74$) from southwest or central Alberta were genetically similar ($P < 0.05$) and more closely related in spring ($P < 0.05$). O111 was not frequently isolated from feces but had location-specific and season-specific PFGE profiles ($P < 0.05$), although isolates from southwest Alberta or those collected in spring were diverse. Human isolates within each serogroup were closely related ($P < 0.05$), but cattle isolates of six O26 strains and ten O111 strains from different seasons and locations were > 90% similar to human isolates of their respective serogroups. The results from this study showed that serogroups O26 and O103 were highly diverse in cattle, but certain strains persisted in geographic regions, with the least genetic diversity among O26 and O103 strains during the spring season. Some O26 and O111 cattle strains had > 90% similarity with human isolates, suggesting human pathogens are present in cattle. However, the diverse nature of the cattle isolates implies

that STEC are readily evolving and that only a fraction of cattle isolates are closely related to those causing human disease.

Key Words: Shiga toxin-producing *Escherichia coli*, non-O157, pulsed-field gel electrophoresis

0602 Isolation and characterization of listeriaphages for control of growth of *Listeria monocytogenes* in dairy foods.

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In this study, two lytic bacteriophages (LMP1 and LMP7) targeting *L. monocytogenes* were isolated from the intestinal content of healthy chickens to identify those with the greatest potential in reducing *L. monocytogenes* in dairy foods. The host specificity of these bacteriophages was determined with different serotypes of *L. monocytogenes* strains by the formation of lytic zones and plaques on host lawns. Genomic and morphological analyses of these phages were also performed to investigate their potential as a means of biocontrol of *L. monocytogenes* in the dairy industry. Lytic activity of *Listeria* bacteriophages was assessed in tryptic soy broth inoculated with *L. monocytogenes* ATCC 7644 or ATCC 19114 and incubated at 30°C for 24 h. Phage lytic activity was also evaluated at 10°C for 5 d in the same composition. LMP1 and LMP7 were able to inhibit the growth of *L. monocytogenes* ATCC 7644 and ATCC 19114 compared with the untreated control both at 30°C and 10°C. LMP1 was more effective than LMP7 against *L. monocytogenes* ATCC 19114; contrary to this, LMP7 was more effective than LMP1 against *L. monocytogenes* ATCC 7644. Morphological characterization from electron microscopy reveals that both LMP1 and LMP7 belong to the *Siphoviridae* family. Bacteriophage genome sequences were determined by next-generation sequencing, and they contain about 40 kb and 47 kb with 69 and 67 coding sequence genes, respectively. Comparative genome analyses could provide some evidence of their different host specificity. The effectiveness of phage cocktail (LMP1 and LMP7) on the growth of *L. monocytogenes* in milk samples was investigated at 30°C and 10°C. The growth of *L. monocytogenes* in milk was effectively inhibited by using the phage cocktail. In conclusion, two listeriaphages (LMP1 and LMP7) exhibiting different host specificity were isolated and further characterized; a phage cocktail with these phages could serve as a tool of biocontrol of *L. monocytogenes* in dairy foods.

Key Words: *Listeria monocytogenes*, phages, biocontrol, dairy foods

0603 Effects of feeding NaturSafe on foodborne pathogens in finishing beef heifers.

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With more judicious use of antibiotics in the future, the beef industry will need new science-based strategies to mitigate foodborne pathogens, especially as standard industry technologies are removed from the diet. In this study, cross-bred heifers (N = 1495; 359 ± 3.4 kg) were utilized in a randomized complete block design at a commercial feedlot to determine the effects of a *Saccharomyces cerevisiae* fermentation product (NaturSafe; Diamond V, Cedar Rapids, IA) on foodborne pathogens when monensin, tylosin, and direct fed microbials (DFM) were not included in the diet. Upon arrival, heifers were allowed ad libitum access to water and long-stemmed hay. During processing, they received a feedlot tag and growth implant and were vaccinated and treated for parasites. Heifers were then blocked by arrival BW and randomly assigned to one of 2 treatments (10 pens/treatment, approximately 75 heifers/pen). Treatments consisted of a diet containing 1) monensin, tylosin, and Bovamine Defend (positive control, PC), or 2) NaturSafe at 18 g/head/d without monensin, tylosin, and the DFM. Diets were fed twice daily with heifers receiving half of the daily dose of treatment in the TMR at each feeding. Cattle were harvested on d 125 and 146 (5 pens per treatment per day). At the abattoir, fecal swabs and subiliac lymph nodes were obtained from 400 animals (200/treatment, 20/pen). Fecal samples were subjected to selective culture for *Salmonella* and *E. coli* O157:H7 enumeration. Only *Salmonella* were enumerated from the lymph nodes. *Salmonella* isolates from feces and lymph nodes were analyzed for virulence (in vitro assay) and antibiotic (ceftiofur, enrofloxacin, and florfenicol) susceptibility. Statistical analyses were performed using ANOVA with Tukey's test for multiple comparisons. Compared to PC, cattle fed NaturSafe had a lower ($P < 0.05$) concentration of *Salmonella* in the feces (74%) and lymph nodes (86%). The fecal concentration of *E. coli* O157:H7 was decreased ($P < 0.05$) by 58%. *Salmonella* isolates from feces and lymph nodes were less ($P < 0.05$) virulent (68% and 66%, respectively) and associated with a decreased expression of *hil*A, a genetic regulator of *Salmonella* invasion into eukaryotic cells. *Salmonella* resistance to select antibiotics was decreased by 17 to 100% (fecal isolates) and 42 to 75% (lymph node isolates). Results from this study indicate that NaturSafe can be used as a pre-harvest food safety intervention in beef cattle when standard industry technologies like monensin, tylosin, and DFM are removed from conventional production diets.

Key Words: *Saccharomyces cerevisiae* fermentation product, cattle, pathogens

0604 Moxidectin residues in tissues of lambs submitted to three programs of gastrointestinal endoparasite control. A. L. G. Monteiro[1], C. H. E. C. Poli*[2], M. A. M. Fernandes[3], F. G. Reyes-Reyes[4], C. J. A. Silva[5], M. D. Bianchi[4], S. Gilaverte[1], and M. T. Peres[1], *[1]UFPR-Universidade Federal do Paraná, Curitiba, Brazil, [2]USU-Utah State University, Logan, [3]UFPR, Curitiba, Brazil, [4]Universidade Estadual de Campinas-UNICAMP, Campinas, Brazil, [5]Instituto Federal de SC, Camboriú, Brazil.*

Moxidectin (MOX) has been reported to induce parasite resistance promoted by frequent drug utilization. To determine dynamic concentrations of drug residues in different sheep tissues according to a gastrointestinal endoparasite control program, two experiments were performed. The first one aimed to determine the time it takes for the MOX concentration to reach the maximum residue limit (MRL) in lamb leg muscles (near the site of drug application (50 μg/kg)) and fat (500 μg/kg). For that, twenty-two lambs were slaughtered on 2, 4, 7, 14, 28, and 42 d after treatment (DAT) with a single dose of MOX (0.2 mg kg^{-1}/body weight). The second experiment aimed to quantify MOX residue in serum, muscle (near and far to the application site), fat, liver, and kidneys of suckling lambs subjected to three programs of endoparasite control: (T1) preventive treatment every 28 d, (T2) treatment when egg count per gram feces (EPG) was equal or higher than 700, and (T3) selective treatment by FAMACHA method (FMC). The experiment was performed in a completely randomized design. The lambs were slaughtered when they reached an average of 30 kg body weight, respecting the time of minimum withdraw period of 28 d. Before slaughtering, blood was collected. Two grams of each tissue was sampled. MOX extraction was based on QuEChERS method. MOX residue was determined using HPLC with mass spectrometry (LC-MS/MS). The depletion curve of MOX for muscle showed a high drug concentration at 2 DAT (1854.2 μg/kg ± 495.0) followed by rapid absorption of the drug at the site of administration, reaching a concentration below MRL at 5 DAT. Longer persistence of MOX was noted at the high concentration, reaching values below the MRL at 17 DAT. Only one sample of fat from the selective treatment group (FAMACHA) showed a concentration of MOX (586.3 $mL \cdot kg^{-1}$) above the MRL. No sample of serum showed MOX residue levels. Significant correlation was observed between MOX residue in fat and omental fat weight ($P < 0.05$; $r = 0.5310$), suggesting that animals with higher fat deposition may have increased residue persistence in their body. The production of suckling lambs with control of gastrointestinal endoparasites by selective (OPG and FAMACHA) or preventive methods (application every 28 d), considering the 28 d withdraw period, presents a low risk of incidence (less than 1%) of high concentration of MOX in muscle, fat, kidney, and liver.

Key Words: FAMACHA, EPG, sheep

0605 Shiga toxin-producing *Escherichia coli* on cattle hides and bacterial transfer from hides to carcasses in Midwestern commercial beef slaughter operations. A. McKiearnan*, N. Cernicchiaro, and M. Sanderson, *Kansas State University, Manhattan.*

Shiga toxin-producing *Escherichia coli* (STEC) are foodborne pathogens that carry Shiga toxin genes (*stx*1 or *stx*2) and can cause serious illnesses in humans. These bacteria, which are mainly shed in the feces of cattle, can contaminate beef carcasses during the hide removal and evisceration processes at harvest. Coliforms, including *E. coli*, are utilized as indicator organisms of fecal contamination of beef carcasses during in -plant processing. The objectives of this study were to determine the frequency of the major seven STEC O serogroups and their associated virulence genes on hide-on beef carcass samples and to determine the distributions of *E. coli* and coliform concentrations from cattle hides and carcasses in commercial slaughter operations. Samples were collected from four large commercial processing plants (two in the northern region and two in the southern region of the Midwestern U.S.), which were visited three times each during summer and fall of 2015. Twenty surface swabs were collected at each sampling station (hide-on, pre-wash, pre-evisceration, post-evisceration, and final product) during each plant visit. Hide-on samples were enriched in *E. coli* broth, subjected to immunomagnetic separation, plated on STEC selective media, and confirmed by PCR. Dilutions from hide-on and carcass samples were plated on *E. coli*/coliform 3M Petrifilm plates. The proportion of positive hide-on samples during summer months was 1.3% for STEC O26, 2.1% for STEC O103, 0.4% for STEC O145, and 21.7% for STEC O157, and no positive samples for STEC serogroups O45, O111, and O121. The proportion of positive fall hide-on samples was 0.8% for STEC O26, 0.8% for STEC O45, 0.4% for STEC O103, 0.8% for STEC O145, and 5.0% for STEC O157, and no positive samples for STEC serogroups O111 and O121. There was a greater number of hide-on samples with higher *E. coli* and coliform concentrations compared to pre-wash samples, demonstrating potential transfer of fecal-origin contamination to the carcasses during hide removal. For pre-evisceration and post-evisceration samples, the number of enumerable samples and the distributions of *E. coli* and coliform concentrations varied by region; the role of evisceration in carcass contamination is unclear and possibly due to plant-to-plant variation. There were few enumerable samples for the final product (before split carcasses enter the cooler), which indicates successful application of

interventions by the processing plants. These data will be inputted into a quantitative microbial risk analysis to model the risk of human illnesses due to STEC along the beef chain.

Key Words: STEC

FOOD SAFETY SYMPOSIUM: THE SPECTRUM OF FOOD SAFETY IMPROVEMENT IN FOODS OF ANIMAL ORIGIN

0606 Have we improved food safety in live cattle?

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A number of technologies for reducing food-borne pathogens have been evaluated in live cattle, such as direct-fed microbials, vaccines, bacteriophages, and bactericidal feed ingredients. Many of these have been targeted to *E. coli* O157:H7, but efficacy in some cases has been variable, while regulatory approval of others has been less than forthcoming. As strategies to control *Salmonella* in live cattle have been even less successful, different approaches may be needed. For *E. coli*, Shiga-toxins are primary causative factors for human disease and are carried on prophages integrated into the bacterial genome. As transfer of these Shiga-toxin phages can convert previously nonpathogenic *E. coli* to pathogens and as these phages can be carried by other bacterial species, such as *Citrobacter freundii*, should we direct more future live animal food safety efforts to better controlling these endogenous phages? Fight phages with phages? Having a phage already integrated in the bacterial genome has been shown to block lysogeny by *stx*-carrying phages of the same species. Alternatively, as *E. coli* are commensal organisms in the bovine gastrointestinal tract and *E. coli* compete within the microflora for access to nutrients and valuable real estate, would it be possible to utilize the strategies of highly-competitive *E. coli* to suppress the growth of other *E. coli* with Shiga toxins? Could the safety of a direct-fed microbial containing a nonpathogenic but highly competitive strain of *E. coli* ever be assured? The CRISPR system evolved to protect prokaryote DNA from integration of viruses and plasmids. Could CRISPR-cas be used to block possible integration sites for Shiga-toxin phages in a highly-competitive nonpathogenic strain of *E. coli*? Should CRISPR-cas be used in this way? As contamination of hides is the primary route leading to contamination of meat; more emphasis on the control of pathogens on hides is warranted. A bacteriophage-based hide wash for control of *E. coli* O157:H7 has been approved by the USDA, but research data have been limited. However, a recent study by our laboratory demonstrated that non-O157 *E. coli* outweigh the pathogenic potential of O157 in feces of slaughter cattle, as serogroups such as O103 and O45 were relatively ubiquitous year-round and 55 to 65% of isolates of these serogroups carried Shiga toxins. New pre-harvest approaches that will more successfully control the gamut of current and potential bacterial pathogens in live cattle are warranted.

Key Words: Shiga toxins, *E. coli*, cattle

0607 Improving food safety in live swine.

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Swine can be colonized by a variety of foodborne pathogens that can be harmful to humans who consume contaminated pork products or who are exposed to waste from swine facilities. The most common foodborne pathogenic bacteria that are associated with swine and pork are *Salmonella* and *Campylobacter*. Illnesses in humans attributed to pork products have declined in recent years due to a tremendous effort put forth by the industry; however, the record is still not perfect. While illnesses still occur, steps such as implementing on-farm biosecurity procedures, reducing exposure to pathogens during transport, and lairage have reduced the horizontal spread of these important pathogens in live swine. The economic and public health significance of intervening to reduce pathogen incidence and transmission will be discussed along with methods under development and future research avenues. Actual and theoretical interventions, such as segregated early weaning, group housing, social stresses, reducing transport stress, limiting lairage exposure, bacteriophage, colicins, and sodium chlorate applications will be described. While challenges indeed remain, work to reduce pathogen carriage in live swine holds promise to reduce human pathogen exposures and resultant illnesses.

Key Words: human pathogen exposure, foodborne pathogens, health

0608 Characterization of zoonotic bacteria from dairy cattle in the era of genomics.

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Dairy farms are well-documented reservoirs for zoonotic pathogens. *Salmonella* spp., *Listeria monocytogenes*, Shiga-toxigenic *Escherichia coli*, and *Campylobacter* spp. are often excreted in the feces of cows, and it is common for infected cows to show no signs of illness and not be recognized as sources of human health risks. Historically, comparisons of bacterial isolates from animals and humans were made using molecular genotyping tools, such as pulsed-field gel electrophoresis and rep-PCR, or targeted sequencing techniques, like multilocus sequence typing. The discriminatory power of these tools has been exploited for strain differentiation and epidemiology tracing, the most widespread example being PulseNet. Decreased costs have made whole genome sequencing (WGS) a viable means of comparing the genomes of large numbers of bacterial isolates. Here, we describe several examples where we have used comparative genomics and

metagenomics to describe relationships between dairy-associated isolates and isolates from other sources and elucidate the ecology of pathogens in dairy farm environments. Genome analysis of 118 *Salmonella enterica* serotype Kentucky (*S.* Kentucky) isolates from dairy, poultry, and humans identified some of the poultry and bovine isolates as sequence type (ST) 152, but there was a phylogenetic distinction between the poultry and bovine isolates. The human isolates were primarily distantly related ST198 strains. Three of the dairy isolates were ST198, suggesting that dairy animals are a potential reservoir of this human pathogen. We further compared the fecal microbial communities of *S.* Kentucky-shedding and non-shedding cows to search for potential shifts in community composition associated with *S.* Kentucky carriage. No significant differences between the two groups were observed, suggesting that *S.* Kentucky is a transient commensal gut inhabitant. For *L. monocytogenes*, we sequenced the genomes of 128 isolates from dairy cows and bulk tank milk and compared them to human-associated *L. monocytogenes* isolates. Phylogenetic inference revealed a high level of diversity among the isolated strains. Multiple sequence and virulence types were identified, including at least four virulence types known to be responsible for large outbreaks. Based on a whole genome phylogenetic analysis, several isolates were closely related to human clinical isolates, such as the strain isolated in the 2011 cantaloupe outbreak that was responsible for multiple deaths. Decreased cost and increased access to WGS is radically changing the understanding of the ecology of bacterial populations. With WGS data, much more subtle changes are readily accessible compared with historic methods of distinguishing strains.

Key Words: *Salmonella*, *Listeria*, dairy

FORAGES AND PASTURE II

0609 Influence of forage diversity on feeding behavior and diet digestibility in lambs. S. Lagrange*[1,2], and J. J. Villalba[2], [1]*INTA EEA, Bordenave, Argentina,* [2]*Utah State University, Logan.*

Diverse combinations of forages with different nutrient profiles and classes of plant secondary compounds (PSC; tannins, saponins) may improve intake and nutrient utilization by herbivores. We tested the effects of increasingly diverse combinations of PSC-containing legumes on intake and diet digestibility in lambs. Freshly-cut birdsfoot trefoil (TRE), sainfoin (SAN), and alfalfa (ALF) at the early flowering stage were offered in ad libitum amounts to forty-two lambs in individual pens assigned to 7 treatments ($n = 6$): single species, a choice of all possible 2-way combinations, or a 3-way choice of the legumes. Composited forage and fecal samples and acid detergent lignin were used to determine in vivo DMD. The change in concentration of BUN from the beginning to the end of the study (24 d) (ΔBUN) was also assessed. Dry matter intake (DMI) and digestible DMI (DDMI) were analyzed as repeated measures designs with lambs (random effect) nested within treatments. A complete random design was used for the remaining variables with treatment as a fixed factor. Lambs preferred ALF > SAN > TRE in 70:30 and 50:35:15 ratios for 2- and 3-way combinations, respectively ($P < 0.05$). Average DMI and DDMI were 10% greater for 2- and 3-way choices than for single species (Table 1). Digestibility values of tannin-containing legumes (SAN and TRE) and their combination were greater than those recorded for the saponin-containing legume (ALF) or ALF/TRE (Table 1). Feeding SAN in a single diet or in combination had lower ΔBUN and greater fecal N/N consumed ratio (Table 1) than ALF, TRE, or ALF/TRE, suggesting a shift in the site of N excretion from urine

Table 0609.
Table 1.

Items	Treatments							SEM	CHOICE vs Single Diets P-Value
	ALF	SAN	TRE	ALF SAN	ALF/ TRE	SAN/ TRE	ALF/ SAN/ TRE		
DM,%	19.7^{a}	18.2^{ab}	16.6^{b}					0.67	
CP,%	16.5^{b}	13.4^{c}	19.3^{a}					0.42	
ADF,%	31.1^{b}	39.3^{a}	31.6^{b}					1.13	
DMI, gr/Kg BW/d	35.9^{ab}	32.4^{b}	27.4^{c}	37.8^{a}	34.3^{ab}	33.5^{ab}	36.0^{ab}	1.88	0.0217
DMD,%	59.3^{d}	68.1^{a}	65.7^{b}	64.2^{b}	61.6^{c}	68.4^{a}	64.6^{b}	0.67	0.5450
DDMI, gr/Kg BW/d	21.3^{b}	22.1^{ab}	18.0^{c}	24.3^{a}	21.0^{b}	22.9^{ab}	23.2^{ab}	1.12	0.0087
Fecal N/N consumed	0.33^{cb}	0.38^{a}	0.28^{d}	0.35^{b}	0.32^{c}	0.35^{b}	0.34^{cb}	0.01	0.3390
ΔBUN, mg/dL	-1.0^{bc}	-4.2^{d}	2.3^{a}	-1.7^{dc}	1.7^{ab}	-0.3^{abc}	0.0^{abc}	1.18	0.3457

Means in a row with different superscripts differ (P < 0.1).

to feces. Combinations of PSC-containing legumes have the potential to enhance intake and digestibility while shifting N loses to feces relative to some legume monocultures.

Key Words: diet mixing, plant secondary compounds, intake

0610 Nutritive quality and forage yield of three *Brassica* varieties for use in livestock grazing systems.

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Brassicas are gaining popularity as high-quality forage for pasture-based livestock producers due to their use to extend the fall grazing season and during the summer forage slump. Little research has been conducted to evaluate forage yield and nutritive value of brassica species. A study was designed to compare forage yield and nutrient composition of 'Barsica' rapeseed (*Brassica napus*), 'Inspiration' canola (*B. napus*), 'Appin' turnip (*B. rapa*), and 'KB Supreme' annual ryegrass (*Lolium multiflorum*). The study was conducted as a completely randomized block (n = 4) design at The Pennsylvania State University Russell Larson Agricultural Research Farm in Rock Springs, PA. Plots were drilled (Wintersteiger Plotseed XL, Salt Lake City, UT) into a prepared seed bed in August 2015 and fertilized with 71 kg N/ha. Potash, P, and lime were added according to soil tests. Forages were sampled biweekly during October and November using a 0.1-m^2 quadrat and clipped to 4 cm. Samples were dried at 60°C using a forced-air oven for 48 h, ground to 1 mm using a Willey Mill (Thomas Scientific Inc., Philadelphia, PA), and submitted to Dairy One Laboratories (Ithaca, NY) for wet chemistry analysis. Statistical analysis was conducted using Proc GLIMMIX (SAS Inc., Carey, NC) with $\alpha = 0.05$. Forage yield was not different among brassicas (1023 ± 108.5 kg DM/ha), which were greater ($P \leq 0.0001$) than ryegrass (242 ± 108.5 kg DM/ha). Although CP was greater ($P < 0.032$) in ryegrass than the brassicas (33.1 vs. 29.2 ± 1.44%), degradable and soluble protein fractions were lower ($P < 0.032$) in ryegrass than all brassicas (76 vs. 84 ± 0.71% and 49 vs. 53 ± 1.12%, respectively). Brassicas contained similar NDF and ADF concentrations (18.7 ± 0.94 and 14.4 ± 0.77%, respectively) but were lower ($P < 0.0001$) than ryegrass (35.4 ± 0.94 and 17.5 ± 0.77%, respectively). Both canola and rapeseed had greater ($P < 0.001$) NE_M and NE_L (1.65 ± 0.02 and 1.72 ± 0.01 Mcal/kg, respectively) than turnip or ryegrass (1.45 ± 0.02 and 1.54 ± 0.01 Mcal/kg, respectively). Inclusion of brassicas in a cool-season pasture rotation has the potential to increase animal productivity and reduce the need for stored feed during periods of perennial cool-season forage shortages, including mid-summer and late fall.

Key Words: *Brassica*, forage, grazing

0611 Effect of early intensive grazing of Kentucky bluegrass on animal performance.

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Kentucky bluegrass (*Poa pratensis* L.), a perennial, cool-season grass, is increasingly dominating pastures in the northern Great Plains, compromising pasture quality due to declining forage quality in the summer months when compared with native forages. Timed grazing can impact plant species and can shift plant communities to a more desired state. A grazing study was conducted at the Central Grassland Research Extension Center, North Dakota, to compare the effect of early-intensive grazing with season-long grazing on Kentucky bluegrass production and on grazing animal performance. Six pastures were assigned to one of two treatments: early intensive grazing and season-long grazing. All pastures were stocked with yearling beef heifers (340 ± 35 kg) at a moderate stocking rate before Kentucky bluegrass reaching the two-leaf stage. The early intensive treatment was grazed for 1.2 mo with a stock density of 0.39 animal units per hectare (AU · ha^{-1}), equivalent to a stocking rate of 0.46 animal unit months per hectare (AUM · ha^{-1}). The season-long treatments were grazed for 4 mo with a stock density of 0.12 AU · ha^{-1}, which is also equivalent to a moderate stocking rate of 0.46 AUM · ha^{-1}. Heifers were removed from the early-intensive treatment when 30% of native vegetation had received some grazing. Due to the shortened grazing time period, stocking density was more than three times higher on the early-intensive treatment. Heifers gained more ($P \leq 0.05$) in season-long pastures, with a corresponding weight loss on the early intensive treatment (0.16 vs. −0.45 kg · d^{-1}, respectively) in 2015. Results from this study show that early intensive grazing negatively influenced animal performance through weight loss and overall lower average daily gains when compared with season long grazing. The production of *P. pratensis* can vary widely in the northern Great Plains, depending on soil and spring moisture conditions; therefore, additional research on utilizing yearling beef cattle to spring graze *P. pratensis* will continue to document animal performance in response to this grazing treatment.

Key Words: early intensive grazing, grazing, heifer, invasive, Kentucky bluegrass, yearling

0612 Frequency of feeding distillers dry grain with solubles as a supplement to beef cows grazing corn residue.

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This study was conducted to evaluate the effects of delivery frequency of distillers dried grains with solubles (DDGS) as a supplement to cows grazing corn residues in the northern

Great Plains. The 36-d study was conducted in the fall of 2015, with 80 first and second calf cows (520 ± 34.5 kg BW). Ten cows were assigned to one of eight paddocks (4 ha each) of corn residue. Four applied treatments with two replications per treatment were no DDGS supplementation (control), DDGS fed daily, DDGS fed every third day, and DDGS fed every sixth day. The DDGS was fed at 0.35% BW per day. Body weight and body condition scores were recorded on two consecutive days at the beginning and end of the study. All cows had ad libitum access to water and a mineral supplement. After corn harvest, corn grain drop was estimated by counting the number of ears on the ground in three 30.5 m rows. Gusty winds in excess of 90 km · h^{-1} before harvest resulted in approximately 1004 kg · ha^{-1} of corn grain on the ground. Above normal temperatures were encountered through the six week course of the study. Average daily gain was greater ($P < 0.05$) following daily (1.57 ± 0.12 kg) and every third day supplementation (1.62 ± 0.12 kg) relative to control (1.22 ± 0.12 kg) or every sixth day supplementation (1.19 ± 0.12 kg). Body condition score change was greater ($P < 0.05$) following daily supplementation (0.7 ± 0.08) relative to every sixth day supplementation (0.4 ± 0.08). There was no difference ($P > 0.05$) in BCS change among control cows and cows supplemented daily or every third day. These results show that under certain conditions, such as mild weather and high grain drop, cows grazing corn residue may not require supplementation. Dried distillers grains with solubles can be supplementally fed every third day to reduce winter labor costs, with no detrimental effects to animal performance.

Key Words: beef cattle, corn residue, dried distillers grains with solubles

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0613 Development of an automated system for measuring supplement intake of grazing animals.

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The objective of this research was to develop and test an automated supplement intake measurement system (SmartFeed, SF), which can be used to measure individual animal supplement intake, behavior, and allow for control of supplement intake to grazing animals. The SF was developed by C-lock Inc., Rapid City, SD, and was designed using a stainless steel feed bin (79 by 71 by 86 cm) that included two weigh cells suspending the bin at two points, an RFID reader and antenna, an adjustable metal framework to limit access to animals at one time, and a data acquisition system that recorded RFID tags and feed bin weights at 1 Hz. A locking door can be added to future SF to control access for individual animals, but the prototype tested in this research did not limit supplement intake. The SF weighs about 100 kg and is self-contained and portable. Over a 14-d test period, 16 RFID-tagged steers (256 ± 31 kg mean BW) grazing dormant native range pasture in Oklahoma had ad lib, 24-h access to SF. The supplement provided in SF was 55% supplements (80% soybean meal and 20% soybean hulls, as-fed basis) and 45% fine mixing salt (as-fed basis) as an intake limiter. During testing, it was determined that SF must be placed on level ground and firmly anchored because the animals will move it if possible. The herd tended to visit SF as a group and exchanged places at the feeder frequently rather than spacing visitation over the day and/or consuming supplement in series. The major considerations for data processing included accounting for rapid animal exchanges at the feeder and weigh scale noise that resulted from animals pushing on the feed bin. Mean daily supplement intake was 1.15 ± 0.50 kg per animal (as-fed basis). The high CV (43%) indicated that considerable variation in daily supplement intake among group-supplemented steers exists. However, the Pearson correlation coefficient between mean daily intake during wk 1 vs. 2 was 0.84, indicating that the ranking of supplement intake was somewhat consistent between weeks. Overall, SF has the potential to measure and, in the future, control individual animal supplement intake in grazing experiments. These capabilities can improve design flexibility and statistical power of experiments, and may have application in nutritional management of range livestock.

Key Words: automation, grazing, supplement intake

0614 Sampling corn silage in bags from the sides.

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Because composition variation in silo bags is expected along the tube, and as nutritionists need to know forage composition before it is consumed, it is necessary to collect representative samples from the sides of the tube. The aim of the study was to determine if the composition of the side samples was similar to that of the face samples. Seven corn silage bags in dairy farms in Cordoba and Santa Fe provinces (Argentina) were sampled. Duplicate samples were taken from 5 different areas of the face of the bag (F1) with a core sampler. Then, 2 to 4 samples from both sides, 2 m forward in the bags, were taken (S). When the front achieved the same place where the side samples were taken, the newly exposed face was sampled again as in F1 (F2). After sampling, samples were stored in a refrigerated box for the rest of the day and sent to the same commercial laboratory to determine percentages of DM, NDF, ADF, CP, and ash by NIR. Nutrient composition of corn silage in F2 and S was compared using a mixed procedure of InfoStat, with silage bag as a random effect and sampling site as a fixed effect. Mean DM percentage (31.8 ± 4.0%) was inside the recommended range for corn silage, although the 80% range is lower than recommended, indicating early cuttings compared to optimum. The other nutrients were in accordance to typical values of corn silage. When evaluating different areas in both F1 and F2, no

Table 0614.

Table 1: Effect of sampling site on nutrient composition in corn silage

Nutrient	F2		S		*P*-value
	Mean	SE	Mean	SE	
DM (%)	32.0[a]	1.65	31.7[a]	1.66	0.3241
NDF (%)	46.6[a]	2.02	46.3[a]	1.94	0.7690
ADF (%)	27.6[a]	1.48	28.1[a]	1.53	0.4415
CP (%)	8.2[a]	0.46	7.8[b]	0.47	0.0001
Ash (%)	5.6[a]	0.27	5.6[a]	0.28	0.8948

Means within rows followed by the same letter are not significantly different (P ≥ 0.05).

differences were found for nutrient composition accounting for the silage bag and type of face (F1 and F2) as random effects. No differences between F2 and S were found in DM, NDF, ADF, and ash content, although CP levels showed different values in the side samples (Table 1). Our results showed that side samples are representative comparing them with the front of the bag regarding most nutrients. Nevertheless, more research is needed to determine a complete side sampling methodology for bagged silage.

Key Words: bagged corn silage, nutrient composition, sampling

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0615 Survey of temporal variation in pasture mineral concentrations and total dietary mineral intake in pasture-based dairy herds. F. Curran*[1,2], D. Wall[3], P. Lonergan[2], and S. Butler[1], *[1]Animal & Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland, [2]School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, [3]Teagasc Crops, Environment and Land Use Program, Johnstown castle Co., Wexford, Ireland.*

In grass-based dairy production systems, grazed pasture represents the sole feed for long periods. Mineral concentrations in pasture vary depending on region, season, plant variety, and fertilization strategy. The objectives of this study were to: (i) benchmark the seasonal variation in pasture mineral concentrations, and (ii) determine the mineral nutritive value of both grazed grass and the total diet for lactating dairy cows. Spring calving dairy farms (n = 44) were selected based on region and soil type and enrolled on the study. Each farm was visited once in March, May, August, and October 2013. These visits were selected to coincide with expected changes in the grass morphology and growth rate from the start (March) to the end (October) of the grazing season. During the week before each visit, pre-grazing grass samples were cut daily for 7 d to a stubble height of 4 cm. At each visit, the grass samples and samples of any other feeds being consumed (silage, concentrate, and other miscellaneous feedstuffs) were collected, and the proportion of each feedstuff in the diet was recorded. The daily grass samples were then mixed to form one composite sample, representative of grass offered to the herd during the preceding week. All samples from each farm were analyzed for mineral concentrations using inductively coupled plasma mass spectrometry (ICP–MS). The mean, range, and standard deviations for each sample analyzed were calculated across the study farms at each time-point. Pasture mineral concentrations did not vary greatly over the four sampling points, with the exception that mean Se concentration was greater at the first sampling time point (0.21 ± 0.18 mg/kg) compared with all other sample collection times (0.04 ± 0.03, 0.07 ± 0.04, 0.03 ± 0.04 mg/kg on visits 2, 3, 4, respectively). On average (range in parentheses), a pasture-only diet would have provided 90% (45–130), 80% (30–125), 50% (8–190), 65% (30–77), and 30% (3–108) of the requirements for lactating cows (National Research Council, 2001) for P, Cu, I, Zn, and Se, respectively. When total dietary mineral intakes were estimated, on average, the diet provided 96%, 153%, 359%, 109%, and 58% of the lactating cow requirements for P, Cu, I, Zn, and Se, respectively. We conclude that, on average, pasture grown on Irish dairy farms is inadequate for P, Cu, I, Zn, and Se to meet cow requirements when fed as the sole feed.

Key Words: minerals, pasture, dairy

0616 Observations of forage yield and steer average daily gain when double cropped forage following crop harvest. K. M. Ulmer*[1], R. G. Bondurant[1], J. L. Gramkow[1], G. W. Lesoing[2], M. E. Drewnoski[1], and J. C. MacDonald[3], *[1]University of Nebraska, Lincoln, [2]University of Nebraska, Auburn, [3]University of Nebraska-Lincoln, Lincoln*.

Two experiments were conducted to evaluate yield of annual forages planted after harvest in cropping systems and to determine the grazing potential. In Experiment 1, a brassica-based 5-species mix was drilled following wheat harvest on August 17 in yr 1 and August 15 in yr 2. Aboveground forage production measured in late October was 2,257 ± 270 and 3,991 ± 270 kg DM/ha in yr 1 and 2, respectively. In both years, land was split into three 2-ha paddocks and stocked according to aboveground forage yield at 909 kg DM per steer. In yr 1, 15 steers (initial BW = 205 kg [SD 16]) were divided into 5 hd groups and grazed for 48 d. In yr 2, 26 steers (initial BW = 266 kg [SD 4]) were divided into 8 to 10 hd groups and grazed for 52 d. Grazing began in mid November and ADG was 1.00 ± 0.019 and 0.70 ± 0.073 kg/hd in yr 1 and 2, respectively. In Experiment 2, half of a corn field was harvested as corn silage (CS) and half as high-moisture corn (HMC). In yr 1, a mix of oats and turnips was drilled on September 9 after CS harvest yielding 1,047 ± 65 kg/ha, and on September 18, the same mix was drilled after HMC yielding 487 ± 117 kg/ha in late October. In yr 1, there was no grazing of the oat–turnip mixture due to herbicide restrictions. In yr 2, oats were drilled on September 3 after CS harvest yielding 3,200 ± 93 kg DM/ha whereas oats drilled on September 17 after HMC harvest yielded 586 ± 95 kg DM/ha. In yr 2, grazing began in mid November with 2 groups of 10 steers per treatment (initial BW = 212 kg [SD 74]) grazing for 62 d. Steers grazing after CS were allocated 795 kg oat forage DM/hd. Steers grazing after HMC were allocated 181 kg oat forage DM and 1,229 kg corn husk and leaf DM per hd. Steer ADG did not differ ($P = 0.27$, SEM = 0.12) among treatments, 0.50 and 0.33 kg for CS and HMC, respectively. Gain per hectare of HMC (109 kg) and CS (153 kg) did not differ ($P = 0.15$, SEM = 1.07). Fall forage production after grain harvest is sufficient to provide cover and adequate forage for growing calves.

Key Words: average daily gain, brassicas, cover crop forages

0617 Banana tree (*Musa sapientum*) forage in sexed Guinea pig (*Cavia porcellus*) fattening. A. R. Sanchez*, *Universidad Tecnica Estatal de Quevedo, Quevedo, Ecuador*.

This research was performed in La Mana canton, in the southeast of Cotopaxi province, whose geographical location is 0°45′35″ S and 7°09′32″ W at an altitude of 240 m above the sea level. The objectives were 1) to determine the effect of Savoie grass (*Panicum maximum* Jacq.) and banana tree leaves (*Musa sapientum*) consumption on guinea pig productive behavior, 2) to determine the effect of sex on guinea pig productive behavior, and 3) to determine treatment yield. A factorial arrangement 2 (forages) × 2 (sexes) within a complete randomized block design with six repetitions was applied. To determine rate differences, a Turkey test ($P \leq 0.05$) was applied and the cost–benefit relationship served as a basis for the economic analysis. Forage consumption, food consumption, live weight (LW), weight gain (WG), food conversion index (FCI), carcass weight (CW), carcass yield (CY), and rent were evaluated. The highest forage consumption (55.40 g MS animal^{-1} d^{-1}), LW (841.11 g.), WG (8.78 g. animal^{-1} d^{-1}), FCI (7.96), CW (598.06 g), and CY (71.0%) were registered for savoie-based treatments. The male guinea pig reported the highest LW (826.00 g.), WG (8.57 g animal^{-1} d^{-1}), FCI (7.96), and CW (576.25 g.), whereas differences among treatments ($P < 0.05$) were shown: savoie per male interaction was significant ($P < 0.05$) for LW (881.0 g.), WG (9.63 g animal^{-1} d^{-1}), FCI (7.01), CW (639.00 g.), CY (72.5%), and 48.3% profitability. Results demonstrate that using tropical forage resources contributes to guinea pig fattening in the studied zone.

Key Words: forage, grasses, feeding, nutrition, guinea pigs

0618 Effect of frame size and season on enteric methane (CH_4) and carbon dioxide (CO_2) emissions in Angus brood cows grazing native tallgrass prairie in central Oklahoma. J. P. S. Neel*, K. E. Turner, P. H. Gowda, and J. L. Steiner, *USDA-ARS-PA-GRL, El Reno, OK*.

A reduction in enteric CH_4 production in ruminants is associated with improved production efficiency. Enteric CH_4 and CO_2 production associated with the livestock industry is of interest due to the impact these emissions might have on global climate change. Our objective was to evaluate the effect of cow frame size (FS) and season on enteric CH_4 and CO_2 production in cattle grazing during summer and fall. Twenty-eight Angus cows (545 ± 49 kg BW) of either medium ($n = 14$) or large FS ($n = 14$) and grazing simultaneously within a native tallgrass prairie pasture in central Oklahoma were used to estimate individual animal enteric CH_4 and CO_2 production daily (via a commercially available breath analyzer) over the summer and fall seasons. Cow FS was categorized based on frame scores generated from individual hip heights. Summer and fall season designations were based on summer and winter solstices and the fall equinox. Statistical analyses were conducted using GLM of SAS. The model included class effects of FS and season and their interaction. As measured at the beginning of the experiment, large-FS cows were heavier ($P < 0.001$) and had a greater frame score ($P < 0.001$) compared with medium-FS cows (609 vs. 480 kg and 6.8 vs. 4.6, respectively). As measured during the experimental period,

large-FS cows produced calves with heavier ($P < 0.01$) 205-d adjusted weaning weights (261 vs. 222 kg). There were no frame size × grazing season interactions with regard to enteric gas production. Large-FS cows produced greater ($P < 0.001$) enteric CH_4 (280 vs. 248 g/d) and CO_2 (9,065 vs. 8,021 g/d) than medium-FS cows. Cows produced higher ($P < 0.001$) amounts of enteric CH_4 and CO_2 in summer than in fall (292 vs. 236 g/d and 9,065 vs. 8,021 g/d, respectively). When expressed as total production (over the entire summer and fall seasons) of CH_4 or CO_2 per weight unit of weaned calf, enteric gas production did not differ between large- and medium-FS cows (0.20 vs. 0.21 kg/kg and 6.4 vs. 6.6 kg/kg, respectively). Further research is needed to relate enteric gas production to herbage nutritive value and animal DMI.

Key Words: beef cows, enteric methane, native prairie

0619 Grazing management: milk production and composition of dairy cows grazing elephant grass.

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The objective of this experiment was to evaluate the effects of strategies of rotational grazing management on milk yield and composition of dairy cows grazing elephant grass (*Pennisetum purpureum* Schum. cv. Cameroon) from December 2015 to February 2016. Treatments corresponded to management strategies characterized by the pregrazing targets of 95% and maximum canopy light interception during regrowth (equivalent to 100 and 135 cm; $LI_{95\%}$ and LI_{Max}, respectively). The postgrazing target was the same and corresponded to 50% of the pregrazing height. Midlactation Holstein × Jersey cows were separated into two groups according to BW, days in milk, age, lactation number, and daily milk yield. The 2.5-ha experimental area was divided up into two sets of 18 paddocks (700 m^2). Twenty-two cows (487.5 ± 13.1 kg) were used as testers and a variable number was used to adjust stocking rate. Milking was performed twice a day at 0500 and 1530 h, milk yield was measured in a daily basis, and milk composition was measured at 10-d intervals. The amount of concentrate mix fed to cows was based on the average milk production for the groups (1 kg of concentrate:3 kg of milk) and offered in two daily individual meals just before milking. The effective values of pre- and postgrazing heights were 100.8/50.5 and 135.6/68.6 cm with average stocking rates of 9.2 and 6.0 cows/ha for $LI_{95\%}$ and LI_{Max}, respectively. The results were analyzed using the PROC MIXED of SAS ($\alpha = 0.05$). Management based on the $LI_{95\%}$ target resulted in an 18.5% increase in milk production (19.2 vs. 16.2 kg of 3.5% fat corrected milk cow^{-1} d^{-1}), lactose (854 vs. 710 g d^{-1}), protein (578 vs. 519 g d^{-1}) and fat yield (677 vs. 569 g d^{-1}), despite no difference in fat content. Protein content was higher for LI_{Max} (3.28 vs. 3.07%) and urea N was higher for $LI_{95\%}$ (13.17 and 11.83 mg dL^{-1}). The results suggest that the $LI_{95\%}$ pregrazing target correspond to a better management strategy because it resulted in increased milk and milk solids production per cow and stocking rate, resulting in increased productivity.

Key Words: light interception, tropical grass, grazing management

Table 0620.

Table 1. Effects of traditional pasture (control) or spring available annual forage crops (SpAFC) on animal performance, plasma metabolites, and ruminal fermentation profile

	Treatments			
Item	Control	SpAFC	SEM	*P*-value
Pasture intake, kg/d	8.10	7.49	0.45	0.20
TMR intake, kg/d	10.9	10.7	0.13	0.13
Total DMI, kg/d	18.9	18.1	0.44	0.08
ADG, kg/d	0.56	0.77	0.14	0.15
Milk yield, kg/d	25.2	23.1	1.24	0.23
Milk fat, %	4.15	3.89	0.26	0.50
Milk fat, kg/d	1.02	0.92	0.09	0.45
Milk true protein, %	3.53	3.63	0.12	0.54
Milk true protein, kg/d	0.86	0.85	0.05	0.83
MUN, mg/dL	13.1	14.7	0.55	0.06
Plasma urea-N, mg/dL	11.9	12.2	0.79	0.66
Plasma NEFA, mEq/L	176	174	5.12	0.72
Ruminal total VFA, m*M*	73.1	75.1	6.40	0.77
Ruminal acetate, mol/100 mol	70.0	69.8	0.79	0.74
Ruminal propionate, mol/100 mol	16.2	16.5	0.50	0.66
Ruminal butyrate, mol/100 mol	11.3	11.1	0.42	0.64

0620 Performance and rumimal metabolism are not changed in lactating dairy cows offered spring available annual forage crops during a short-term grazing experiment. K. A. Juntwait*, A. F. Brito, K. S. O'Connor, R. G. Smith, K. M. Aragona, C. P. Ghedini, and A. B. D. Pereira, *University of New Hampshire, Durham*.

Spring available annual forage crops (AFC) can potentially be used to extend the grazing season by increasing pasture production. We aimed to determine the impact of spring available AFC on pasture production and animal performance during a short-term grazing experiment. Fourteen multiparous and 2 primiparous lactating organically certified Jersey cows were randomly assigned to either a traditional legume–grass pasture mix (control treatment; $n = 8$ cows) or a spring AFC mix of wheat, triticale, barley, cereal rye, and hairy vetch strip-tilled into a traditional pasture (SpAFC treatment; $n = 8$ cows). The botanical composition (DM basis) for the control averaged 70% grasses, 17% legumes, and 13% other (broadleaf, weeds, and dead), whereas that for SpAFC averaged 60% grasses, 14% legumes, 13% AFC grasses, 4% AFC legumes, and 9% other. Cows averaged 433 ± 48 kg of BW and 83 ± 50 DIM for the control group and 416 ± 46 kg of BW and 86 ± 43 DIM for the SpAFC group. A 14-d adaptation period was followed by a 7-d sampling period. Pasture nutrient composition during the sampling period averaged 16.0 and 15.1% CP, 53.3 and 56% NDF, and 34.6 and 32.1% ADF for the control and the SpAFC, respectively. Pasture biomass averaged 3,038 ± 303 and 4,052 ± 353 kg of DM/ha for the control and SpAFC, respectively. Cows were fed a total mixed ration (TMR) and milked twice daily and had access to a new strip of pasture after the afternoon milking. Pasture intake was estimated using chromium oxide and IVDMD. Ruminal fluid was sampled using an esophageal tube immediately after the morning milking with samples analyzed for VFA. Results are shown in Table 1. There were no significant differences in pasture and TMR intake comparing the control with SpAFC, but a trend ($P = 0.08$) was observed for increased total DMI (+0.8 kg/d) in cows fed the control treatment. Contents and yields of milk and milk fat and protein and ADG did not differ between treatments. A trend ($P = 0.06$) for greater MUN was observed with feeding the SpAFC rather than the control treatment. No significant differences were observed in the plasma concentrations of urea N and NEFA or in the ruminal concentration of total VFA. Strip-tilling spring available AFC into a perennial grass–legume pasture mix increased herbage biomass production and did not affect animal performance of lactating Jersey cows in the Northeastern United States.

Key Words: annual forage crops, dairy cows, grazing

0621 Performance and ruminal metabolism in lactating dairy cows offered summer available annual forage crops during a short-term grazing experiment. K. A. Juntwait*, A. F. Brito, K. S. O'Connor, R. G. Smith, K. M. Aragona, C. P. Ghedini, and A. B. D. Pereira, *University of New Hampshire, Durham*.

Summer available annual forage crops (AFC) have the potential to increase pasture production during times of heat and drought in the Northeastern United States. The objective of this study was to determine the impact of summer available AFC on pasture production and animal performance during a short-term grazing experiment. Sixteen multiparous and 4 primiparous organically certified lactating Jersey cows were randomly assigned to 1 of 2 treatments: traditional legume–grass pasture mix (control; $n = 10$ cows) or a summer AFC

Table 0621.

Table 1. Effects of traditional pasture (control) or summer available annual forage crops (SuAFC) on animal performance, plasma metabolites, and ruminal fermentation profile

	Treatments			
Item	Control	SuAFC	SEM	*P*-value
Pasture intake, kg/d	8.26	8.75	0.73	0.51
TMR intake, kg/d	11.2	11.6	0.38	0.32
Total DMI, kg/d	19.6	20.3	0.82	0.41
ADG, kg/d	0.65	0.57	0.22	0.71
Milk yield, kg/d	17.1	17.0	0.60	0.86
Milk fat, %	4.43	5.02	0.14	<0.01
Milk fat, kg/d	0.78	0.93	0.04	0.02
Milk true protein, %	3.49	3.73	0.08	0.05
Milk true protein, kg/d	0.61	0.69	0.03	0.05
MUN, mg/dL	11.8	10.8	0.39	0.09
Plasma urea-N, mg/dL	10.6	8.92	0.49	<0.01
Plasma NEFA, mEq/L	174	168	6.88	0.34
Ruminal total VFA, m*M*	5.34	5.07	7.37	0.95
Ruminal acetate, mol/100 mol	71.8	71.8	0.81	0.92
Ruminal propionate, mol/100 mol	15.5	15.6	0.31	0.71
Ruminal butyrate, mol/100 mol	10.6	10.5	0.40	0.93

mix of millet, teff, buckwheat, oats, and chickling vetch strip-tilled into a traditional pasture (SuAFC; n = 10 cows). The botanical composition (DM basis) for the control averaged 69% grasses, 11% legumes, and 20% other (broadleaf, weeds, and dead), whereas that for SuAFC averaged 61% grasses, 13% legume, 1% AFC grasses, 2% AFC legumes, 12% AFC broadleaf, and 11% other. Cows averaged 434 ± 46 kg of BW and 146 ± 61 DIM for the control and 449 ± 53 kg of BW and 140 ± 57 DIM for the SuAFC. A 14-d adaptation period was followed by a 7-d sampling period. Pasture nutrient composition during the sampling period averaged 12.9 and 14.8% CP, 53.1 and 50.1% NDF, and 35 and 38.8% ADF for the control and SuAFC, respectively. Pasture biomass averaged 2,774 ± 275 and 2,588 ± 272 kg of DM/ha for the control and SuAFC, respectively. Cows were fed a total mixed ration (TMR) and milked twice daily and had access to a new strip of pasture after the afternoon milking. Pasture intake was estimated using chromium oxide and IVDMD. Ruminal fluid was sampled using an esophageal tube immediately after the morning milking with samples analyzed for VFA. Results are shown in Table 1. There were no significant differences in pasture, TMR, total DMI, ADG, and milk yield between the control and SuAFC. Milk fat and protein concentrations and yield were all significantly greater in cows offered SuAFC than in cows offered the control. A trend (P = 0.09) for lower MUN in cows fed SuAFC vs. cows fed the control treatment was observed. Cows offered SuAFC had less (P < 0.01) concentration of plasma urea N than those offered the control. Ruminal concentrations of total VFA and plasma NEFA did not differ between treatments. Strip-tilling summer available AFC into perennial grass–legume pasture mix did not change pasture biomass production compared with the control but increased the concentrations and yields of milk fat and protein.

Key Words: annual forage crops, dairy cows, grazing

0622 Fluctuation of soil carbon dioxide emission in agrosilvopastoral system managed with sheep.

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The burning of fossil fuels and the misuse of land in the agricultural sector has been raising the concentration of carbon dioxide (CO_2), which causes global temperature rise causing climate imbalance. The use of integrated systems such as agrosilvipastoral is vitally important in mitigating this gas. This research aimed to evaluate the CO_2 in soils intercropped with corn and Massai grass with subsequent implementation of a silvopastoral system with sheep grazing. The experiment was performed at Sao Paulo State University in Brazil from April to May 2012 and February 2013 to September 2014. Carbon dioxide emissions were assessed weekly from soil on intercropping corn and Massai grass 15 d before the corn harvest and 1 mo after. Carbon dioxide assessments were also performed every 15 d in three different treatments: silvopastoral Massai grass with eucalyptus spacing by 6.0 by 1.5 m with grazing assess, silvopastoral Massai grass with eucalyptus spacing by 12.0 by 1.5 m, and Massai grass without eucalyptus system with grazing assess in a completely randomized design with repeated measures with two longitudinal factors (2 yr of evaluations and two seasons: dry and rainy season). The CO_2 emission on intercropping corn and Massai grass remained constant a week after harvesting of maize with an average of 2.43 μmol CO_2 $m^{-2}{\cdot}s^{-1}$. Two weeks after the harvest, there was reduction in CO_2 emissions of 34.98% or 0.85 μmol CO_2 $m^{-2}{\cdot}s^{-1}$. The average flux of CO_2 emission in the silvopastoral system did not differ between treatments (P > 0.05). In the summer (rainy season), there were higher CO_2 emission values compared with the winter (dry season) (P < 0.05), with a reduction of 44.46%, or 2.33 μmol $m^{-2}{\cdot}s^{-}1$, in the CO_2 emissions. Comparing the years of measure, we can denote that in the first year, there was the highest values of CO_2 emissions compared with the second year of measure (P < 0.05), with a reduction of 16.44%, or 0.73 μmol CO_2 $m^{-2}{\cdot}s^{-1}$. Therefore, the corn harvest reduces the emission of CO_2 in the soil. However, the introduction of trees in the pastoral system did not change the CO_2 emissions. The CO_2 emission was modified only by climatic factors. These results can be explained because the silvopastoral system was in an implementation phase when the eucalyptus trees had an average height between 1.7 and 4.7 m in first and second year, respectively, and were not providing the expected shading as the silvopastoral system.

Key Words: intermittent stocking, climatic changes, tropical pasture

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0623 Yield and quality evaluation of ensiled Johnsongrass as a potential forage for beef cattle.

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Johnsongrass (*Sorghum halepense*) is a nonnative invasive species that is commonly used for hay production. Johnsongrass could be ensiled to avoid long drying times associated with hay production. The objective of this study was to examine the nutritive value and digestibility of Johnsongrass conserved as silage when harvested at four maturity levels: 3-wk, boot, flower, and dough. A preexisting stand of Johnsongrass was split into 16 plots in May 2015 at the J. Phil Campbell Research Station at the University of Georgia in Watkinsville, GA. Each plot was then randomly assigned to one of the four treatments. After reaching the proper stage, botanical separation and growth stage data were collected before harvesting to obtain DM yield. During the growing season, two harvests were designated for ensilage. After these harvests, forage was allowed to

wilt to approximately 50% DM. Wilted forage was packed into mini-silos constructed with 90-cm lengths of 10-cm diameter polyvinyl chloride pipe. Forage was packed to a density of 2.4 kg/L. The silos were sealed and allowed to ferment for 10 wk. After fermentation, all samples were frozen until subsequent nutritive value and fermentation characteristics could be determined. Statistical analysis was performed in JMP (SAS Inst. Inc., Cary, NC) with treatment as a main effect and harvest date as a random variable. Treatment did not have a significant effect on DM yield ($P = 0.09$). Neutral detergent fiber, ADF, and lignin increased ($P < 0.001$) as maturity at harvest increased from 3-wk (52, 35, and 6.0%, respectively) to dough (62, 41, and 7.9%, respectively). However, CP and relative forage quality decreased ($P < 0.01$) as maturity at harvest increased from 3-wk (108 and 14.9%, respectively) to dough (86 and 12.2%, respectively). Forage maturity did not affect nonstructural carbohydrates ($P = 0.06$). After fermentation, pH was similar ($P = 0.06$) across maturities; however, total VFA and ammonia was greater ($P < 0.03$) for forage harvested at 3 wk (7.7 and 1.4%, respectively) compared with dough (5.7 and 0.9%, respectively). These data indicate that Johnsongrass can provide high-quality forage if not allowed to mature past the boot stage and can be ensiled, providing an alternate method of conservation.

Key Words: Johnsongrass, silage, digestibility

0624 Evaluation of warm-season annual forages on forage production and stocking rate.

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A 2-yr study was conducted to evaluate four warm-season annual forages in a southeastern forage-finishing beef production system. Forage treatments were brown midrib sorghum × sudangrass (*Sorghum bicolor* var. *bicolor* × *bicolor* var. *sudanense*) (BMR; Honey Graze/AS6201), sorghum × sudangrass (SS; Sugargrazer/AS5201), pearl millet [*Pennisetum glaucum* (L.) R. Br.] (PM; Tifleaf III), or pearl millet planted with crabgrass [*Digitaria sanguinalis* (L.) Scop.] (PMCG; Tifleaf III + Red River) planted at a seeding rate of 22.4, 22.4, 16.8, and 11.2 + 5.6 kg ha^{-1}, respectively. Sixteen pastures (0.81 ha) were assigned to one of four forage treatments in a randomized complete block design. Pastures were subdivided into two 0.405-ha paddocks for rotational grazing. British-cross beef steers ($n = 32$; 438 ± 49 kg) were stratified by weight and randomly assigned to 1 of the 16 pastures for forage finishing. Put-and-take grazing was used to maintain a forage allowance of 1,600 to 4,500 kg ha^{-1}. Pastures were grazed in 2014 and 2015 for 70 and 63 d, respectively. Forage yield was measured by clipping, in triplicate, a 4.3-m^2 area with a plot harvester on d 0 and every 14 d thereafter, whereas metabolic BW were measured on d 0 and every 34 d thereafter until termination of the trial. Statistical analysis was conducted using the MIXED procedure in SAS 9.4 (SAS Inst. Inc., Cary, NC) with main effects of treatment, year, and the interaction. Analysis of main effects revealed that DM yield in 2014 was greater for BMR and SS compared with PM and PMCG at d 0 ($P < 0.05$; 1,657, 1,958, 1,205, and 1,297 kg h^{-1}, respectively) and at d 14 ($P < 0.05$; 4,007, 4,670, 3,485, and 2,962 kg h^{-1}, respectively). In 2015, DM yield was greater at d 0 for BMR, SS, and PM compared with PMCG ($P < 0.05$; 2,548, 2,755, 3,016, and 2,039 kg h^{-1}, respectively) and at d 42 for BMR compared with SS, with PM and PMCG as intermediates ($P < 0.05$; 2,880, 1,577, 2,294, and 2,219 kg h^{-1}, respectively). Average daily gain was significantly ($P < 0.05$) higher for steers grazing BMR (0.90 kg/d) compared with steers grazing SS and PMCG (0.68 and 0.62 kg/d, respectively) but did not differ from steers grazing PM ($P > 0.05$; 0.79 kg/d). These findings suggest that BMR, SS, PM, and PMCG may all be used in beef cattle production systems but BMR may outperform SS, PM, and PMCG on the parameters of forage yield and animal performance.

Key Words: warm-season annual forages, beef, performance

0625 Microbiota attachment and structural components of *Lolium perenne* L. and *Festuca arundinacea* Schreb. during in vitro fermentation.

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The objective of this research was to evaluate the effect of lignin aggregation in *Lolium perenne* and *Festuca arundinacea* on microbiota attachment and cell wall components during in vitro degradation. Stages of senescence (0, 30, and 60%) were measured in summer and winter. Leaf tissue structure and cell wall components were studied using histochemistry technique. An in vitro fermentation test was performed during 72 h, and microbiota attachment to grass residues was studied using scanning electron microscopy. The experimental design was split plot, and PROC MIXED of SAS was used to evaluate the stage effect, whereas means were compared with a Tukey test. The central vein (CV) of 0% senescence showed higher lignified tissue in summer than in winter, whereas for 30 and 60% senescence, lignified tissue was higher in *Lolium* compared with *Festuca* ($P < 0.05$). The extension of the vascular

bundle sheath (EVBS) of the CV contributed the most to leaf lignification ($P < 0.05$). Senescence affected IVDMD, and total VFA production of *Lolium* and *Festuca* at 30% senescence was lower in winter, but in summer, is was higher compared with 60% senescence leaves ($P < 0.05$). Microbiota cell wall attachment was higher in 0% senescent leaves in both grasses, but in 30 and 60% senescent leaves, microbiota was reduced and attached to lignified walls of fibers and vessels of xylem ($P < 0.05$). It is concluded that leaves cell aging of *Lolium* appears as lignification of the EVBS with higher values in summer, whereas no differences were found in *Festuca*. The oldest leaves of *Festuca* showed higher NDF and ADF, which affected in vitro response and fermentative variables of the ruminal inoculum and microbiota attachment. As far as we know, this is the first contribution about tissue identification during leaf lignification of *Lolium* and *Festuca* in winter and summer.

Key Words: leaf structure, lignified tissue, microbiota attachment

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0626 Correlation of fermentation characteristics with intake and digestibility of alfalfa silage in gestating ewes. V. Niyigena*[1], K. P. Coffey[2], W. K. Coblentz[3], A. N. Young[1], D. Philipp[2], H. L. Bartimus[4], and R. T. Rhein[1], *[1]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [2]University of Arkansas, Division of Agriculture, Fayetteville, [3]U.S. Dairy Forage Research Center, Marshfield, WI, [4]Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO*.

Baled silage production provides benefits to farmers because it reduces leaf losses and requires a shorter wilting time, thereby limiting risks of exposure to rain compared with making hay. Our objective was to investigate the correlation of alfalfa silage fermentation parameters with intake and digestibility in gestating ewes. Alfalfa from 3 field blocks was baled in large round bales at a mean moisture concentration of 59.1 ± 4.30% and then wrapped with plastic on the day of baling or 1, 2, or 3 d after baling; this resulted in considerable variability in silage fermentation measurements. Following approximately 5 mo of storage, the alfalfa was chopped and then offered for individual ad libitum consumption by 16 gestating ewes (63.5 ± 1.71 kg average BW) where total feces were collected for 7 d following a 10-d dietary adaptation in each of 3 different periods. Diets were rerandomized to different ewes for each period such that ewes were not offered the same treatment in any period. Data were analyzed using PROC CORR of SAS to determine the correlation between alfalfa fermentation parameters with intake and digestibility measurements. Dry matter and OM intakes were positively correlated ($P < 0.05$) with silage moisture and lactic acid and propionate concentrations and negatively correlated ($P < 0.05$) with ADF concentrations. Dry matter and OM digestibilities were positively correlated ($P < 0.05$) with proportion of lactic acid to total acids (mol/100 mol) but negatively correlated ($P < 0.05$) with ADF concentration, and OM digestibility was also positively correlated ($P < 0.05$) with silage pH. Digestibility of ADF was positively correlated ($P < 0.05$) with silage pH but negatively correlated with water content, lactic acid, total acids, and propionate. Digestible DM and OM intakes (g/kg BW) were positively correlated ($P < 0.05$) with water content of silage, total silage acids, lactic acid, propionate, and butyrate. Therefore, managing alfalfa silage to ensure more desirable fermentation should also result in greater intake of digestible OM, which should improve overall energy status of ruminants. The study was supported in part by USDA-ARS specific cooperative agreement 58-3655-4-052.

Key Words: alfalfa, digestibility, fermentation

0627 A Bayesian approach to unmixed diet composition. N. Vargas Jurado*, K. M. Eskridge, and R. M. Lewis, *University of Nebraska-Lincoln, Lincoln*.

Accurately measuring diet composition is key to delineating feed efficiency, but under grazing conditions, doing so is challenging. Plant-wax markers can be used to estimate the composition of diet mixtures. However, traditional methodologies such as nonnegative least squares (NNLS) ignore variability in and relationships (covariances) between such markers. More recently, Bayesian hierarchical models for linear unmixing (BHLU) have been successfully used for estimating mixing proportions in hyperspectral image analysis

Table 0627.

Table 1. Efficiency of BHLU under four specifications and NNLS

Plant mixture	BDU	BDG	BCU	BCG	NNLS
NMSE					
2	14.4	52.2	11.0	34.0	23.2
3	25.3	66.1	25.1	45.7	39.2
8	321.1	417.1	210.4	463.3	431.8
CP					
2	0.97	0.74	0.91	0.76	0.72
3	0.98	0.89	0.98	0.85	0.73
8	0.18	0.16	0.12	0.17	0.17

and could be applied to estimate diet composition. The objective of the present study was to determine the efficiency of BHLU under five scenarios: 1) BHLU with no covariance and uniform priors, 2) BHLU with no covariance and Gaussian priors, 3) BHLU with covariances and uniform priors, 4) BHLU with covariances and Gaussian priors, and, for completeness, 5) NNLS. A simulation study was performed using *n*-alkane and long-chain alcohol concentrations measured on eight forage species in western rangelands: *Bouteloua gracilis*, *Bromus tectorum*, *Amorpha canescens*, *Schizachyrium scoparium*, *Hesperostipa comata*, *Bouteloua curtipendula*, *Melilotus officinalis*, and *Pascopyrum smithii*. Three mixtures were formed: 1) the two plants *M. officinalis* and *B. tectorum*; 2) the three plants *M. officinalis*, *B. tectorum*, and *B. gracilis*; and 3) all eight plants. For the two- and three-plant mixtures, proportions were drawn from a Dirichlet distribution. The eight-plant mixture reflected the composition of a field in spring. Covariances between markers were specified based on observed correlations. In each case, 900 samples were drawn. Efficiency was assessed through normalized mean squared error (NMSE) and coverage probability (CP). Accounting for covariances between markers increased efficiency of estimation, as shown by lower NMSE and increased CP (Table 1). Gaussian priors increased errors and reduced coverage. Although not entirely comparable with Bayesian methods, NNLS performed reasonably well in terms of NMSE but achieved lower CP. In the eight-plant scenario, all methods performed poorly, suggesting that delineating individual plants grazed in complex swards will be difficult.

Key Words: diet composition, plant-wax markers, Bayesian inference

0628 Dry matter yields and nutritional composition of corn and sorghum for silage in Florida.

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The objective of this retrospective study was to determine the effect of forage type and planting season on DM yield and nutritional composition of corn and sorghum for silage. Data were obtained from hybrid test trials performed by University of Florida. Evaluated forages included corn, forage sorghum (FS), and sorghum Sudan (SS) planted during spring and summer of each year from 2008 to 2014. Plantings occurred on March 17 (±13 d) and July 17 (±3 d) for corn and April 16 (±9 d) and July 18 (±2 d) for sorghum species during spring and summer seasons, respectively. Nutritional composition of harvested and nonensiled samples was determined using NIRS (Dairyland Labs, WI). Data were analyzed using Proc MIXED of SAS. The statistical model included the effects of year (random; df = 6), the treatments (fixed; df = 5), and the residual error (df = 30). Orthogonal contrasts were used to test the effect of planting season (contrast 1), corn vs. sorghum (contrast 2), interaction of season and corn vs. sorghum (contrast 3), FS vs. SS (contrast 4), and the interaction of season (FS vs. SS; contrast 5). Dry matter yield was greater ($P <$??) for corn than for sorghum. Summer planting resulted in 30 to 35% lower ($P <$??) DM yields than spring planting in all forages. Dry matter yields did not differ ($P >$??) between sorghum species. Corn had lower ($P <$??) concentrations of NDF, greater ($P <$??) concentrations of starch, and greater ($P <$??) NDF digestibility than sorghum species. Sorghum Sudan had greater ($P <$??) concentrations of NDF than FS. In conclusion, spring season forages yielded more DM of better nutritional quality than summer season forages. Also corn yields more DM of better nutritional quality than sorghum forages.

Key Words: corn, sorghum, silage.

0629 Influence of plant population, maturity and ensiling time on fermentation profile, nitrogen fractions, and starch digestibility in earlage.

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The objective of this study was to evaluate the effect of plant population, maturity at harvest, and ensiling time on

Table 0628.

Table 1. Effect of planting season on yield and composition of different corn (CN), forage sorghum (FS) and sorghum Sudan (SS) for silage.

	Spring			Summer				*P* value[1]				
	CN	FS	SS	CN	FS	SS	SEM	1	2	3	4	5
DM Yield, ton/acre	8.9	7.8	8.3	6.1	5.4	5.4	0.46	0.01	0.02	0.75	0.57	0.48
DM, %	30.8	29.7	30.0	31.8	29.0	28.6	0.68	0.36	0.01	0.02	0.92	0.47
CP, %	8.4	7.1	6.8	8.2	7.0	7.8	0.47	0.47	0.01	0.35	0.59	0.21
NDF, %	41.8	55.9	58.9	43.9	56.3	58.8	1.15	0.12	0.01	0.26	0.01	0.46
NDFD, % NDF	60.0	52.9	47.9	52.2	48.5	45.4	2.20	0.01	0.01	0.18	0.05	0.63
Starch, %	34.3	17.3	16.5	31.3	14.1	10.8	2.39	0.01	0.01	0.52	0.26	0.51

[1] For testing orthogonal contrasts.

fermentation profile, N fractions, and ruminal in vitro starch digestibility (ivSD; 7 h incubations on dried and 4-mm ground samples) in earlage (contains husks, kernels, and cob). Samples from 4 hybrids (used as experimental unit), each planted at 4 different plant populations (64,000 [64K], 79,000 [79K], 94,000 [94K] or 109,000 [109K] plants/ha) and harvested at 2 maturities (one-half kernel milk line [1/2ML] or black layer [BL]), were collected at harvest, inoculated (Buchneri 500; Lallemand Animal Nutrition, Milkwaukee, WI), and ensiled in vacuum-sealed bags for 30, 60, 120, and 240 d. Ensiled and fresh samples were analyzed at Dairyland Laboratories Inc. (Arcadia, WI). Data were analyzed using Proc Mixed of SAS with the fixed effects of ensiling time, plant population, maturity, and their interactions. Regressions to determine linear relationships were performed using Proc Reg in SAS. Except for greater (P = 0.01) DM content for 64K than for 94K and 109K or slightly greater ivSD for 94K than for other treatments (P = 0.04; 65.5 vs. 63.3% of starch, on average), no effects of plant population were observed (P > 0.10). Although contents of DM, CP, starch, and sugars were greater (P > 0.01), lactate, acetate, 1,2-propanediol, ethanol, and total acid concentrations were lower and, thus, pH was greater in BL earlage. Furthermore, soluble CP and ammonia N concentrations and ivSD were reduced by 5.5, 1.0, and 8.3 percentage units, respectively, in BL than in 1/2ML. Measurements of pH were greater (P = 0.001) for 30 d than the other ensiling times in relationship to a shift in fermentation from lactate (P = 0.001) toward acetate and 1,2-propanediol (P = 0.001) as fermentation progressed. Gradual increases were observed (P < 0.001) from 30 to 240 d for soluble CP (40.6, 47.6, 49.7 and 69.5% of CP) and ammonia N (4.3, 5.4, 5.9, and 9.6% of N). Likewise, the ivSD measurements increased with ensiling time (P < 0.001; 57.9, 59.9, 67.8, and 69.9% of starch). Both ammonia N (R^2 = 0.42, P = 0.001) and soluble CP (R^2 = 0.45, P = 0.001) were positively related to ivSD. Fermentation profile, N fractions, and ivSD of earlage were influenced to a greater extent by ensiling time and maturity than by plant populations. Ammonia N and soluble CP were both good indicators of ivSD in earlage.

Key Words: earlage, ensiling time, starch digestibility

0630 Replacing alfalfa silage with birdsfoot trefoil silage varying in tannin content in lactating cow diets. U. C. Hymes Fecht*, *USDA ARS Dairy Forage Research Center, Madison, WI.*

Silages made from birdsfoot trefoil (BFT) containing 3 levels of condensed tannins (CT) were compared with alfalfa silage (AS) as the principal forage in the diets of lactating dairy cows. Thirty-five multiparous and 15 primiparous Holstein cows were fed a covariate diet for 2 wk and then blocked by parity and DIM and randomly assigned to 1 of 5 diets in a trial of randomized complete block design. Experimental diets were fed as total mixed ration for 12 wk and contained 48% (DM basis) AS or 16% AS plus 32% BFT with low CT (BFTL), normal CT (BFTN), or high CT (BFTH) or a mixture with equal DM from all 3 BFT silages. The BFTL, BFTN, and BFTH contained 5.1, 8.4, and 14.8 g CT/kg DM, respectively. The balance of dietary DM was fed as corn silage, high-moisture shelled corn, soybean meal, soy hulls, Energy Booster, and macro- and trace minerals plus vitamins A, D, and E. Diets were formulated to 16.5% CP and 30% NDF. Statistical analyses were performed using the mixed procedures of SAS. Intake and yield of milk, ECM, true protein, lactose, and SNF were greater (P < ??) on BFTL and BFTN than on AS and BFTH, whereas the BFT mix was intermediate. Apparent N efficiency also was numerically higher (P > ??) on BFTL and BFTN than on the other 3 diets; MUN was lower (P < ??) on all BFT diets than on AS. These results suggest that CT concentrations of approximately 5 to 8 g/kg DM in BFT improve utilization of forage nutrients for milk production.

Key Words: birdsfoot trefoil, condensed tannins, milk production

Table 0630.

Table 1. Production results

	Legume silage source						
Item	AS	BFTL	BFTN	BFTH	BFT mix	SEM	P > F
DMI, kg/d	24.0^{bc}	25.6^{a}	25.4^{a}	23.2^{c}	24.9^{ab}	0.41	< 0.01
Milk, kg/d	36.6^{b}	40.1^{a}	39.5^{a}	36.3^{b}	38.6^{ab}	0.95	0.02
ECM, kg/d	34.7^{bc}	38.3^{a}	37.3^{ab}	33.8^{c}	35.8^{abc}	1.13	0.04
Fat, kg/d	1.39	1.55	1.53	1.36	1.42	0.061	0.11
True protein, kg/d	1.09^{bc}	1.21^{a}	1.15^{ab}	1.06^{c}	1.10^{bc}	0.030	0.01
Lactose, kg/d	1.74^{bc}	1.92^{a}	1.84^{ab}	1.71^{c}	1.84^{ab}	0.048	0.02
SNF, kg/d	3.16^{bc}	3.48^{a}	3.32^{ab}	3.09^{c}	3.26^{abc}	0.084	0.02
MUN, mg/dL	10.3^{a}	9.1^{bc}	9.5^{ab}	9.1^{bc}	8.6^{c}	0.29	< 0.01
Milk-N/N intake, %	26.4	28.0	28.1	26.7	26.3	0.80	0.29

^{a,b,c} Means within a row with different superscript differ (P < 0.05).

0631 Bacterial and fungal community structure of conventional and brown midrib corn hybrids ensiled with or without a combo inoculant at high dry matter concentrations. J. J. Romero*[1,2], Y. H. Joo[3], Y. Zhao[4], J. Park[3], M. A. Balseca-Paredes[1], E. Gutierrez-Rodriguez[5], and M. S. Castillo[1], *[1]Department of Crop Science, North Carolina State University, Raleigh, [2]Animal and Veterinary Sciences, University of Maine, Orono, [3]Division of Applied Life Science (BK21Plus, Inst. of Agri. & Life Sci.), Gyeongsang National University, Jinju, the Republic of Korea,[4]Department of Animal Nutrition and Feed Science, China Agricultural University, Beijing, P. R. China, [5]Department of Food, Bioprocessing, and Nutrition Sciences, North Carolina State University, Raleigh*.

The objective was to evaluate the effects of a combo inoculant on the microbial community structure of 4 corn hybrids ensiled at high DM. Treatment design was the factorial combination of 4 corn types (HYB) ensiled with (INO) and without (CON) inoculant. Corn hybrids were TMF2R737 and F2F817 (A and B; 44.0 and 38.1% DM, respectively; from Mycogen) and P2089YHR and P1449XR (C and D; 42.0 and 41.3% DM, respectively; from Pioneer). F2F817 and D were brown midrib mutants. The inoculant added contained *Lactobacillus buchneri* and *Pediococcus pentosaceus* (4×10^5 and 1×10^5cfu/g of fresh corn). Experimental design was a complete randomized design with treatments replicated 6 times (silos). Corn was chopped, treated or not with inoculant, packed into 7.6-L bucket silos, and stored for 100 d. At d 0, neither HYB nor INO affected the relative abundances of Enterobacteriaceae (61.4 ± 4.54%) and Brucellaceae (3.8 ± 1.24%) bacterial families. F2F817 had more abundance ($P \leq 0.05$) of Rhizobiaceae (5.2 vs. 2.41 ± 0.48%) and Pseudomonadaceae (3.3 vs. 1.8 ± 0.17%) families, compared with A and C. For fungi, 45% (±4.17) consisted of unidentified fungal sequences followed by unidentified sequences of the Tremellales order, which were more abundant in C vs. the others (21.4 vs. 9.5; $P \leq 0.05$). At d 100, a HYB × inoculation effect was observed for the Lactobacillaceae and Leuconostocaceae bacterial families ($P < 0.02$). For the former, INO increased its abundance in all HYB (99.1 vs. 58.9 ± 5.3%) but to a larger extent for B (98.3 vs. 34.3%), and for the latter, INO reduced its abundance in all HYB (0.1 vs. 11.3 ± 3.58%), except C (0.06 vs. 6.67), and to a larger extent in B (0.7 vs. 28.7). INO decreased ($P < 0.01$) the Enterobacteriaceae (0.6 vs. 23.5 ± 1.16%), Streptococcaceae (0.1 vs. 4.6 ± 0.54%), Aeromonadaceae (0.01 vs. 0.55 ± 0.03%), and Brucellaceae (0.01 vs. 0.39 ± 0.05%) families. For fungi, INO had less abundance ($P < 0.01$) of Pichiaceae (6.5 vs. 47.3 ± 5.19%) but more of the Debaryomycetaceae (63.1 vs. 17.3 ± 4.1%) and Mucoraceae (2.7 vs. 0.8 ± 0.53%) families when compared with CON. The results indicate that epiphytic microbial composition differ depending on HYB and that after ensiling, INO favors the dominance of the Lactobacillaceae and Debaryomycetaceae families compared with a more diverse microbial community in the CON.

Key Words: corn silage, bacterial and fungal diversity, combo inoculant

0632 Bacterial and fungal community structure of oats ensiled with or without a combo inoculant. J. J. Romero*[1,2], Y. Zhao[3], M. A. Balseca-Paredes[1], Y. H. Joo[4], J. Park[4], E. Gutierrez-Rodriguez[5], and M. S. Castillo[1], *[1]Department of Crop Science, North Carolina State University, Raleigh, [2]Animal and Veterinary Sciences, University of Maine, Orono, [3]Department of Animal Nutrition and Feed Science, China Agricultural University, Beijing, P. R. China, [4]Division of Applied Life Science (BK21Plus, Insti. of Agri. & Life Sci.), Gyeongsang National University, Jinju, the Republic of Korea, [5]Department of Food, Bioprocessing, and Nutrition Sciences, North Carolina State University, Raleigh*.

The objective was to evaluate the effects of a combo inoculant on the microbial community structure of oats ensiled at high DM concentrations (44.0%). From each of 6 sections in a field, whole oats at heading stage were mowed, wilted for 21 h, chopped, treated (INO) or not (CON) with inoculant, packed into 19-L plastic bucket silos, and ensiled for 217 d. The inoculant added contained *Lactobacillus buchneri* and *Pediococcus pentosaceus* (4×10^5 and 1×10^5 cfu/g of fresh oats). The V4 region of the 16S rRNA gene and the ITS-1 region were amplified and sequenced using an Illumina MiSeq platform for describing the bacterial and fungal communities, respectively. Experimental design was a complete randomized design replicated 6 times (silos). At d 0, there were no differences due to INO for the relative abundance of the Leuconostocaceae (82.9 ± 4.27%), Enterobacteriaceae (15.2 ± 3.52%), Streptococcaceae (0.5 ± 0.10%), and Pseudomonadaceae (0.2 ± 0.13%) bacterial families. For fungi, most of the total relative abundance consisted of unidentified sequences (56.9 ± 6.46%). INO had a higher abundance of the Davidiellaceae family (34.3 vs. 19.6 ± 4.47%) and a lower abundance of unidentified sequences of the Pleosporales order (1.5 vs. 3.2 ± 0.40%) vs. CON ($P \leq 0.05$). No differences between INO and CON were observed for the Pleosporaceae (5.1 ± 2.08%), Nectriaceae (1.9 ± 0.51%), and Debaryomycetaceae (0.6 ± 0.35%) families. At d 217, INO had a lower relative abundance of Leuconostocaceae (42.3 vs. 95.8 ± 4.64%) and a higher relative abundance of Lactobacillaceae (57.4 vs. 3.9 ± 4.65%) bacterial family vs. CON ($P < 0.01$). No effects of INO were observed on the Enterobacteriaceae family (0.05 vs. 0.03 ± 0.02%). For fungi, there were no differences between INO and CON for the relative abundance of Pichiaceae, Trichocomaceae, and Debaryomycetaceae (0.33 ± 0.22%) families and unidentified sequences of the Saccharomycetales order (13.9

± 11.4%), Ascomycota phylum (5.9 ± 4.0%), and Fungi kingdom (1.46 ± 0.96%). However, there was a large numerical decrease of Pichiaceae (41.2 vs. 82.5 ± 20.68%) and increase of Trichocomaceae (14.0 vs. 1.9 ± 6.71%) families in INO vs. CON ($P < 0.23$). In conclusion, INO had only a relative minor influence on the epiphytic fungi but not on the epiphytic bacterial composition. After ensiling, INO favored the dominance of Lactobacillaceae compared with Leuconostocaceae bacterial family in CON. No effects of INO were observed on the fungal community at d 217, but a large numerical decrease was observed in Pichiaceae and increase in Trichocomaceae fungal families vs. CON.

Key Words: oats haylage, bacterial and fungal diversity, combo inoculant

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0633 Microbial count, fermentation, and aerobic stability of regular and brown midrib corn hybrids ensiled with or without a combo inoculant at high moisture concentrations. J. J. Romero*[1,2], J. Park[3], M. A. Balseca-Paredes[1], Y. Zhao[4], Y. H. Joo[3], A. Heitman[1], E. Gutierrez-Rodriguez[5], and M. S. Castillo[1], *[1]Department of Crop Science, North Carolina State University, Raleigh, [2]Animal and Veterinary Sciences, University of Maine, Orono, [3]Division of Applied Life Science (BK21Plus, Insti. of Agri. & Life Sci.), Gyeongsang National University, Jinju, the Republic of Korea,[4]Department of Animal Nutrition and Feed Science, China Agricultural University, Beijing, P. R. China, [5]Department of Food, Bioprocessing, and Nutrition Sciences, North Carolina State University, Raleigh*.

The objective was to evaluate the effects of a combo inoculant on microbial count, fermentation, and aerobic stability of 4 hybrids of corn ensiled at high moisture concentrations. Treatment design was the factorial combination of 4 corn types ensiled with (INO) and without (CON) inoculant. Corn types (HYB) were TMF2R737 and F2F817 (A and B, respectively; from Mycogen) and P2089YHR and P1449XR (C and D, respectively; from Pioneer). F2F817 and D were brown midrib hybrids. The inoculant added contained *Lactobacillus buchneri* and *Pediococcus pentosaceus* (4×10^5 and 1×10^5 cfu/g of fresh corn). Experimental design was a complete randomized design with 6 replicates (silos). Corn was chopped, treated or not with inoculant, packed into 7.6-L bucket silos, and stored for 100 d. At d 0, there were differences due solely to hybrids ($P \leq 0.05$). The percent DM was 30.5, 26.3, 31.1, and 31.5 for A, B, C, and D, respectively; lactic acid bacteria (LAB) count (log cfu/g of fresh corn) was similar for C and D (8.4) and both were greater than A and B (7.7 ± 0.23); yeast count was greatest in C (6.8 vs. 6.0 ± 0.14) and mold count was lowest in D vs. the others (4.6 vs. 5.2 ± 0.15; $P \leq 0.05$). At opening, INO increased ($P \leq 0.05$) LAB (9.3 vs. 7.1 ± 0.29), acetic acid (3.44 vs. 1.32 ± 0.35% of DM), and 1,2-propanediol for all HYB (0.7 vs. 0.0) except D (0.3 ± 0.11% of DM; INO × HYB, $P < 0.01$); decreased yeast (3.1 vs. 4.6 ± 0.45) and molds (1.5 vs. 3.0 ± 0.61); and extended the aerobic stability (582 vs. 111 ± 128 h) vs. CON. However, INO decreased ($P \leq 0.05$) DM recovery (95.6 vs. 97.4 ± 1.05%) and lactic acid for all HYB (4.2 vs. 7.6) except A (4.9 ± 0.59% of DM; INO × HYB, $P < 0.01$) and WSC (1.2 vs. 2.3 ± 0.17% of DM) vs. CON. Also, INO increased pH for all HYB (4.1 vs. 3.9) except D (3.9 ± 0.03; INO × HYB, $P < 0.01$) and decreased ethanol only for D (0.8 vs. 1.3) but not for the others (0.6 ± 0.08% of DM; INO × HYB, $P < 0.01$). The results indicate that the inoculant used consistently improved aerobic stability across HYB by increasing acetic acid and reducing fungal counts but reduced DM recovery of the corn ensiled at high moisture.

Key Words: corn silage, microbial counts, combo inoculant

0634 Forage quality of two different pasture systems incorporating warm and cool season forages for grazing organic dairy cattle. K. E. Ruh*[1,2], B. J. Heins[1], and J. Paulson[3], *[1]University of Minnesota West Central Research and Outreach Center, Morris, [2]University of Minnesota, Saint Paul, [3]University of Minnesota Extension, Rochester*.

Two pasture systems (perennial and annual grass species) with enhanced in-field and landscape-level species diversity were analyzed for forage quality characteristics across the grazing season at the West Central Outreach and Research Center organic dairy in Morris, MN, for 3 yr. System 1 was a diverse mixture of cool season grasses and legumes (perennial ryegrass, white clover, red clover, chicory, orchardgrass, meadow bromegrass, alfalfa, and meadow fescue). System 2 was a combination of perennial polycultures and annual warm-season grasses (BMR sorghum-sudangrass and teff grass). Grazing of lactating cows was initiated when forages were 20 to 30 cm tall, and strip size was adjusted to leave 7 to 13 cm of refusals. Random samples of pasture forage were sampled every other day when a group of cows moved to a new paddock. Pasture clippings were randomly collected in a 0.76-m^2 square of pasture. Forage samples were sent to Rock River Laboratory, Inc., Watertown, WI, and were analyzed with NIR spectrophotometry for DM, CP, and total tract NDF digestibility (TTNDFD). Data were analyzed using the MIXED procedure of SAS. Independent variables for analyses were the fixed effects of system (perennial [1] or perennial–annual [2]), month (June to October), forage (perennial grass pasture, oats/turnips mix, BMR sorghum-sudangrass, or teff grass), year (2013, 2014, and 2015), and their interactions, and date of harvest was a random variable. The DM was 23.3 and 22.4% for systems 1 and 2, respectively ($P = 0.44$). The CP was 23.0 and 18.0% for systems 1 and 2, respectively ($P < 0.001$). The CP for system 1 was 20.9% in 2013, 23.2% in 2014, and 24.7% in 2015 ($P < 0.05$). The CP for system 2 was

14.6% in 2013, 18.9% in 2014, and 20.5% in 2015, and 2013 was lower ($P < 0.05$) than 2014 and 2015. The TTNDFD was 54.6% and 54.9% for system 1 and system 2, respectively ($P = 0.84$). The TTNDFD was 63.8% in 2013, 48.0% in 2014, and 51.9% in 2015 for perennial grass pastures ($P < 0.01$) and 59.3% in 2013, 46.3% in 2014, and 59.0% in 2015 for warm season annual grasses. In summary, CP was greater in perennial cool-season pasture systems; however, TTNDFD and DM did not differ between pasture systems. Yearly effects and weather may affect forage quality in both pasture production systems.

Key Words: grazing, teff, sorghum-sudangrass

0635 Meta-analysis of the effect of homolactic and facultative heterolactic bacteria inoculation on silage quality II: Aerobic stability and yeast, mold and clostridia counts.

A. S. Oliveira*[1], Z. G. Weinberg[2], A. A. P. Cervantes[3], K. G. Arriola[3], I. M. Ogunade[3], Y. Jiang[3], D. Kim[3], M. C. M. Gonçalves[4], D. Vyas[3], and A. T. Adesogan[3], *[1]Universidade Federal de Mato Grosso – Sinop, Sinop, Brazil, [2]Department of Food Quality and Safety, Agricultural Research Organization, The Volcani Center, Rishon Le Zion, Israel, [3]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [4]Instituto Federal Goiano, Rio Verde, Brazil*.

Data from 120 peer-reviewed papers were summarized to evaluate the effects of homolactic and facultative heterolactic bacteria (HAB; *Lactobacillus plantarum*, *Pediococcus pentosaceus*, *Enterococcus faecium*, *Lactobacillus rhamnosus*, or their combinations) inoculation on aerobic stability and microbial profile of silages. The effects were statistically analyzed by comparing raw mean differences between inoculant and control treatment means that had been weighted by inverse variance using random models. Heterogeneity sources evaluated by meta-regression included crop species, application rate (AR; $<10^4$, 10^5 to 10^6 or $>10^7$ cfu/g, representing 3.7, 93.6 and 2.7% of studies, respectively), HAB species, and silo type (laboratory or farm-scale; 92.2 and 7.8% of studies, respectively) as covariates. Corn/sorghum, temperate and tropical grasses, sugarcane, alfalfa, other legumes, and other crops silages accounted for 22.8, 32.3, 7.8, 10.2, 4.8, 12.9, and 9.2% of the silages, respectively. High heterogeneity (I^2 statistic > 50%) was detected for all response variables. No interactions ($P > 0.05$) between the covariates were detected. Inoculation did not affect aerobic stability (2.4 h; $P = 0.33$, $n = 44$) but reduced counts (log cfu/g as fed) of Clostridia (−2.31 log cfu/g; $P < 0.01$, $n = 7$) mainly in grass silage studies ($n = 6$). Inoculation did not affect mold counts in corn/sorghum silages (0.05; $P = 0.73$, $n = 15$), but it reduced mold counts in temperate (−0.50; $P < 0.01$, $n = 10$) and tropical grasses (−1.68; $P = 0.04$, $n = 2$). Inoculation increased yeast counts (0.30; $P < 0.01$, $n = 82$). Inoculation with HAB did not affect aerobic stability, but it increased the growth of yeasts in all crops and reduced clostridia and mold populations in tropical and temperate grass silages.

Key Words: clostridia, *Lactobacillus plantarum*, mold, yeast

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0636 Meta-analysis of the effect silage inoculation with homolactic or facultative heterolactic bacteria on the performance of dairy cows.

A. S. Oliveira*[1], Z. G. Weinberg[2], A. A. P. Cervantes[3], K. G. Arriola[3], I. M. Ogunade[3], Y. Jiang[3], D. Kim[3], M. C. M. Gonçalves[4], D. Vyas[3], and A. T. Adesogan[3], *[1]Universidade Federal de Mato Grosso – Sinop, Sinop, Brazil, [2]Department of Food Quality and Safety, Agricultural Research Organization, The Volcani Center, Rishon Le Zion, Israel, [3]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [4]Instituto Federal Goiano, Rio Verde, Brazil*.

Data from 13 peer-reviewed papers were summarized to examine the effect of silage inoculation with homolactic or facultative heterolactic bacteria (HAB) on the performance of dairy cows. The effects were compared by raw mean differences (RMD) between inoculant and control treatment means and weighted by inverse variance using random-effect models. Heterogeneity sources evaluated by meta-regression and included as covariates crop species (grass, alfalfa, corn, or mixtures of silages representing 68.8, 12.5, 6.3, and 12.5% of experiments, respectively), HAB species (*Lactobacillus plantarum* or HAB combinations were each used in 50% of the studies), diet type (total mixed ration [TMR] vs. non-TMR were used in 25 and 75% of the studies, respectively), and level of milk yield of control cows (<22 or >22 kg/d were produced in 56.3 and 43.7%, respectively, of the studies). All studies had HAB application rates of 10^5 to 10^6 cfu/g fed. High heterogeneity was detected for DMI (I^2 statistic = 71.5%), milk yield ($I^2 = 81.6\%$), and milk protein concentration ($I^2 = 88.7\%$), whereas moderate heterogeneity was detected for milk fat concentration ($I^2 = 49.1\%$). No interaction ($P > 0.10$) was detected between the covariates. Inoculation with HAB increased DMI (RMD = 0.66 [0.22, 1.10] kg/d; $P < 0.01$, $n = 11$), did not affect milk yield in cows producing <22 kg of milk/d (RMD = −0.89 [−1.93, 0.13] kg/d [$P = 0.09$]; milk yield for control cows = 19.60 ± 1.88 kg/d; $n = 9$), but increased milk yield in cows producing >22 kg/d (RMD = 1.07 [0.26, 1.88] kg/d [$P < 0.01$]; milk yield of control cows = 29.92 ± 8.64 kg/d; $n = 6$). Inoculation with HAB tended to increase milk fat concentration (RMD = 0.06 [−0.004, 0.11] % milk; $P = 0.07$, $n = 15$) and increased milk protein concentration (RMD = 0.10 [0.05, 0.15] % milk; $P < 0.01$, $n = 13$, $n = 2$ outliers). However, there was a trend for inoculation with a mixture of HAB species to give a higher milk protein response (RMD = 0.15 [0.02, 0.25] % milk; $P = 0.02$, $n = 6$)

than inoculation with *L. plantarum* alone (RMD = 0.04 [0.01, 0.07] % milk; $P < 0.01$, $n = 7$). Inoculation with HAB with improved the performance of dairy cows producing more than 22 kg of milk/d but did not affect that of those producing lower quantities of milk.

Key Words: forage conservation

0637 Screening of microorganism and effects of different bacterial additives on fermentation quality of rye silage harvested at dough stage.

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This study was investigated to select a new inoculant and estimate its effects on rye silage harvested at dough stage. Twenty-four rye silages were collected from the commercial beef cattle farms. A total of 180 dominant microorganisms from these rye silages were selected and identified as *Lactobacillus* spp. Those were confirmed the antimicrobial activities against such as mycotoxigenic fungi through antagonism screening. The isolates also were analyzed for acidification ability through monitoring a change of bromophenol blue color and pH of MRS broth. Finally, the isolates were evaluated for fibrinolysis ability through the enzyme plate assay test using four enzymes (cellulase, xylanase, esterase, and chitinase). Eight isolates among 180 isolates indicated antimicrobial activities against *Fusarium moniliforme*. Two isolates indicated strong acidification ability (R4-26 and R7-24). In enzyme plate assay test, one isolate was effective for all enzymes (R48-27). Selected isolates R48-27 (LP1) and R4-26 (LP2) were evaluated on rye silage to improve fermentation quality. Rye forage was grown at the research farm of Gyeongsang National University, Jinju, the Republic of Korea, and harvested at dough stage (46% DM). The forages were divided into five treatments: CON (distilled water at 2 mL/kg of fresh forage), LP1 (*Lactobacillus plantarum* R48-27 at 4.0×10^4 cfu/g of fresh forage), LP2 (*L. plantarum* R4-26 at 4.0×10^4 cfu/g of fresh forage), MIX (mixture of LP1 and LP2 at 1:1 ratio), and LB (*Lactobacillus buchneri* at 4.0×10^4cfu/g of fresh forage). The forage was chopped and ensiled into 10-L mini-silos with 4 replications for 100 d. The NDF concentration was higher ($P < 0.05$) in CON and MIX silages compared with the other silages, whereas ADF concentration was lower ($P < 0.05$) in LP2 silage than the other silages. The LB silage produced the lowest pH that was equated with higher lactate production ($P < 0.05$), whereas the LP2 silage produced the highest acetate and propionate ($P < 0.05$). The LB silage resulted in the highest lactate-to-acetate ratio ($P < 0.05$). Mold was not detected only in the LP2 silage. In conclusion, the new inoculant (LP2) could be suggested to improve the silage safety, which has a strong effect against mycotoxin fungi.

Key Words: rye silage, inoculant, fermentation quality

0638 Effects of cow and bag type on the undigested neutral detergent fiber after two hundred forty hours in situ incubation.

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The effect of cow and in situ bag type on undigested NDF (uNDF) content of corn silage, wheat straw, and alfalfa silage after 240 h in situ incubation were evaluated in three rumen-cannulated Holstein cows. Two corn silages, a wheat straw, and an alfalfa silage sample were dried and ground to pass through a 2.5-mm screen. After thorough mixing, 1 , 2, and 5 g of each forage were placed into F57 Ankom bags (4 by 5 cm), Ankom 5- by 10-cm nylon bags (part number R0510), or Ankom 10- by 20-cm nylon bags (part number R1020), respectively. There were three duplicates for each treatment within each cow. Sample mass to surface area by bag was 25, 20, and 12.5 mg cm^{-2}, respectively. The residual NDF was analyzed after 240 h incubation. Data was analyzed by SPSS 19.0. Within each forage, the effect of cow and bag type on uNDF within forages was determined by ANOVA. Means were compared by Duncan's multiple range test. The contents of the uNDF significantly differed due to bag type ($P < 0.001$). The content of uNDF in F57 bags was significantly higher than in R0510 and R1020 nylon bags ($P < 0.05$) and there was no significant difference in uNDF between R0510 and R1020 nylon bags ($P > 0.05$). The uNDF differed within cow for wheat straw ($P < 0.001$). Bag type and effective surface area should be taken into consideration when measuring uNDF by in situ methods; the estimate of uNDF in relatively indigestible materials, such as wheat straw, may also be affected by cow.

Key Words: undigested neutral detergent fiber, in situ, bag type

0639 WS Immunodetection of the Cry toxin in leaves of transgenic maize hybrids. G. Balieiro Neto*[1], A. W. P. Freitas[2], R. Botelho Ferraz Branco[2], K. Maria Roncato Duarte[2], F. Porto Pela[3], and M. D. Baruffi[3], *[1]Sao Paulo State Agency Agribusiness Technology, Ribeirao Preto, Brazil, [2]São Paulo State Agency Agribusiness Technology, Ribeirao Preto, Brazil, [3]University of São Paulo, Ribeirao Preto, Brazil*.

This assay aimed to evaluate the Cry toxins concentration in the last completely expanded leaf at 7, 14, 28, 35, 70, 84, and 96 d after planting of five corn hybrids. The evaluated hybrids were Syngenta Impact TL TG, Monsanto DKB 390 VT PRO II, Monsanto AG 8088 PRO II, Biomatrix 2B655 Herculex from Dow, and Syngenta 7205 Viptera. To analyze the toxin concentrations, antibodies were produced and a PTA-ELISA was developed. The positive controls used to produce the calibration curves were Sigma-Aldrich BF412b (Cry1Ab), Sigma-Aldrich BF418b (Cry1F), and Sigma-Aldrich BF423b (Vip3Aa20). The experimental design was randomized blocks in a factorial arrangement 5 (hybrid) × 7 (samples) with five repetitions. There were a significant interaction between hybrid and sampling period. The mean concentrations of the Cry toxins in the hybrids Herculex, AG 8088 PRO II, DKB 390 VT PRO II, Viptera, and Impacto were 7.58, 13.05, 16.81, 22.67, and 34.05 µg/g of fresh tissue, respectively. The mean concentration of Cry toxins were 16.77, 15.16, 18.46, 22.87, 22.85, 20.62, and 15.98 µg/g of fresh tissue at 7, 14, 28, 35, 70, 84, and 96 d after planting. Higher concentration of Cry toxin occurred between 35 and 70 d after planting and the hybrids with the higher concentrations were Viptera and Impacto with concentrations of 34.6 and 39.6 µg/g of fresh tissue, respectively. This information can integrate selection criteria of hybrids for cultivation in different regions according to the level of infestation of pests and resistance thereof to different Cry toxin concentrations.

Key Words: corn, Cry toxin, OGM, PTA ELISA

0640 The effect of defoliation severity during late autumn–winter on herbage production, regrowth, and nitrogen uptake. G. Cun*, G. R. Edwards, and R. H. Bryant, *Lincoln University, Lincoln, New Zealand*.

Nitrate leaching is an important environmental concern in livestock production in temperate pastures with leaching losses often high in late autumn/winter. Management strategies are sought to reduce nitrate leaching by enhancing pasture growth and uptake of nitrogen (N) over the winter period. The objective of this experiment was to determine the effect of five postgrazing heights on herbage production, quality, and N uptake of a diverse pasture mixture containing *Lolium perenne* (perennial ryegrass), *Trifolium repens* (white clover), *Cichorium intybus* (chicory), *Plantago lanceolata* (plantain), and *Medicago sativa* (lucerne) during the late autumn winter season. Pasture areas were defoliated to five different residual heights (20, 30, 40, 50, and 60 mm) by a push lawn mower in a randomized block design with four replicates. All swards were allowed to regrow for 112 d and herbage accumulated over the regrowth period was measured. Swards defoliated to 20, 30, and 40 mm had greater herbage regrowth (1,884, 1,508, and 1,322 kg DM/ha, respectively) compared with those defoliated to 60 mm (1,289 kg DM/ha) over 112 d. Repeated measures analysis on N concentration of herbage showed a significant interaction ($P = 0.012$) of defoliation treatment with time. For the 20-mm defoliation, N concentration increased from 18.8 to 29.7 g N/kg whereas the 60-mm defoliation decreased from 26.1 to 24.9 g N/kg during the regrowth period. During this 112-d regrowth period, pastures defoliated to 20 mm accumulated 56.01 kg N/ha compared with 32.07 kg N/ha in plots defoliated to 60 mm. The results indicate severely grazing to postgrazing heights <40 mm may improve growth and N uptake in the late autumn/winter period.

Key Words: grazing management, nitrogen uptake, defoliation severity

Table 0641.

Table 1. Biomass yield and quality of tall wheatgrass (TW) in fall interseeded with hairy vetch in the previous year.

	Treatments*			
Variable	TWCon	TWHV	p-value	SEM
DM yield, kg/ha	502.92	526.67	0.7016	52.44
DM, %	53.46[a]	45.12[b]	0.0039	1.30
NDF, %	68.21[a]	65.21[b]	0.0058	0.63
ADF, %	38.49[a]	36.54[b]	0.0227	0.45
ADL, %	3.51[a]	3.85[b]	0.0317	0.10
IVDMD, %	43.35	47.52	0.1976	2.03

* Control, no interseeding (TWCon) and TW + HV interseeding (TWHV)
[a,b] P <0.05

0641 Tall wheatgrass biomass yield and quality after interseeding with hairy vetch. M. Menghini[1,2], H. M. Arelovich*[1,2,3], M. F. Martínez[1], R. D. Bravo[1], and M. D. Chamadoira[1], *[1]Dto. Agronomia, Universidad Nacional del Sur, Bahia Blanca, Argentina, [2]CIC, Bahia Blanca, Argentina, [3]CERZOS, Bahia Blanca, Argentina*.

Tall wheatgrass (TW; *Thinopyrum ponticum*) is a reliable perennial temperate grass frequently used as a pasture in southwest semiarid Argentina. However, grass quality and biomass yield is affected by soil fertility. Mixes with annual legumes well adapted to the area such as hairy vetch (HV; *Vicia villosa*) may affect grass biomass yield and nutritive value. The aim of this study was to evaluate the effect of interseeding HV within an existing TW pasture on the biomass yield and nutritional value measured in fall, once the life cycle of the legume is finished. The experimental site was located at 62°00′56″ W, 38°10′16″ S. Pastures arranged in plots of 9 m^2 were used as experimental units. The treatments were control, no interseeding (TWCon), and TW + HV interseeding at a density rate of 20 $kg \cdot ha^{-1}$ (TWHV) in a complete block design ($n = 3$). Interseeding dates for HV were March 20 and 22 of 2013 and 2014, respectively, with a similar biomass yield composition of 80 and 83% for HV in the spring of both years. The plots were manually clipped at 8 cm height on March 21, 2014 (Y1), and May 12, 2015 (Y2). Subsamples of 0.4 m^2 were obtained from each plot to determine forage DM content and biomass yield, CP, NDF, ADF, ADL, and in vitro DM digestibility (IVDMD). Data were analyzed as a mixed model and means were compared by Tukey ($\alpha = 0.05$). An interaction treatment by year was only apparent for CP ($P < 0.05$). Then, CP concentration was analyzed for each treatment; TWCon was 8.2 and 3.8% vs. a higher level for TWHV 13.5 and 6.8% for Y1 and Y2, respectively ($P < 0.05$). The year mean for the rest of the variables are shown in the table. Except for ADL, which was higher for TWHV, the DM, NDF, and ADF contents resulted lower for TWHV than for TWCon ($P < 0.05$), whereas for DM yield and IVDMD, the differences attributed to the interseeding were not significant. Interseeding HV into TW existing pastures improve the nutritional value of the TW regrowth.

Key Words: *Vicia villosa*, *Thinopyrum ponticum*, intercropping

0642 Effect of canopy height on the nutritive value of elephant grass silage. E. B. Alves, I. L. De Oliveira, J. R. Gervasio, M. S. Bastos, S. M. Da Silva, J. O. Gusmao, L. M. Lima, and T. F. Bernardes*, *Federal University of Lavras, Lavras, Brazil*.

The ideal canopy height (CH) to harvest elephant grass for making silage has not been determined. Therefore, the objective of this study was to evaluate the yield of elephant grass (*Pennisetum purpureum* cv. Cameroon) and the silages produced from plants harvested at five CH: 100, 140, 180, 220, and 260 cm (described as CH100, CH140, CH180, CH220 and CH260, respectively). The experiment consisted of 25 plots with four rows each. The plants used to assess forage yield and to produce the silages were cut at ground level from the two central rows of each plot every time the canopy reached the target height. To make silages, the plants were chopped with a theoretical cut length of 20 mm and packed to a wet density of 688 kg/m^3 in 15-L laboratory silos. To measure effluent production, 10 kg of sand were placed on the bottom of the silos. The silos were sealed with plastic lids, weighed, and maintained at room temperature for 60 d. At silo opening, silage was removed and subsamples were taken to determine fermentation end products, microbial counts (bacteria, yeasts, and molds), and nutritive value. The experimental design was randomized blocks with five repetitions. The data were analyzed by the mixed-model method using the MIXED procedure (SAS Institute, 2004). The means were compared by a Tukey test at 5%. Canopy height was considered a fixed effect and block was considered a random effect. CH100 and CH140 had the lowest yield (on average, 12.8 ton DM/ha) and CH260 had the highest (22.4 ton DM/ha). CH180 and CH220 showed an intermediate production (on average, 17.3 ton DM/ha). The DM concentration of the plants before ensiling ranged from 11.6 to 21.5% ($P < 0.001$). Canopy height did not affect fermentative and microbial characteristics of the silages. Effluent losses were greater ($P < 0.0001$) in silages with plants harvested at CH100 (58.4 kg/ton of fresh forage), whereas the silages from CH260 had the lowest effluent production (24.1 kg/ton of fresh forage). The in vitro digestibility of the silages produced with plants harvested at CH100, CH140, and CH180 was greater (on average, 69.9%; $P = 0.0007$) than that of the other treatments (57.1%). As no differences among treatments were observed in terms of fermentation quality, it is possible to conclude that the right CH to produce elephant grass silage range from 180 to 220 cm due to the greater balance between forage yield and silage digestibility.

Key Words: cut-and-carry system, forage harvesting, tropical forage

0643 Compost inclusion level in soil on chemical composition and in vitro dry matter digestibility of native and improved cactus forage varieties. J. A. Santos-Haliscak*[1], J. Kawas[1], H. Fimbres-Durazo[1], G. Moreno-Degollado[1], R. E. Vázquez-Alvarado[1], E. Olivares-Sáenz[1], and H. Andrade-Montemayor[2], *[1]Universidad Autonoma de Nuevo Leon, San Nicolas de los Garza, Mexico, [2]Universidad Autónoma de Querétaro, Querétaro, Mexico*.

The objective of this study was to determine DM and protein production per hectare, chemical composition, and in vitro digestibility of two cactus varieties planted in soil with three compost levels. A randomized complete block design with a

factorial arrangement of treatments, with the two cactus varieties, one with spines (WS) and one without spines (WOS), four seasons (summer, fall, and winter of 2013 and spring 2014) and three levels of compost (0, 61, and 122 tons/ha) was conducted. Compost was purchased from a local feedlot. The WS variety was Forrajero Mina and the WOS was COPENA F1. These were planted in double rows, with a spacing of 0.5 m between plants and 0.6 m between rows in 1.2-m-wide beds. The design included 5 beds (repetitions), for a total of 300 plants per variety and 600 for the entire experiment. The WS variety had higher concentrations of NDF (30.5 vs. 22.3%; $P = 0.001$), hemicellulose (17.5 vs. 7.9%; $P = 0.001$), ash in NDF (4.09 vs. 3.14%; $P = 0.005$), iron (59.8 vs. 49.8 ppm; $P = 0.020$), and manganese (41.1 vs. 34.3 ppm; $P = 0.005$), whereas the WOS variety had higher concentrations of lignin (1.4 vs. 0.7%; $P = 0.001$), ash in ADF (0.92 vs. 0.45%; $P = 0.03$), calcium (3.1 vs. 2.9%; $P = 0.001$), and zinc (44.6 vs. 39.0 ppm; $P = 0.03$). In vitro DM digestibility was higher (79 vs. 67%; $P = 0.001$) for the WOS variety. The inclusion of compost increased DM (2.8 to 4.4 tons/ha; $P = 0.018$) and CP (196 to 556 kg/ha; $P = 0.001$) production, lignin (0.83 to 1.22%; $P = 0.008$), phosphorus (0.10 to 0.23%; $P = 0.001$), and zinc (36.7 to 44.1 ppm; $P = 0.025$) while decreasing the concentration of ash in ADF (0.93 to 0.51%; $P = 0.031$). The two cactus varieties had high ash and moisture content, which may reduce the energy density of this feed for livestock. Nitrogen associated with the ADF fraction (0.65%) may reduce nitrogen availability for bacteria in the rumen.

Key Words: cactus, chemical composition, in vitro digestibility, compost.

0644 Neutral detergent fiber digestibility of diets supplemented with soy hulls, corn stover, or alkali–ethanol–treated stover in lactating dairy cows. D. M. Donnelly*[1], L. C. de Resende[2], and D. K. Combs[3], *[1]Department of Dairy Science, University of Wisconsin-Madison, Madison, [2]University of Wisconsin-Madison, Madison, [3]Department of Dairy Science, University of Wisconsin, Madison*.

The objective of this study was to evaluate the digestibility of diets supplemented with three sources of NDF: soy hulls, untreated corn stover, or corn stover treated with NaOH and ethanol. Total tract apparent DM and NDF digestibility were measured with eight lactating Holstein cows in a replicated 4 × 4 Latin square design with four 21-d periods. The diets consisted of a low-fiber control diet (25% of diet DM as NDF) and treatment diets containing the control diet supplemented with 2.1 kg of soy hulls, untreated corn stover, or NaOH/ethanol–treated stover. Treatment diets contained approximately 30% of diet DM as NDF. Feed intake, orts, and milk yield were recorded daily. During the third week of each period, 12 fecal samples were collected to cover a 24-h period and composited. Milk collected from the last four milkings of each period was analyzed for milk composition. Data was evaluated using PROC MIXED (SAS version 9.3) with cow within block and period as random effects and treatment set as a fixed effect. Milk yield, milk fat percentage, and DMI did not differ among treatments ($P > 0.05$). Intake of NDF and iNDF intake as a percentage of BW were similar across treatments. Cows fed the control diet and the diet with supplemented soy hulls had higher DM digestibility (57.7 and 60.0% DMD, respectively) compared with cows fed diets supplemented with untreated stover (52.4%; $P < 0.0001$). The DM digestibility of the diet with supplemented treated stover was similar to both the untreated stover and soy hull rations. In vivo NDF digestibility was lowest when cows were fed the untreated stover ration. Digestibility of NDF was improved when soy hulls or treated

Table 0644.

	Control	Soy Hulls	Treated Stover	Untreated Stover	SEM	P - Value
MY, kg	28.0	30.7	27.9	29.9	3.3	0.36
Fat, %	4.4	4.1	4.2	4.4	0.3	0.39
DMI, kg	29.1	30.3	29.6	28.7	1.2	0.28
NDF Intake, kg	10.1	10.5	10.3	10.0	0.4	0.28
DMD, %	57.7[a]	60.0 [a]	54.8 [ab]	52.4 [b]	1.6	< 0.0001
In Vivo NDFD, %	35.6[a]	41.63[b]	38.2 [ab]	31.9 [c]	1.5	< 0.0001
NDF Intake, %BW	1.39	1.44	1.40	1.36	0.08	0.24
iNDF Intake, % BW	0.140	0.149	0.145	0.142	0.008	0.24

stover were added to the diets ($P < 0.0001$). The NaOH/ethanol treatment process appears to improve the DM and NDF digestibility of corn stover to values similar to those of soy hulls. Supplemental fiber did not affect milk yield, DMI, or fiber intake.

Key Words: in vivo, neutral detergent fiber, NaOH

0645 Yield and nutritive value of photoperiod-sensitive sorghum and sorghum-sudangrass in central Wisconsin. E. Remick*[1], H. Su[2], W. K. Coblentz[3], and M. Akins[2], *[1]University of Wisconsin-Madison, Madison, [2]University of Wisconsin, Madison, [3]U.S. Dairy Forage Research Center, Marshfield, WI.*

A study was conducted to evaluate the yield and nutrient composition of photoperiod-sensitive (PS) and non-PS forage sorghum, sorghum-sudangrass, and sudangrass compared with corn planted on 2 dates and harvested using single- or multiple-cut harvest strategies at 2 research stations (Marshfield and Hancock), each located in central Wisconsin. At each site, treatments were arranged in a randomized complete block design with 4 replicates. The experiment was analyzed as a split-split-plot design with planting date (early or mid June) designated as the main plot, harvest strategy (single cut or multiple cut) as the subplot, and 8 forage cultivars (corn silage, PS forage sorghum, PS sorghum-sudangrass, forage sorghum, BMR forage sorghum, sorghum-sudangrass, BMR sorghum sudangrass, or PS-BMR sudangrass) designated as the sub-subplot treatment factor. Multiple-cut plots were harvested in late August and early October with single-cut plots harvested only in early October. Data were independently analyzed for each location. Overall, forage yields were numerically greater for Hancock plots compared with Marshfield plots (Table 1). At Hancock, DM yields were greater for the early compared with late planting date (16,225 vs. 12,080 kg DM/ha; $P = 0.014$), but there were no effects of planting date at Marshfield (overall mean = 8,228 kg DM/ha; $P = 0.90$). The lack of response at Marshfield was likely due to delayed germination of early planted plots following heavy rains. At both sites, the single-cut harvest (17,517 kg DM/ha at Hancock and 11,729 kg DM/ha at Marshfield) was greater ($P < 0.01$) than the multiple-cut harvest system (10,789 kg DM/ha at Hancock and 4,726 kg DM/ha at Marshfield). There were yield differences for variety as well as variety by harvest type interactions ($P < 0.01$) at both locations (Table 1). At both sites, the multiple-cut harvest strategy reduced yields of all hybrids. The sorghum-sudangrass and PS sorghum-sudangrass varieties had the greatest numerical yields among the sorghum types tested under both harvest strategies. Reduced yields of varieties harvested using multiple-cut strategies may reflect reduced tillering and regrowth capabilities of certain varieties. Using a single harvest, several sorghum forage types has similar or better forage yields compared with corn silage.

Key Words: forage sorghum, sorghum-sudangrass photoperiod sensitive

0646 Cutting interval and water application influence *Sericea lespedeza* yields and condensed tannin content. L. C. Nuti*[1], J. P. Muir[2], E. A. Duffus[1], Y. Jung[1], A. A. James[1], N. M. Cherry[3], and G. R. Newton[1], *[1]Prairie View A&M University, Prairie View, TX, [2]Tarleton State University, Stephenville, TX, [3]Texas A&M AgriLife Research, Stephenville, TX.*

Sericea lespedeza (SL; *Lespedeza cuneata*) contains tannins that may provide beneficial effects in gastrointestinal nematode suppression in small ruminants. The objective of the present work was to investigate the effect of cutting frequency and water application on forage yield, total tannin content, and active protein bound to tannins. *Sericea lespedeza* was grown in 30 raised boxes (1.5 m^2 by 0.3 m) containing a commercial potting soil mixture. Established (yr 3) SL was randomly assigned to a cutting interval of 30, 45, or 60 d over a 120-d trial period. Within each cutting frequency, boxes were randomly assigned to a watering treatment of ambient rainfall or 2.5 or 5.0 cm of applied water per week (AWW). At the designated harvest intervals, SL was cut to a height of 12.5 cm and weighed (wet weight). The effect of cutting frequency and water treatments were analyzed using SAS 9.3 general linear model procedure for repeated measure design. No interaction was detected between cutting frequencies and water application rates. Cutting interval ($P < 0.08$) and water treatments ($P < 0.03$) influenced overall wet weight yield of SL over the 120-d growing period. A 45-d cutting interval produced more SL forage ($P < 0.07$; 8.43 ± 0.39 kg) when compared with a 30-d cutting interval (7.15 ± 0.39 kg) but was similar to yields obtained on Day 60 (7.56 ± 0.39 kg). Plants supplemented with 5 cm AWW produced more SL forage (8.61 ± 0.4) than plants grown under ambient conditions (7.12 ± 0.4 kg; $P < 0.03$) or supplemented with 2.5 cm AWW (7.42 ± 0.34 kg; $P < 0.9$). *Sericea lespedeza* was then sun dried and condensed tannin (CT) and protein-bound (PB) CT were determined using 50 μg DM and the protein precipitable phenolics method of Hagerman and Butler (1978). Total CT was not influenced by water application rates ($P > 0.1$). A cutting interval of 45 d increased the amount of plant CT (153.18 ± 12.95 μg; $P > 0.01$) when compared with the 30- (100.75 ± 11.51 μg) or 60-d (107.73 ± 15.86 μg) cutting intervals. Concentrations of PB CT were not influenced by cutting interval or water application rates. Growth of SL under ambient conditions in Texas is good but can be improved with irrigation. A 45-d cutting interval maximizes plant yield and total tannin concentrations.

Key Words: *Sericea lespedeza*, growth, tannins

0647 A comparison of in vitro rumen digestibility and fermentation indices of tannin-rich chestnut meal. J. H. Park*[1], J. W. Jang[1], J. H. Kim[1], H. J. Lee[2], Y. H. Joo[2], S. S. Lee[2], I. H. Choi[3], and S. C. Kim[1,2], *[1]Department of Animal Science, Gyeongsang National University, Jinju, the Republic of Korea, [2]Division of Applied Life Science (BK21Plus, Insti. of Agri. & Life Sci.), Gyeongsang National University, Jinju, the Republic of Korea, [3]Department of Companion Animal & Animal Resources Science, Joongbu University, Geumsan, the Republic of Korea*.

This study was conducted to estimate in vitro rumen digestibility and fermentation indices of tannin rich chestnut meal probiotic using a novel wireless automated gas production system. The chestnut separated to whole chestnut (WCP), endodermis (EDP), or kernel (KNP) and then ground by cutting mill. The ground chestnuts were mixed with combo inoculant (*Lactobacillus acidophilus*, 1.0×10^6 cfu/g; *Saccharomyces cerevisiae*, 1.0×10^6 cfu/g; and *Bacillus subtilis*, 4.5×10^6 cfu/g), individually placed into 10-L mini-silos, and incubated at 39°C for 4 d to produce each chestnut probiotic. Each chestnut probiotic (0.5 g) was placed into the incubation bottles with rumen fluid mixture (40 mL), which was mixed with Van Soest medium in a 2:1 ratio. Rumen fluid was collected from cannulated Hanwoo heifers. Four replicates in each treatment with three blanks were incubated at 39°C for 48 h, and gas pressure was measured at 30 min intervals. The bottle contents were centrifuged at the end of incubation. The supernatant was used for pH, ammonia N, and VFA and the residue was used for in vitro digestibility of DM (IVDMD) and NDF (IVNDFD). The KNP (76.5 and 60.1%) had greater ($P < 0.05$) IVDMD and IVNDFD, respectively, than WCP (49.5 and 19.2%, respectively) or EDP (46.1 and 20.1%, respectively). The KNP had greatest ($P < 0.05$) concentrations of total VFA (116 m*M*/L), propionate (26.6%), and butyrate (23.4%), whereas EDP had greatest ($P < 0.05$) pH (6.60) and concentrations of ammonia N (35.9 mg N/100 mL) and valerate (52.5%). Acetate concentration and acetate-to-propionate ratio in WCP (52.6% and 2.12, respectively) and EDP (52.5% and 2.14, respectively) were higher ($P < 0.05$) than those in KNP (46.4% and 1.75, respectively). The rapidly fermentable fraction (0.72 vs. 0.28 mL/g) in KNP was greater ($P < 0.05$) than in WCP. The KNP (4.93 mL/g, 5.65 mL/g, and 0.29%/h) had greatest ($P < 0.05$) total fermentable fractions and fractional fermentable rate. The lag phases (4.69 and 4.81 vs. 3.72 h) in EDP and KNP were greater ($P < 0.05$) than in WCP. In conclusion, it is suggested that KNP could be used to improve the rumen fermentation characteristics for ruminants.

Key Words: chestnut, digestibility, fermentation characteristics

0648 Inoculant effects on bermudagrass silage nutritive value and fermentation characteristics. E. C. Freitas[1], J. M. D. Sanchez*[2], F. A. Kuhawara[3], U. Cecato[4], J. M. B. Vendramini[5], and A. Aguiar[1], *[1]DeLaval Manufacturing, Bannockburn, IL, [2]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [3]Sao Paulo State University, Botucatu, Brazil, [4]UFL, Ona, FL, [5]UF/IFAS, Range Cattle Research and Education Center, Ona, FL*.

The objective of this study was to investigate the nutritive value and fermentation parameters of 'Jiggs' bermudagrass (*Cynodon dactylon* L.) silage treated with FeedTech microbial inoculants M20XC and M25AS (2×10^6 cfu/g of treated forage [as fed]) and F600 and F20 (2×10^6 cfu/g of treated forage [as fed]) or control (C). The experiment was conducted in Florida in 2014. Plots (experimental units, 3 by 2 m) were staged on August 15 at an 8-cm stubble height and fertilized with 80 kg N/ha. Forage was harvested with a 4-wk regrowth interval, immediately packed into a mini-silo at a density of approximately 382 kg fresh forage/m^3, and ensiled for 106 d. Treatments were distributed in a randomized complete block design with 5 replicates. The data were analyzed using PROC MIXED with treatment as a fixed effect and block as a random effect. There was an increase on DM recovery ($P = 0.04$; 99.7 vs. 84.4%) and IVTD ($P = 0.06$; 57.8 vs. 53.8%) on silage treated with M20XC compared with the control. No differences were detected among treatments on DM, CP, ADF, NDF, and NDFD ($P > 0.10$). Silage pH, acetic acid, propionic acid, butyric acid, and ammonia concentrations were similar among treatments ($P > 0.10$). However, there was a trend ($P = 0.14$) that M20XC had the greatest concentration of acetic acid between treatments. There was no effect ($P > 0.27$) of inoculants on mold and yeast count (mean = 1.7 and 1.3 log cfu/g, respectively) and mycotoxins (aflotoxin, vomitoxin, zearalenone, and T2) among treatments. FeedTech M20XC may be an efficient inoculant to increase DM recovery and IVTD of bermudagrass silage in the Southeastern United States.

Key Words: grass, silage, inoculants

0649 The effect of a microbial inoculant at two application rates on the aerobic stability of high-moisture corn. E. Benjamim da Silva*, R. M. Savage, S. A. Polukis, M. L. Smith, A. E. Laubach, K. M. Pacer, and L. Kung Jr., *University of Delaware, Newark*.

The purpose of this study was to evaluate the effect of a microbial inoculant at two application rates on the fermentation and aerobic stability of high-moisture corn (HMC). High-moisture corn (74% DM) was 1) untreated (control), 2) treated with *Lactobacillus buchneri* (NCIMB 30139) at an application rate of 400,000 cfu/g of fresh material (LB400), or 3) treated with *L. buchneri* (NCIMB 30139) at a rate of

600,000 cfu/g of fresh material (LB600). The inoculant was supplied by Volac Intl., Ltd., United Kingdom. Five replicated lab silos (7.5 L) for each treatment were packed (density of 658 kg DM/m^3) and ensiled for 30 and 92 d between 21 and 23°C. Data were analyzed as a 3 × 2 factorial arrangement of treatments with the main effects of treatment, day, and their interaction. High-moisture corn was analyzed for fermentation end products, number of yeasts, and aerobic stability. At 92 d, the pH of LB400 and LB600 (4.48 and 4.47) was higher ($P < 0.01$) than that of control (4.33). All treatments had similar concentrations of lactic acid at 30 d, but by 92 d, lactic acid concentrations decreased ($P < 0.01$) in LB400 and LB600 (0.36 and 0.41%) compared with untreated HMC (0.58%). At 30 d, treatment with LB400 and LB600 (0.36 and 0.30%) had higher ($P < 0.01$) concentrations of acetic acid compared with control (0.05%). At 92 d, untreated HMC (0.15%) had lower ($P < 0.01$) concentrations of acetic acid than LB400 and LB600 (0.79 and 0.86%). Treatment with LB400 and LB600 (0.32 to 0.55%) increased ($P < 0.01$) 1,2-propanediol concentrations compared with untreated HMC (0.00 to 0.09%) at both 30 and 92 d. At both ensiling times, HMC treated with LB400 and LB600 (<2.00 to 2.97 log cfu/g) had fewer ($P < 0.01$) yeasts than control HMC (4.04 to 5.93 log cfu/g). At 30 and 92 d, treatment with LB400 and LB600 (>217 h) greatly increased ($P < 0.01$) aerobic stability compared with untreated HMC (16 to 56 h). This experiment showed that inoculation with *L. buchneri* (NCIMB 30139) can improve the fermentation characteristics and the aerobic stability of HMC.

Key Words: aerobic stability, high-moisture corn, *Lactobacillus buchneri*

0650 Meta-analysis of the effect of homolactic and facultative heterolactic bacteria inoculation on silage quality: III Dry matter recovery, chemical composition and in vitro digestibility.

A. S. Oliveira*[1], Z. G. Weinberg[2], A. A. P. Cervantes[3], K. G. Arriola[3], I. M. Ogunade[3], Y. Jiang[3], D. Kim[3], M. C. M. Gonçalves[4], D. Vyas[3], and A. T. Adesogan[3], *[1]Universidade Federal de Mato Grosso – Sinop, Sinop, Brazil, [2]Department of Food Quality and Safety, Agricultural Research Organization, The Volcani Center, Rishon Le Zion, Israel, [3]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [4]Instituto Federal Goiano, Rio Verde, Brazil*.

Data from 120 peer-reviewed papers were summarized to evaluate the effects of inoculation with homolactic and facultative heterolactic acid bacteria (HAB) on DM recovery (DMR), chemical composition, and 48-h in vitro DM digestibility (IV-DMD) of silages. The effects were statistically analyzed by comparing raw mean differences between inoculant and control treatment means that had been weighted by inverse variance using random models. Heterogeneity sources evaluated by meta-regression included crop species, application rate (<10^4, 10^5 to 10^6, or >10^7 cfu/g, which represented 3.7, 93.6, and 2.7% of the studies, respectively), HAB species, and silo type (laboratory or farm-scale, which represented 92.2 and 7.8% of the studies, respectively) as covariates. Corn/sorghum, temperate and tropical grasses, sugarcane, alfalfa, other legumes, and other crops silages represented 22.8, 32.3, 7.8, 10.2, 4.8, 12.9, and 9.2% of the silages, respectively. No interactions ($P > 0.05$) between the covariates were detected. High heterogeneity (I^2 statistic > 50%) was observed for all response variables, except ADIN ($I^2 = 41.6\%$) and water-soluble carbohydrates (WSC; $I^2 = 0$). Inoculation did not affect DMR of corn/sorghum silages ($P = 0.10$, $n = 18$) but increased DMR ($P < 0.05$) of temperate grasses (2.89%; $n = 10$) and tropical grasses (2.89%; $n = 8$) and reduced DMR of sugarcane (−2.87%; $P < 0.01$). Inoculation did not affect the DM concentration of corn/sorghum silages ($P = 0.80$, $n = 45$) and sugarcane ($P = 0.11$, $n = 14$) but increased DM ($P < 0.05$) of temperate grasses (0.60%; $n = 54$), tropical grasses (0.45%; $n = 17$), alfalfa (0.31%; $n = 11$), other legumes (0.77%; $n = 30$), and other crops silages (0.86%; $n = 20$). Inoculation did not affect CP concentration ($P = 0.56$, $n = 106$), tended to reduce ADIN concentration (−0.13% nitrogen; $P = 0.09$, $n = 9$), and reduced WSC concentration (−0.32% DM; $P < 0.01$, $n = 150$) and lignin concentration (−0.28% DM; $P = 0.01$, $n = 20$), but it did not affect IV-DMD ($P = 0.24$, $n = 33$). Inoculation with HAB did not improve DMR of corn/sorghum silages, but it improved those of tropical and temperate grass silages and reduced that of sugarcane silages. Inoculation with HAB did not improve chemical composition or IV-DMD of silages.

Key Words: forage conservation, *Lactobacillus plantarum*

0651 Percentages of alfalfa and grass in fresh and ensiled binary mixtures using near infrared reflectance spectroscopy: Developing a robust calibration.

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Evaluating alfalfa and grass content of alfalfa–grass mixtures is useful for quantifying forage and diet quality. No studies have attempted to evaluate percent alfalfa content of silages and no commercial forage laboratory currently offers this service. Our objective was to develop a robust near-infrared reflectance spectroscopy (NIRS) method to estimate percent composition of binary alfalfa–grass mixtures in the Northeastern United States. Alfalfa–grass samples were collected across New York state over 4 growing seasons and hand separated, and a subset was separately ensiled. Dry samples were coarsely ground, mixed in known proportions, and reground for analysis by NIRS at Dairy One Forage Laboratory, Ithaca,

NY. Samples were mixed to range from 0 to 100% alfalfa for NIRS calibration, with a total of 741 individual samples from 2011, 2012, and 2014 used for calibration. Prediction equations were developed using three NIRS instruments. Dairy One calibrated a Foss 6500 NIRS instrument as well as two newer generation Foss XDS instruments, analyzing most samples with all three instruments. A total of 1,480 spectra were collected for calibration, with samples packed twice and scanned in duplicate. Calibration statistics were similar for the three instruments. Close agreement between R2 (0.99) and 1-VR (0.99) for all three equations indicates consistent results among the cross-validation groups and suggests that the calibration models are robust. There was no benefit in separate sample calibrations for fresh and fermented samples. Spectra from the three instruments were combined to develop and support a single calibration for use in a commercial setting across multiple platforms. Calibrations for grass and alfalfa percent worked well with all instruments and equally well with fresh versus ensiled forage. The three prediction equations had relative prediction deviation values of 4.35, 4.97, and 4.62, indicating calibrations were satisfactory. A diverse set of 98 samples from 2015 were used for validation of the equations. Mixture content was predicted with good precision and accuracy showing biases of 2.49 and SE of prediction of 5.06, with R2 of 0.972, using the equation developed across multiple instruments. These data indicate that with selection of a robust set of calibration samples over many environments, NIRS can be used to determine the botanical composition of alfalfa–grass samples, regardless of whether they are fresh or ensiled, and that replicate scans from multiple instruments can be combined to develop a single calibration that will perform with equal efficiency across different instruments.

Key Words: forage evaluation, botanical composition

0652 Comparison of dry matter measurements between three hand-held near-infrared units with oven drying at sixty degrees Celsius for forty-eight hours.

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This study compared DM predictions of three hand-held near infrared spectrophotometer (NIRS) units (Moisture Tracker, Digi-Star Inc., Fort Atkinson, WI) to conventional oven drying at 60°C using two alfalfa and two corn silages. Corn and alfalfa silages (1,500 g) obtained from the University of Wisconsin Dairy Cattle Center (DCC) and the Arlington Research Station (ARS) were analyzed for DM daily for 20 d. Three NIRS calibrations were also tested within each unit: NIRf, NIRa, and NIRb. The DM predicted from the factory-preset calibrations was NIRf. NIRa was an adjusted DM prediction, where the average difference between oven-dried forage and NIRf determined on duplicate forage samples for 3 d before the experiment was used as a bias adjustment for all subsequent DM determinations. NIRb was a bias-adjusted DM prediction based on the average difference between oven-dried forage and NIRf over the 20-d experiment. NIRb was determined on each forage sample after the experiment had been completed. Each forage was scanned 20 times by each NIRS unit. The average predicted DM from the 20 scans was recorded as the forage DM. The process was repeated three times with each NIRS unit. Two 100-g subsamples of each forage were then oven-dried for 48 h at 60°C daily. Data was analyzed using PROC MIXED (SAS, version 9.3), with method, day, feed, method × day, and method × feed as fixed effects and equipment as the random effect. Oven DM of ARS and DCC alfalfa silages was 37.34 and 48.52%, respectively. Oven DM of ARS and DCC corn silages was 34.69 and 37.41% DM, respectively. NIRf DM predictions were significantly different from their respective oven values for ARS corn silage and ARS haylage ($P < 0.0001$), and NIRf DM tended to differ from oven DM for DCC Corn Silage; $P = 0.06$). NIRf and oven DM for DCC haylage were similar ($P = 0.99$). All NIRb DM values were similar to oven-dried DM for all four forages ($P > 0.05$). The hand-held NIRS units accurately predicted DM content of the alfalfa and corn silages when the factory preset calibrations were corrected for bias.

Key Words: dairy cattle, dry matter, near-infrared

0653 Grazing intensities and season affect N_2O emissions in a tropical pastureland.

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The study assessed a tropical pasture in Brazil to determine how grazing height and season influences N_2O production and consumption. Nitrous oxide fluxes were measured over 2 yr in a Marandu palisade grass pasture with 3 grazing heights (15, 25, and 35 cm), 6 replicates, and 4 seasons (spring, summer, autumn and winter) using static closed chamber and chromatography quantification. The N_2O flux (μg N_2O-N m^{-2} h^{-1}) was integrated by linear interpolation to cumulative emissions. The patters of N_2O fluxes were displayed by using means and SEM. The data were submitted to ANOVA by using R statistical software. When significant, a polynomial orthogonal contrast was done. Nitrous oxide emissions were maximum following rainfall events and application of urea fertilizer (Fig. 1). Nitrous oxide emissions were greatest in the summers whereas lower fluxes associated with frequent instances of N_2O uptake in other seasons. The topmost rate of N_2O emissions was measured in the second week of December 2013 when mean fluxes were 469, 394, and 279 μg N_2O-N

m^{-2} h^{-1} for 15, 25, and 35 cm of pasture heights, respectively.

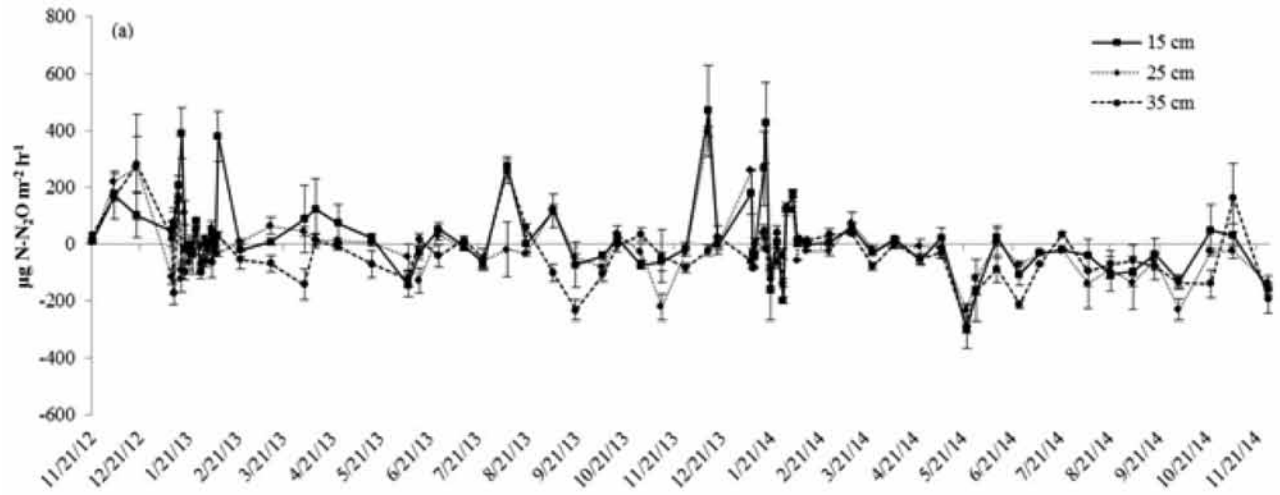

Fig 0653.

Figure 1. N_2O flux (μg N_2O-N m^{-2} h^{-1}) for three grassland intensities (15, 25, and 35 cm) during two years of evaluation (November 21, 2012 to November 26, 2014).

Negative fluxes were detected in approximately 60% of all N_2O sampling especially in the spring and autumn of the yr 2 when lower values of water-filled pore space were also recorded. The highest rate of N_2O consumption was measured on May 23, 2014, when mean fluxes were −299, −235, and −287 μg N_2O-N m^{-2} h^{-1} for pastures heights of 15, 25, and 35 cm, respectively. Grazing intensity was significantly correlated with N_2O flux during the summer. There was a linear reduction in annual cumulative N_2O emissions ($P < 0.05$) with decreasing grazing intensities for both years. The total N_2O emissions were 300.1, 41.6, and −48.3 mg N_2O-N m^{-2} in yr 1 and −153.2, −263.7, and −298.7 mg N_2O-N m^{-2} in yr 2 for 15, 25, and 35 cm of pasture heights, respectively. The greater grazing intensity had the highest levels of N_2O emissions in all seasons except for in the spring of yr 1. The grassland intensity on cumulative N_2O emissions was negatively linear in the annual analysis ($P < 0.05$) driven by the negative associations observed in the summer ($P < 0.05$) and even more so in the autumn ($P < 0.001$). There was a negative linear effect of pasture height on the amount of N_2O emitted/consumed. High stocking rates in the grazing systems influenced the increment of N_2O production, although lower grazing intensities contributes to N_2O mitigation in tropical pastures.

Key Words: continuous stocking, greenhouse gas, pasture height

0654 Impact of foliar spray on yield and chemical composition of alfalfa hay. S. Acharya* and D. P. Casper, *Dairy Science Department, South Dakota State University, Brookings*.

The study objective was to determine the response to foliar nutrient application (proprietary product) on DM yield and chemical composition of second-cutting alfalfa hay. Two fields with a total area of 38.4 ha were selected, where half of the second-cutting alfalfa hay field was sprayed as the Test and half of the field was unsprayed as the Control. The spraying rate was 23.4 L/ha. Crop was planted following established standard procedure of alfalfa, and the interval between first and second cutting was 28 d. Each field was divided into four replications, two represented by Control Plot and two by Test Plot. After harvesting alfalfa and drying in the field, hay was square baled (at moisture level of 14.2%) and weighed and samples were taken using a standard hay probe bale sampler later on. A total of eight hay samples (4 samples from each field) were sent to a commercial laboratory for analysis of nutrient composition. Dry matter yield was increased ($P < 0.01$) for Test (1.48 and 1.34 mt/ha for Test and Control, respectively) compared with Control. Similarly, digestible DM was also found improved ($P < 0.01$) for Test Plot (0.93 and 0.80 mt/ha) compared with Control. Crude protein percentage was increased ($P < 0.05$) for Test Plot (21.1 and 19.1%) compared with Control. There was a trend ($P < 0.10$) of increase in in vitro DM digestibility (62.6 and 59.8 5) and a numerical increase in NDF digestibility (52.1 and 50.8%) for Test compared with Control. This could be explained by a significantly ($P < 0.05$) lower lignin content of Test (8.07 and 8.71%) compared with Control. The nonfiber carbohydrates content was higher ($P < 0.05$) for Test (22.2 and 21.3%) compared with Control. This could further

be explained by a significant ($P < 0.01$) higher NE for lactation content for Test alfalfa (1.28 and 1.19 Mcal/kg) compared with Control. The use of foliar nutrient sprays increase DM yield and nutrient digestibility of alfalfa, thus being able to support more milk yield and feed efficiency.

Key Words: foliar spray, alfalfa, chemical composition

0655 Evaluation of in vitro gas production and energy available in low-lignin alfalfa varieties. K. P. Ortega*, G. Getachew, D. H. Putnam, and E. J. DePeters, *University of California, Davis, Davis*.

Lignin is composed of cross-linked phenolic compounds that impact forage quality. As forage plants mature, lignin concentration increases and DM and fiber digestibility decrease. Low-lignin alfalfa varieties offer potential for improved forage quality and animal production as well as increased yield by allowing for harvests at later maturity while maintaining high digestibility. Lignin synthesis in alfalfa was reduced by genetic manipulation through suppressing enzymes in the lignin biosynthetic pathway. In the current study, two genetically modified alfalfa lines (LL) and their respective controls (CL) were used to study the effect of reduced lignin content on in vitro gas production and predicted ME concentration. Sixty-four samples, that is, four alfalfa lines (two LL and two CL), four field replicates, two cuttings (cut 1 and 3), and two cutting schedules (28 and 35 d), were used. An in vitro technique was used to determine differences in in vitro gas production and predicted ME concentration between two CL and two LL varieties of alfalfa. Alfalfa samples were compared at cuttings 1 and 3 as well as cutting schedules that occurred at 28 and 35 d. Ground alfalfa samples were incubated in buffered rumen fluid using an in vitro gas technique at various time points over 72 h to determine the influence of lignin on rate and extent of in vitro gas production. Four in vitro incubations were conducted, and rate and extent of gas production were calculated using an exponential model. The ME was estimated using the 24 h gas production and CP content of each sample as described by Menke and Steingass (1988). Total ME ($P < 0.0001$) and rate of gas production ($P < 0.0001$) were higher in the LL varieties than the CL varieties, whereas no significant difference was found in extent of gas production. Low-lignin alfalfa varieties offer potential to increase the ME concentration in alfalfa, which needs to be further evaluated by animal feeding studies.

Key Words: alfalfa, low lignin, in vitro gas production, metabolizable energy

0656 WS Influence of supplement type and monensin addition on utilization of low-quality, cool-season forage by beef cattle. D. W. Bohnert*[1], M. C. Rodrigues[1], M. C. Vieira[1], K. C. Swanson[2], S. J. Falck[3], and R. F. Cooke[1], *[1]Oregon State University – EOARC Burns, Burns, [2]North Dakota State University, Fargo, [3]USDA-ARS, EOARC Burns, Burns, OR*.

Two studies were conducted to evaluate the influence of supplement composition and monensin addition on intake and digestibility of a low-quality (4.5% CP), cool-season forage as well as cow performance. Treatments included a nonsupplemented control (CON), approximately 30% CP supplements consisting of corn and urea (CU), CU + monensin (200 mg/d; CU+M), dried distillers' grains (DDGS), or DDGS + monensin (200 mg/d; DDGS+M). In Experiment 1, 5 steers were used in an incomplete 5 × 4 Latin square with four 28-d periods to compare the effects of monensin and supplement type on forage intake, digestibility, and ruminal fermentation characteristics. Forage intake tended to be greater with supplementation ($P = 0.06$), was greater with DDGS compared with CU ($P = 0.03$), and was decreased with monensin addition ($P = 0.04$). Ruminal pH was increased with monensin; however, it was increased more with monensin addition to the DDGS supplement compared with the CU supplement ($P < 0.01$). In Experiment 2, 80 late gestation cows were stratified by age, BCS, and BW and randomly allotted to treatments (20 pens; 4 cows/pen and 4 pens/treatment). Precalving and postcalving BCS change were more positive with supplementation ($P < 0.01$), whereas monensin addition to the supplements benefited precalving ($P = 0.02$) and postcalving ($P = 0.02$) BCS change a greater amount with the CU supplement compared with the DDGS supplement. Monensin addition, irrespective of supplement type, reduced forage intake while maintaining performance of beef cattle consuming low-quality forage.

Key Words: cattle, cool-season, forage, ionophore, monensin, supplementation

0657 WS Methods to increase productivity of spring calving production systems in the Nebraska Sandhills. D. Broadhead*[1], A. Stalker[1], J. A. Musgrave[2], and R. N. Funston[3], *[1]University of Nebraska-Lincoln, North Platte, [2]University of Nebraska, Lincoln, [3]University of Nebraska, North Platte*.

A 2-yr study evaluated effects of late-gestation supplementation, postpartum progestin administration, and creep feeding on productivity of March calving cows. In yr 1, 120 crossbred cows (BW 479 ± 57 kg) were assigned to 1 of 4 levels of late-gestation supplementation, 1 of 2 levels of postpartum progestin, and 1 of 2 levels of creep feed in a 4 × 2 × 2 factorial arrangement of treatments in a completely random design. The

four supplement levels fed were 1) 0 kg/d Dec. 1 to Mar. 1, 2) 0.41 kg/d DM Dec. 1 to Mar. 1, 3) 0.41 kg/d DM Jan. 15 to Mar. 1, or 4) 0.82 kg/d DM Jan. 15 to Mar. 1 while cows grazed dormant upland range. Levels of exogenous progesterone postpartum were 1) controlled internal drug release device for 7 d or 2) no progesterone administration. Creep feed levels were 1) unrestricted access by the calf to creep feed, which contained an intake limiter, or 2) no access to creep feed. The higher levels of late-gestation supplementation increased cow BW ($P < 0.05$) and increased cow BCS ($P < 0.05$) but did not affect ($P > 0.12$) reproductive measures or calf performance. Exogenous progesterone administration postpartum did not affect ($P > 0.13$) cow or calf performance. Allowing calves access to creep feed increased ($P < 0.01$) calf BW at weaning by 21 kg.

Key Words: creep feed, progesterone, supplement

0658 Performance of stocker cattle grazing 'Tifton 85' bermudagrass supplemented with dried distillers' grains on per-animal and per-area bases: A two-year summary.

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The supply of dried distillers' grains (DDG) generated from the ethanol industry provides great opportunities for feed additives and supplementation of stocker cattle. The objective of this study was to evaluate performance of stocker calves grazing 'Tifton 85' bermudagrass [*Cynodon dactylon* (L.) Pers.] when supplemented daily with varying levels of DDG. Steers ($n = 96$ [4 testers pasture^{-1} yr^{-1}], 363 ± 3.7 kg initial BW, and approximately 15 mo of age) were stratified by BW and randomly allocated to each of 16 pastures (0.7 ± 0.01 ha) across 2 yr (2014 and 2015). Pastures were randomly allocated to each of 4 levels of DDG supplementation for about 110 d at 0, 0.25, 0.5, or 1% BW hd^{-1} d^{-1}. Steers were group fed daily at 0800 h and weighed every 21 d. Grazer animals were added to pastures based on visual and forage mass assessments to maintain a similar forage allowance among pastures. Data were analyzed using SAS PROC MIXED or PROC GLIMMIX. Least squares means were calculated for treatments and separated using *F*-protected *t* tests with the Tukey–Kramer adjustment. Average daily gain was greatest ($P < 0.05$) from steers offered 1% BW DDG (1.25 kg/d) and least from non-DDG steers (0.77 kg/d), with 0.25 and 0.5% BW being intermediate (1.05 and 1.12 kg/d, respectively). Additional gain from DDG supplementation was greater ($P < 0.05$) from 1% BW DDG (0.68 kg/d) than from 0.25 and 0.5% BW steers (0.47 and 0.54 kg/d, respectively). There was a trend ($P = 0.13$) toward increased supplemental feed to additional gain ratios of 4.2, 5.4, and 7.2 for 0.25, 0.5, and 1% BW DDG, respectively, indicating that higher levels of DDG supplementation resulted in substitution of forage in the diet. There was no measurable difference ($P = 0.33$) in stocking rate (318 kg = 1 steer) among treatments (overall mean = 12.4 hd/ha), whereas gain per area was greatest ($P < 0.05$) at 1,883 kg/ha from pastures offered DDG at 1% BW followed by intermediate values of 1,268 kg/ha at 0.25% and 1,399 kg/ha at 0.5% BW. Pastures receiving no supplementation had steers gaining 906 kg/ha. Supplementation of stocker calves with DDG while grazing Tifton 85 bermudagrass is a viable management strategy to optimize gain per animal or per area.

Key Words: Tifton 85 bermudagrass, dried distillers' grains, stocker, supplement

0659 Monensin effects on early-weaned beef calves grazing annual ryegrass pastures.

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The objective of this study was to evaluate the effects of monensin on performance of early weaned beef calves grazing annual ryegrass (*Lolium multiflorium*). The experiment was conducted at the University of Florida/Institute of Food and Agricultural Sciences Range Cattle Research and Education Center, Ona, FL, from January 12 to April 14, 2015. Treatments were calves receiving monensin (20 mg/kg of estimated total DMI) or control (no monensin) distributed in a randomized complete block design with four replicates. Calves were weaned with 81 ± 6 kg BW at 84 ± 20 d of age. Calves were supplemented with 1% BW concentrate (18% CP and 78% TDN) daily. Four calves were allocated to each pastures (0.3 ha, experimental unit) in a continuous and fixed stocking rate. Herbage mass and nutritive value were evaluated every 14 d, and calf BW was recorded every 28 d. Blood samples were collected at the termination of the study. Data were analyzed using the Proc Mixed of SAS with treatment as fixed effect and block as random effect. There was no difference ($P \geq 0.05$) in herbage mass (mean = 1,450 kg/ha), CP (mean = 22.2%), and in vitro digestible OM (mean = 78.7%) between treatments. Calves receiving monensin had greater ADG (0.71 vs. 0.57 kg/d; $P = 0.003$) and tended to have greater IGF-1 (89.5 vs. 67.9 ng/mL; $P = 0.09$) but there was no difference ($P \geq 0.05$) in BUN (mean = 26.7 mg/dL), glucose (mean = 86.3 mg/dL), and insulin (mean = 2.31 uIU/mL). The incidence of coccidiosis was lesser (0.49 vs. 1.35 log count) for calves receiving monensin. Adding monensin to the concentrate supplement

is a feasible management practice to improve performance of early weaned calves grazing annual ryegrass pastures.

Key Words: supplementation, beef cattle, monensin

0660 Reduced enteric methane emissions on legume versus grass irrigated pastures. J. W. MacAdam*[1], K. A. Beauchemin[2], A. I. Bolletta[3], and L. R. Pitcher[4], *[1]Department of Plants, Soils, and Climate, Utah State University, Logan, [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]National Institute of Agricultural Technology, Bordenave, Argentina, [4]Utah State University, Logan*.

Life cycle assessment that compared the cow–calf and feedlot phases of beef production in western Canada demonstrated that the greatest source of greenhouse gas emissions, in carbon dioxide equivalents (CO_2 eq.), was enteric methane (CH_4). Furthermore, the cow–calf phase was responsible for approximately 80% of CO_2 eq. Perennial legume forages contain less fiber than grasses and are, therefore, more digestible, and condensed tannins (CT) have been reported to reduce ruminant enteric methane emissions. Our objective was to measure enteric CH_4 emissions of beef cows and heifers grazing irrigated pastures. We compared a grass with two nonbloating legumes, one that had CT and one that did not. Our treatments were meadow bromegrass (*Bromus riparius* Rehmann), CT-containing birdsfoot trefoil (*Lotus corniculatus* L.), and non-CT cicer milkvetch (*Astragalus cicer* L.). The study was a randomized complete block design with 5 replications. The experimental unit was a 0.365-ha rotationally stocked pasture containing one forage treatment and one cow in late gestation (616 ± 8 kg; 2014) or two heifers (each 439 ± 7 kg; 2015). Following a 5- (2014) or 2-wk (2015) adjustment period, enteric methane was sampled on 4 d/wk for 5 wk on 1 (2014) or 2 (2015) reps/wk using the sulfur hexafluoride method (Johnson et al., 2007). Forage disappearance from pastures was estimated from pre- minus postgrazing herbage DM, measured using a rising plate meter calibrated for each species. This value is presented as percent of BW. The herbage of the cultivar of birdsfoot trefoil used in this study, *Langille*, contained 20 to 30 mg CT/g DM whereas the CT concentration of the other two pasture species was negligible. We conclude that methane emissions were reduced by approximately half for cows grazing legumes compared with grass and by approximately one-third for heifers grazing legumes compared with grass. However, there did not appear to be an effect of CT on enteric CH_4 emissions.

Key Words: birdsfoot trefoil, cicer milkvetch, meadow bromegrass

0661 Milk production, rumination, and body condition score of organic dairy cattle grazing two pasture systems incorporating warm and cool season forages. K. E. Ruh*[1,2], B. J. Heins[2], and J. Paulson[3], *[1]University of Minnesota, Saint Paul, [2]University of Minnesota West Central Research and Outreach Center, Morris, MN, [3]University of Minnesota Extension, Rochester*.

Organic dairy cows ($n = 90$) of Holstein and crossbred genetics were used to evaluate the effect of two pasture production systems (perennial versus perennial/annual systems) over two grazing seasons (May to October of 2014 and 2015) on milk production, milk components (fat, protein, MUN, and SCS), rumination (min/d), BCS, and BW. Cows were assigned to one of two pasture systems: 1) system 1, a diverse mixture of cool season grasses and legumes (perennial ryegrass, white clover, red clover, chicory, orchardgrass, meadow bromegrass, alfalfa, and meadow fescue), or 2) system 2, the same combination of perennial polycultures and annual warm season grasses (brown midrib sorghum-sudangrass [BMRSS] and teff grass). Cows rotationally grazed pasture and moved to a new paddock every 2 d and were supplemented corn (2.27 kg/d) and provided free-choice mineral on pasture. Weekly milk production, monthly milk components, and biweekly BW and BCS were recorded for each of the six replicate groups. Activity and rumination time (daily) were monitored electronically using HR-LD Tags (SCR Engineers Ltd., Netanya, Israel) for the grazing season. The PROC MIXED of SAS was used for statistical analysis, and independent variables were fixed effects of system (1 or 2), forage (perennial grass, BMRSS, or teff) nested within system, year (2014 or 2015),

Table 0660.

Table 1. Enteric methane emissions and forage allowance on irrigated pastures

	Birdsfoot trefoil	Cicer milkvetch	Meadow bromegrass
Enteric methane (g/head/d)			
Cows, 2014	167b	159b	355a
Heifers, 2015	152b	145b	215a
Forage disappearance (kg DM/d/kg BW)			
Cows, 2014	1.63a	2.04a	2.17a
Heifers, 2015	1.99b	2.68a	1.62b

Numbers within a row followed by different letters are statistically different at $P < 0.05$.

system nested within year, and week nested within system, with replicate nested within system as a random effect with repeated measures. System 1 and system 2 cows had similar ($P > 0.05$) milk production (14.7 and 14.8 kg/d, respectively), fat percentage (3.92 vs. 3.80%, respectively), protein percentage (3.21 vs. 3.17%, respectively), MUN (12.5 and 11.5 mg/dL, respectively), and SCS (4.05 and 4.07, respectively). There was a significant yearly effect ($P < 0.05$) for milk production, MUN, and SCS for both systems. Milk production was higher ($P < 0.05$) in 2015 compared with 2014 (15.6 vs. 13.9 kg/d, respectively). There was no effect ($P > 0.05$) of forage type on milk production, fat, protein, MUN, or SCS. Cows in system 1 had greater ($P < 0.05$) daily rumination (530 min/d) compared with cows in system 2 (470 min/d). The BW (485 and 497 kg) and BCS (3.10 and 3.06) were similar ($P > 0.05$) for system 1 and 2, respectively. In summary, warm season annual forages may be incorporated into grazing systems for organic dairy cattle while maintaining milk production and quality.

Key Words: grazing, BMR sorghum-sudangrass, teff

0662 Evaluation of production, rumination, milk fatty acid profile, and profitability for organic dairy cattle fed sprouted barley fodder. B. J. Heins*[1], J. Paulson[2], and H. Chester-Jones[3], *[1]University of Minnesota West Central Research and Outreach Center, Morris, [2]University of Minnesota Extension, Rochester, [3]University of Minnesota Southern Research and Outreach Center, Waseca*.

Certified-organic cows (n = 36) were used to evaluate the effect of feeding sprouted barley fodder to dairy cows on production, SCS, BW, BCS, daily rumination, milk fatty acid profile, and profitability. Cows were assigned to one of two replicated treatment groups (4 groups; n = 9 cows each group): 1) no fodder supplementation or 2) fodder supplementation at 9.1 kg/cow per day. Supplement was fed with a total mixed ration of organic corn silage, alfalfa haylage, and an organic grain mix (corn and minerals). The fodder replaced 2.7 kg of DM of organic corn. The no-fodder cows were fed 3.6 kg of organic grain in the supplement. The study was conducted at the University of Minnesota's West Central Research and Outreach Center, Morris, MN. For 70 d during the summer of 2015, 28 fodder trays (0.6 by 1.8 m) from a FarmTek Fodder Pro system were filled with 4.1 kg of presoaked barley grain, which was soaked for 24 h, to produce sprouted barley fodder. Each tray was automatically watered three times a day for 4 min each time. Weekly milk production, monthly milk components, and biweekly BW and BCS were recorded for each of the four replicate groups. Activity and rumination time (daily) were monitored electronically using HR-LD Tags (SCR Engineers Ltd., Netanya, Israel). Data were analyzed using the MIXED procedure of SAS on a pen basis. Independent variables for analyses were the fixed effects week of study and fodder supplementation group and replicate was a random effect. Milk production and SCS were not different ($P > 0.05$) for the fodder (12.3 kg/d and 3.63, respectively) and no-fodder (13.3 kg/d and 3.55, respectively) supplementation groups. Furthermore, BW (503 kg vs. 505 kg) and BCS (3.17 vs. 3.17) for fodder and no-fodder cows were not different. The fodder cows tended ($P < 0.10$) to have less rumination (519 vs. 550 min/d) compared with the no-fodder cows. The fodder cows tended ($P < 0.10$) to have a lower omega 6:omega 3 ratio (1.16 vs. 1.40) than the no-fodder cows. Net income per cow per day was similar for fodder ($2.96 vs. $3.18 cow/d) and no-fodder cows, respectively. In summary, the results show that sprouted barley fodder may have no benefit in an organic production system.

Key Words: sprouted fodder, production, organic

0663 Effect of tillage and planting date of wheat pasture on forage production and calf performance. P. A. Beck*[1], W. Galyen[2], T. Hess[3], and D. S. Hubbell III[3], *[1]University of Arkansas SWREC, Hope, [2]University of Arkansas, Fayetteville, [3]University of Arkansas Livestock and Forestry Research Station, Batesville*.

The objectives of this experiment were to determine how fall wheat forage production and animal performance are affected by establishment method (conventional tillage [CT] vs. no-till [NT]) and timing in dedicated wheat fields (1.6 ha). No-till pastures were planted on August 15 (n = 8), September 1 (n = 8), or September 15 (n = 8) and CT pastures were planted on September 1 (n = 3) or September 15 (n = 3). Preconditioned steers (n = 236; 245 ± 21.1 kg BW) were placed on wheat pasture when forage mass reached a minimum of 1,100 kg DM/ha. Steers were destocked from pastures on 23 February 2015 and 11 February 2016. Forage mass was estimated monthly using a calibrated rising plate meter, with 20 plate readings per pasture. Data were analyzed as a randomized complete block design using the mixed procedure of SAS (SAS Inst. Inc., Cary, NC). Forage mass in November for NT did not differ (P = 0.91) between the August 15 (1,525 ± 386 kg/ha) and September 1 (1,548 ± 386 kg/ha) planting dates but was greater than (P = 0.05) the September 15 planting date (1,153 ± 386 kg/ha). November forage mass for CT planted on September 1 (1,982 ± 426 kg/ha) tended (P = 0.10) to be greater than that for CT planted on September 15 (1,444 ± 426 kg/ha) and NT planted on August 15 or September 1. No-till planting on September 15 (1,153 ± 386 kg/ha) produced less ($P \leq 0.05$) forage in November than other planting methods. The average starting date of grazing was November 26 for CT planted on September 1 or September 15 and NT planted on August 15 or September 1 whereas the average starting date of grazing was delayed ($P < 0.01$) until December 8 for the NT September 15 planting. Initial forage allowance (3.79 ± 0.93 kg forage DM/kg steer BW) did not differ ($P \geq 0.84$) among tillage methods and planting dates and, therefore, ADG (1.24 ± 0.10 kg/d) did

not differ ($P = 0.63$) among planting methods. Steer grazing days per hectare and BW gain per hectare were reduced ($P \leq 0.02$) by NT planting on September 15. Planting wheat pasture in mid August using NT did not result in improved forage production or animal gains compared with CT or NT on September 1. If planting is delayed until mid September, use of CT provides advantages over NT.

Key Words: Wheat pasture, tillage, planting date, steers

0664 Impact of high-energy forages on grass-finished steer performance and carcass merit.

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The research objective was to compare high-energy forage options during the finishing period for Upper Midwestern forage-finished beef production systems. Twelve 0.80-ha pastures were randomly assigned to 1 of 3 forage treatments including mixed pasture (MIX), simple cereal grain/brassica mixture (SIMP), and complex cereal grain/brassica mixture (COMP). Red Angus–influenced steers (439.99 kg ± 4.21 BW; $n = 24$) were stratified by BW and randomly assigned to 1 of 12 paddocks and were grazed for a 76-d finishing period. Steers had ad libitum access to water, free choice mineral, and supplemental hay and were allowed access to strips in each grazing treatment, which were back fenced to allow for forage regrowth. Overnight fasted BW was measured on d 0, 36, 66, and 76. At the end of the finishing period, steers were slaughtered under federal inspection and carcass data were collected 48 h postmortem. Data were analyzed using Proc Mixed (SAS version 9.4) where paddock was the experimental unit. Steers had different d 0 to 76 BW gains ($P < 0.01$), where gains were greatest for MIX (90.15 kg ± 3.32) followed by COMP (73.71 kg ± 3.32) and then SIMP (64.64 ± 3.32). Although overall BW gains were greatest for steers in MIX, there was a tendency ($P = 0.11$) for d 67 to 76 gains to be highest in COMP and least for MIX (19.28 kg ± 2.07 and 12.47 kg ± 2.07, respectively).There was a treatment × period interaction for d 76 BW ($P < 0.01$), where steers on COMP and SIMP had less BW (514 kg ± 4.7 and 505 kg ± 4.7, respectively) than those on MIX (530 kg ± 4.7), yet each had greater ($P < 0.01$) dressing percents (56.95% ± 0.44 and 59.96% ± 0.44 versus 54.67% ± 0.44, respectively).There were no differences ($P > 0.05$) among steer carcasses from all treatments for HCW, backfat, LM area, KPH, YG, and marbling score. These data indicate that steers grazing all treatments had reasonable gains and carcass merit and that these systems can be a viable component of forage-finishing systems in the Upper Midwest.

Key Words: brassicas, beef, grass finished

0665 Effect of stocking rate on performance, diet selection, and apparent total-tract digestibility among heifers grazing cover crops.

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Grazing cover crops can increase lands available for cattle production and reduce costs associated with winter feeding. Unfortunately, data are limited on stocking rates that allow optimal utilization of cover crops by cattle. We evaluated effects of stocking rate among heifers (573 ± 9.5 kg BW) grazing cover crops. Cover crop pasture (12.1 ha) consisted of a mixture of annual ryegrass (*Lolium multiflorum*; 66.5%), radish (*Raphanus sativus*; 20%), and purple top turnip (*Brassica rapa*; 13.5%). Pasture was divided into 12 paddocks. Heifers were blocked by weight before initiation of the experiment and randomly assigned to 1 of 4 BW blocks. Stocking rate treatments were designed to obtain 45, 55, or 65% forage utilization and were achieved by randomly assigning 3, 4, or 5 heifers within each BW block to paddocks. All paddocks in 3 BW blocks contained a ruminally cannulated heifer to facilitate measures of diet selection, and heifers were allowed to graze for 48 d. Heifers were weighed on consecutive days at the beginning and end of the experiment and on d 9 to 22. Heifers were provided TiO_2 from d 14 to 23, and composite fecal samples (d 18 to 24) allowed estimates of fecal output. Estimates of DMI and diet digestibility were obtained from determination of fecal and diet acid detergent insoluble ash. Initial, intermediate, and final diet samples were collected on d 2, 24, and 46 by ruminal evacuation. Fecal and diet samples were analyzed for DM, OM, NDF, and ADF. Reductions in stocking rate tended to increase intermediate (linear effect, $P = 0.06$) and overall (linear effect, $P = 0.10$) ADG. However, estimates of DMI tended (quadratic effect, $P = 0.07$) to be less as stocking rate was reduced. Reduced stocking rate tended (quadratic effect, $P = 0.06$) to increase diet DM; however, stocking rate had no impact ($P \geq 0.15$) among diet OM, NDF, and ADF. Estimates of DM and OM digestibility decreased (quadratic effect, $P < 0.01$) with reduced stocking rate. Similarly, reduced stocking rate tended (linear effect, $P = 0.06$) to reduce NDF digestibility, but stocking rate had no effect ($P \geq 0.23$) among estimates of ADF digestibility. These data indicate that reduced stocking rate among heifers grazing cover crops tends to increase performance. It is unclear why estimates of DMI and diet digestibility decreased with reduced stocking rate.

Key Words: cattle, cover crops, stocking rate

0666 The physiological consequences of ingesting a toxic plant (*Diplotaxis tenuifolia*) and medicinal supplements influence subsequent foraging decisions by sheep. F. H. Catanese[1], J. J. Villalba*[2], and R. A. Distel[1], [1]*Universidad Nacional del Sur, Bahia Blanca, Argentina,* [2]*Utah State University, Logan*.

There is a large group of highly nutritious plants that are commonly avoided by grazing livestock due to the presence of toxic plant secondary compounds. Our hypothesis was that aversion toward toxic plants is learned and that their negative postingestive effects could be attenuated by specific nutrients. Therefore, we determined the impact of supplements on physiological parameters and feeding behavior in Merino sheep consuming *Diplotaxis tenuifolia* ("Wild rocket"), a plant with high concentration of glucosinolates (37.2 ± 3.6 μmol/g). Thirty-six sheep were randomly assigned to four feeding treatments in a split-plot design with lambs (n = 9) nested within treatment: Wild rocket (DT), Wild rocket and a protein (160 g/d) supplement (DT+P), Wild rocket and a protein supplement containing iodine (10 mg/d) and copper (40 mg/d) (DT+P+M), or alfalfa pellets (CTRL) in amounts that paired the ingestion of Wild rocket in DT. Toward the end of a 35-d exposure period, sheep in DT showed the lowest intake of Wild rocket (P = 0.04) as well as reduced concentrations of plasma thyroid hormones (T3 and T4; P < 0.001 and P = 0.05, respectively) and the enzyme alanine aminotransferase (P = 0.02) and a trend toward reduced hemoglobin concentration (P = 0.07) relative to sheep in DT+P and DT+P+M, which, in turn, showed concentrations of hormones and hepatic enzymes similar to those recorded in CTRL. Total serum protein and albumin levels were greater (P = 0.03 and P = 0.04, respectively) in supplemented than in unsupplemented sheep fed Wild rocket, which could have elicited a protective effect on glucosinolate ingestion. Foraging behavior was evaluated in an experimental arena where animals could select among randomly distributed buckets containing a fixed amount of Wild rocket or variable amounts of barley grain. Regardless of barley grain availability, sheep in DT showed lower intake and lower time spent eating Wild rocket than sheep in DT+P or in DT+P+M (19.0 vs. 48.5 and 43.2 ± 6.0 g [P = 0.007] and 26.8 vs. 54.4 and 48.9 ± 4.78 s [P = 0.005], respectively). Sheep in CTRL showed intake levels of Wild rocket and behavioral responses similar to those observed in supplemented sheep. In conclusion, nutritional supplements have the potential to attenuate the negative postingestive effects of glucosinolates in Wild rocket and enhance the utilization of the plant at pasture. A negative feeding experience with Wild rocket is needed for animals to display the typical pattern of aversion commonly observed in grazing conditions.

Key Words: feeding behavior, food aversions, glucosinolates

0667 Lining bunker wall with oxygen barrier film reduces nutrient losses of corn silages. L. M. Lima, J. P. Dos Santos, I. L. De Oliveira, J. O. Gusmao, M. S. Bastos, S. M. Da Silva, E. B. Alves, J. R. Gervasio, and T. F. Bernardes*, *Federal University of Lavras, Lavras, Brazil*.

Spoiled silage at the shoulders of bunker silo is common. The objective of this study was to evaluate the effect of two systems for covering corn silage in bunker silos. The first system comprised a sheet of 45-μm-thick oxygen barrier film (OB; polyethylene + ethylene-vinyl alcohol) placed along the length of the sidewall before filling, with approximately 2 m of excess draped over the wall. After filling, the excess film was pulled over the wall, and a sheet of polyethylene was placed on top. The second system involved using a standard sheet (ST) of 180-μm-thick polyethylene film. Eight commercial bunker silos were divided into two parts lengthwise so that half of the silo was covered with OB and other with ST system. During the filling, three bags with chopped corn were buried in the central part of the bunkers (CORE) in three 10-m-apart sections. After filling, 18 bags (9 per covering system) were buried in the upper layer of the three sections. These bags were placed at three distances from the bunker walls (0 to 50, 51 to 100, and 101 to 150 cm). During unloading, the bags were removed from the silos to determine the DM losses, fermentation end products, and nutritive value. The Milk2006 spreadsheet was used to estimate milk per ton of DM. The experiment was set up as randomized blocks with eight replicates (silos). Two orthogonal contrasts were tested to compare silages under the two covering systems with that in the CORE (OB versus CORE and ST versus CORE). Three orthogonal contrasts compared the distances from the bunker walls (OB50 versus ST50, OB100 versus ST100, and OB150 versus ST 150). Variables were analyzed with the PROC MIXED procedure of the SAS at 5%. The OB method produced well-fermented silages, which were similar to the CORE, whereas the PE system showed less lactic acid and greater pH and mold counts compared with the CORE. The PE method had 116.2 kg of milk/ton less than the CORE (P = 0.0016), as the OB system and the CORE were similar (1,258.3 and 1,294.0 kg/ton, respectively). Regarding the distances from the walls, the effects were more pronounced in the corner zones (0 to 50 cm). OB50 silages had better fermentation profile and lower spoiled microorganisms and DM losses than ST50. Corn silage at the shoulders has quality similar to the CORE when the OB system is used.

Key Words: aerobic deterioration, bunker silo, silage covering

0668 Effects of method and storage time on the nutritive value of sugarcane for dairy cattle.
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Fresh chopped sugarcane is an important forage source for dairy cattle in tropical environments; however, daily harvest has been a major constraint for producers. Therefore, the objective of this study was to evaluate two storage methods (stem and whole plant) in different times on the nutritive value, microbial counts, and DM losses to extend the intervals between harvests. Two experiments were performed for 2 yr (Experiment 1 and 2). In both experiments, 288 plants of sugarcane were manually collected during the crop harvesting window. Leaves were removed from 144 plants and other part remained intact (whole plants). Sugarcane stems and plants were split into 18 bunches (8 stems or plants per bunch) and placed on the ground in a barn at ambient temperature for 0, 2, 4, 6, 8, and 10 d. For each day of evaluation, three bunches of each treatment were weighed to determine DM losses. Afterward, bunches were chopped to assess nutritive value and microbial counts (bacteria, yeasts, and molds). In experiment 2, additionally to these parameters was assessed the leaf carbon balance (CO_2 uptake during photosynthesis minus CO_2 loss during respiration) in sugarcane plants. Treatments were arranged in a completed randomized design with repeated measurements over time. The data were analyzed by the mixed-model method using the MIXED procedure (SAS Institute, 2004). The means were compared using a Tukey test at the 5% probability. In both experiments, DM and NDF concentrations and in vitro DM digestibility were lower in stems compared with whole plants. Storage time had an inconsistent effect on chemical composition and microbial counts. Only DM losses were affected by the interaction between method and storage time. Whole plants reached losses more than 90 kg MS/ton at 6 and 8 d in the experiment 1 and 2, respectively. On the other hand, stems showed the maximum DM losses at 10 d (55.1 and 35.0 kg MS/ton for experiment 1 and 2, respectively). The carbon balance of leaves in whole plants was negative due to respiration losses from 2 d storage, which might explain the rise in DM losses. Overall, sugarcane stems is the most effective method to store forage under a cut-and-carry system because stems have greater nutritive value and take up less space in the barn with a long duration of aerobic stability (10 d).

Key Words: cut-and-carry system, forage harvesting, tropical forage

0669 Bunk heating of rations containing corn silage with various inoculants, a stabilizer, or wet grain byproducts: A field survey.
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Inoculation of corn silage with *Lactobacillus buchneri* (LB) retards yeast growth and delays heating of corn silage exposed to air. The objective of this survey was to quantify the effects of LB inoculation of corn silage on temperature stability of total mixed ration (TMR) containing corn silage with or without added wet feeds (12 with whey, 9 with wet distillers' grains, and 5 with wet corn gluten). Effects of adding a feed stabilizer ($n = 6$) to the TMR also were monitored. Samples of 57 TMR as delivered to the bunk at 55 dairies in the Upper Midwest were obtained during June of 2015. These TMR samples were exposed to air at room temperature and TMR temperatures were recorded after 6, 12, 24, 36, 48, 60, and 72 h of air exposure by an individual not familiar with the silage treatments or TMR additions. Although 9 different silage inoculants were used, only one of the inoculants contained LB. When compared with the TMR containing corn silage with other inoculants, TMR containing corn silage treated with LB had TMR temperatures that were 2, 5, and 7°C lower ($P < 0.05$) at 6, 12, and 24 h. Temperature responses differed among the various wet feeds that were added. Including wet distillers' grains in the TMR resulted in a 6°C greater ($P < 0.05$) temperature by 24 h but differences thereafter were not significant ($P > 0.10$). Including wet gluten or whey in the TMR resulted in temperatures that were 7°C and 5°C greater ($P < 0.05$), respectively, at 12 h than TMR not containing these wet feeds. Total mixed rations containing wet grains plus corn silage treated with LB had temperatures that were 3, 7, and 8°C lower ($P < 0.02$) at 6, 12, and 24 h than those TMR containing wet grain plus corn silage not treated with LB. Addition of the feed stabilizer failed to significantly alter the TMR temperature at any time. In conclusion, LB inoculation of corn silage that was included in the TMR reduced heating of the TMR as delivered to lactating cows for 24 h whether or not wet feeds were included in the TMR.

Key Words: corn silage, inoculants, temperature stability

0670 The effect of *Lactobacillus brevis* and fibrolytic enzymes on fermentation of switchgrass silages.

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The objective of this study was to determine the effect of *Lactobacillus*, enzymes, and *Lactobacillus* + enzymes mixture on fermentation characteristics, nutritive value, and microbial diversity of switchgrass silage. Switchgrass (*Panicum virgatum* L.) was harvested at vegetable stage and treated with distilled water (control), *Lactobacillus brevis*, fibrolytic enzymes, and *L. brevis* + fibrolytic enzymes (denoted C, LB, E, and LB+E, respectively) before ensiling. Treated switchgrass was ensiled in sealed 1.0-L plastic jars. Inoculation accelerated the decline of silage pH. Compared with other treatments, LB+E had the greatest decline ($P < 0.05$) in pH during the first 3 d of ensiling. After 30 d, for C, LB, E, and LB+E, pH declined to 5.3, 4.6, 4.8, and 3.7, respectively. There was no butyric acid detected in LB and LB+E. Lactic acid concentration of LB and LB+E increased by 5.53 times and 21.75 times than that of C, respectively. Acetic acid concentration of LB and LB+E decreased by 36.34 and 9.40%, respectively. NH_3–N concentration of LB, LB+E, and E decreased by 67.7, 74.55, and 69.88%, respectively. Treatments with enzymes (E and LB+E) effectively ($P < 0.05$) decreased NDF and ADF concentration. Neutral detergent fiber concentration of E and LB+E decreased by 8.09 and 8.43%, respectively. Acid detergent fiber concentration of E and LB+E decreased by 3.03 and 10.88%, respectively. Crude protein content of C, LB, E, and LB+E was 77.6, 96.2, 88.0, and 97.0 g/kg DM, respectively, suggesting that inoculation increased CP content of switchgrass silage ($P < 0.05$). The 16S rRNA gene-based pyrosequencing was used to analyze the community of the 30-d silage, and results indicated that the diversity of microorganisms differed among treatments ($P < 0.05$). *Enterobacter* was the dominant genus in C, and the relative abundance of *Enterobacter* was 53.60%. *Enterobacter* was the dominant species in E, although the relative abundance of *Enterobacter* decreased to 40.67% and that of *Lactobacillus* increased to 26.13% in E. In LB and LB+E, *Lactobacillus* was the advantageous species (91.19 and 96.89%, respectively), and *Enterobacter* was effectively inhibited. In conclusion, the addition of bacterial and enzymatic additives can improve the switchgrass silage fermentation quality at different extent. Adding the mixture of *L. brevis* and fibrolytic enzymes worked more efficient than adding either *L. brevis* or fibrolytic enzymes, respectively.

Key Words: switchgrass silage, fermentation characteristics, nutritive value

0671 Effects of wrapping time delays on fermentation characteristics of baled alfalfa silages.

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Baled silage is an attractive forage conservation approach for small and mid-sized dairy or beef producers, partly because it limits the risks associated with baling dry hay during wet or unstable weather conditions. Our objectives were to test the effects of delayed wrapping on silage fermentation and the storage characteristics of baled alfalfa silages. A secondary objective was to evaluate a prototype bale wrap containing an O_2–limiting barrier, against an identical polyethylene wrap without the O_2 barrier. Sixty-four 1.19- by 1.25-m round bales of alfalfa were made from 4 field blocks at a mean moisture concentration of 59.1 ± 4.3% and a mean initial wet bale weight of 473 ± 26.4 kg. Large-round bales were wrapped in plastic film within 4 h of baling (d 0) or after delays of 1, 2, or 3 d and then stored for 97 d. All bales were wrapped with 7 polyethylene layers. At wrapping, internal bale temperatures were greater for all bales with wrapping delays compared with bales wrapped on d 0 (54.9 vs. 34.9°C; $P < 0.01$) and linearly increased ($P < 0.01$) to a maximum of 63.9°C after a 3-d delay. No internal bale temperature for any treatment combination exceeded 30°C by 23 d after baling. Concentrations of water=soluble carbohydrates linearly declined with bale temperature at wrapping ($y = -0.039x + 6.5\%$; $r^2 = 0.634$); conversely, the buffering capacity of pre-ensiled forages linearly increased with bale temperature ($y = 2.98x + 316$ mEq/kg DM; $r^2 = 0.759$). Total silage fermentation acids were greatest when bales were wrapped on d 0 compared with bales wrapped with 1-, 2-, or 3-d time delays (4.64 vs. 2.26%; $P < 0.01$) and declined with both linear ($P < 0.01$) and quadratic ($P < 0.01$) effects of time delay. Similar responses were observed for lactic acid but without the quadratic effect of time ($P = 0.18$). Butyric acid also was detected and was greatest within bales wrapped on d 0 compared with those wrapped after 1, 2, or 3 d (0.99 vs. 0.38%; $P < 0.01$), and a similar response (0.68 vs. 0.52%; $P < 0.01$) was observed for NH_3–N (% of DM). Bale wrap had no effect on any silage fermentation response ($P \geq 0.07$), likely because of the conservative (7-layer) wrapping protocol. Silage fermentation characteristics deteriorated with time delays before wrapping, but responses were exacerbated when delays exceeded 1 d.

Key Words: alfalfa, baled silage, fermentation

0672 Effects of wrapping time delays on the nutritive value of baled alfalfa silages. W. K. Coblentz*[1], K. P. Coffey[2], and E. A. Chow[3], [1]*U.S. Dairy Forage Research Center, Marshfield, WI,* [2]*University of Arkansas, Division of Agriculture, Fayetteville,* [3]*Kuraray America, Inc., Pasadena, TX.*

Baled silages are an attractive forage conservation option, especially for small and mid-sized beef and dairy producers. Our objectives were to test the effects of delayed wrapping on the nutritive value of baled alfalfa silages on a pre- and post-storage basis. A secondary objective was to evaluate a prototype bale wrap containing an O_2–limiting barrier against an identical polyethylene wrap without the O_2 barrier. Sixty-four 1.19- by 1.25-m large-round bales were wrapped in plastic film within 4 h of baling (d 0) or after delays of 1, 2, or 3 d. All bales were wrapped with 7 polyethylene layers. The internal bale temperature for all bales declined to <30°C by 23 d after baling, regardless of wrapping time delay. Internal bale temperatures ranged from 34.9 to 63.9°C, 38.1 to 66.7°C, and 29.7 to 39.6°C when determined at the time of wrapping, as the maximum temperature during storage, and as mean for the initial 23 d of storage, respectively. In each case, these responses were explained by linear ($P < 0.01$) effects of time delay; a quadratic ($P = 0.01$) effect of time also was observed for the 23-d mean temperature. After completing a 97-d storage period, NDF concentrations could be linearly related to internal bale temperature at wrapping ($y = 0.14x + 40.5\%$; $r^2 = 0.67$). Concentrations of neutral-detergent insoluble CP ($y = -0.0009x^2 + 0.16x - 1.3\%$ of DM; $R^2 = 0.84$) and acid-detergent insoluble CP ($y = -0.0003x^2 - 0.014x + 2.1\%$ of DM; $R^2 = 0.70$) both quadratically increased with internal bale temperature at wrapping. Energy density calculated as TDN with the summative approach declined in a quadratic relationship with internal bale temperature at wrapping ($y = -0.0039x^2 + 0.31x + 51.2\%$ of DM; $R^2 = 0.61$), which represented a loss of approximately 3 TDN units when wrapping was delayed by 3 d. Generally, responses were less clear when samples of unfermented forage were obtained immediately before bales were wrapped in polyethylene. The type of bale wrap had no effect ($P \geq 0.32$) on any aspect of forage nutritive value, likely because of the conservative (7-layer) wrapping protocol. The nutritive value of fermented round-bale silages deteriorated with time delays before wrapping, but responses were exacerbated with delays longer than 1 d.

Key Words: alfalfa, baled silage, nutritive value

0673 Effects of corn planting density and maturity on yield and nutritional quality of corn silage. G. Ferreira* and C. L. Teets, *Virginia Polytechnic Institute and State University, Blacksburg.*

The objective of this study was to determine the effects of planting density and maturity on yield and nutritional quality of corn for silage in a double-crop rotation system. The study was performed at an 800-cow dairy farm located in southern Virginia. Corn was planted in experimental plots within 2 cornfields, one of which was irrigated with a central-pivot irrigation system. Planting densities were 55, 70, 85, and 100 seeds/ha (× 1,000) in 4 replicates per cornfield (2 fields × 4 densities × 4 replicates = 32 plots total). Plots were twelve 50-m-long rows separated by 76 cm. The irrigated cornfield was watered with approximately 100 mm of water before silking. At one-fourth and three-fourths milk-line stages of maturity (early and late, respectively), 10 plants from each plot were cut (15 cm above ground), weighed, chopped, mixed, and analyzed using wet chemistry. Additionally, 200 to 400 g of chopped material were placed into mini-silos and analyzed after 60 d. Data was analyzed as a completely randomized design with repeated measures. The statistical model included the fixed effects of density (D) and irrigation (I), the interaction of D × I, the whole-plot error, the fixed effect of maturity (M), and the interactions of M × D, M × I, and M × D × I. Dry matter yield linearly increased ($P < 0.01$) when increasing planting density at both maturity stages. Concentrations of CP, NDF, and starch of the fresh material were not affected ($P > 0.13$) by planting density at any maturity stage. Maturity did not change CP ($P > 0.20$) and NDF ($P > 0.54$) concentrations but increased starch ($P < 0.01$) and decreased ($P < 0.01$) sugars concentrations in the fresh materials. The decrease in sugars concentration with maturity was greater ($P < 0.05$) for

Table 0673.

Effect of corn planting density (plants/ha x 1000; D), irrigation (I) and maturity (M) on yield and nutritional quality of corn silage.

	Early Maturity								Late Maturity									P value						
	No Irrigation				Irrigation				No Irrigation				Irrigation											
	55	70	85	100	55	70	85	100	55	70	85	100	55	70	85	100	SEM	I	D	IxD	M	MxI	MxD	MxIxD
Plant Weight, kg/plant	0.350	0.302	0.270	0.234	0.427	0.328	0.293	0.280	0.421	0.346	0.281	0.276	0.430	0.398	0.329	0.290	0.017	0.01	0.01	0.97	0.01	0.38	0.38	0.06
DM Yield, kg/ha x 1000	18.5	19.6	21.4	22.5	22.7	20.9	22.8	26.3	22.3	22.5	22.4	26.4	22.9	25.3	25.5	27.2	1.9	0.01	0.01	0.99	0.01	0.38	0.58	0.09
DM, %	32.0	31.6	31.0	32.2	30.3	29.0	28.7	30.1	37.6	37.5	37.9	36.5	33.7	33.9	33.1	31.9	1.32	0.01	0.63	0.95	0.01	0.04	0.16	0.92
CP, %	10.0	10.1	10.6	10.2	10.9	10.7	10.8	10.6	10.0	9.9	10.1	10.6	10.0	10.2	10.6	10.9	0.53	0.08	0.49	0.99	0.20	0.47	0.29	0.48
NDF, %	38.0	39.8	38.8	40.3	41.0	40.3	42.6	39.5	38.0	39.2	39.9	42.1	38.0	38.7	40.1	40.8	1.98	0.36	0.18	0.34	0.54	0.16	0.39	0.83
Starch, %	34.6	35.3	34.8	34.3	30.3	31.8	30.5	32.8	37.6	36.9	37.1	34.9	34.5	38.1	37.0	32.4	2.07	0.01	0.26	0.62	0.01	0.11	0.12	0.43
Sugars, %	17.4	14.4	16.1	14.1	11.3	13.2	16.5	12.8	10.0	8.1	8.3	8.3	8.5	8.3	10.7	8.3	1.61	0.06	0.01	0.01	0.01	0.05	0.84	0.62
Silage pH	3.65	3.71	3.71	3.74	3.65	3.65	3.61	3.66	3.80	3.82	3.82	3.85	3.78	3.79	3.78	3.80	0.30	0.01	0.11	0.34	0.01	0.11	0.94	0.62
DM Silage, %	30.5	30.9	30.3	30.9	28.5	27.1	28.8	28.9	35.4	35.9	35.9	35.5	32.7	32.4	31.9	31.5	1.14	0.01	0.98	0.75	0.01	0.16	0.63	0.66
Ash Silage, %	4.9	4.9	4.3	4.5	4.7	4.4	4.6	4.4	4.2	4.3	4.3	4.4	3.6	3.7	3.8	4.3	0.39	0.04	0.92	0.62	0.01	0.27	0.10	0.68
CP Silage, %	10.5	11.2	11.2	10.9	10.7	10.9	11.5	10.9	9.2	9.7	10.2	10.1	9.7	11.0	10.7	10.9	0.48	0.07	0.05	0.79	0.01	0.05	0.64	0.12
NDF Silage, %	44.1	46.9	44.1	45.5	44.7	45.6	45.4	41.1	39.2	39.4	43.9	44.3	39.8	37.2	39.0	40.7	2.00	0.03	0.65	0.17	0.01	0.26	0.02	0.26
Starch Silage, %	28.5	27.3	29.6	28.4	28.9	31.9	28.9	31.6	31.7	35.1	28.9	26.8	32.1	32.8	31.6	28.5	2.25	0.14	0.14	0.82	0.05	0.38	0.02	0.14
Sugars Silage, %	6.2	7.6	7.1	6.6	8.9	8.2	7.7	8.6	2.3	1.9	2.0	2.3	3.1	2.5	2.4	2.3	1.07	0.01	0.91	0.59	0.01	0.07	0.73	0.43

nonirrigated than for irrigated corn (6.8 and 3.5 percentage units, respectively). A cubic effect ($P < 0.01$) of planting density on sugars concentration was observed for fresh samples. Planting density did not affect silage pH ($P > 0.11$) but late maturity silages had greater pH ($P < 0.01$) than early maturity silages (3.81 vs. 3.67, respectively). The concentrations of NDF, starch, and sugars of silages did not change with planting density ($P > 0.14$). In conclusion, increasing planting density increased DM yields while minimally affecting the nutritional composition of corn silage at any maturity stage.

Key Words: planting density, corn silage, nutritional quality

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9674 Effect of homolactic bacteria inoculation and aerobic stress during ensiling on the nutritional and fiber digestibility characteristics of spring triticale. L. C. Solórzano*[1], L. L. Solorzano[2], A. A. Rodriguez[1], and J. A. Teisberg[4], *[1]University of Puerto Rico, Mayagüez, [2]Lankin, Fitchburg, WI, [3]Nurealm, LLC, Hutisford, WI.*

Silage is often aerobically stressed during storage due to improper management, weather, or mechanical issues, resulting in diminished silage quality. The effect of homolactic bacteria inoculation (HBI; supplying >9.1 × 10^{10} cfu/g containing *Lactobacillus plantarum*, *Enterococcus faecium*, *Lactococcus lactis*, *Pediococcus pentosaceus*, and *Pediococcus acidilactici*) and aerobic stress during ensiling on fresh whole plant spring triticale (x Triticosecale spp.) was evaluated. Triticale was fermented for 120 d at a temperature of 20 to 23°C using 3-L capacity PVC mini-silos fitted with two-way mechanics to vent gas. Sixteen mini-silos were filled with about 2 kg of the crop at about 35% DM and 5.2% soluble carbohydrates (DM basis). Four treatments were A) no HBI with gas vent closed, B) HBI with gas vent closed, C) no HBI with gas vent open during the ensiling period, and D) HBI with gas vent open during the ensiling period. Upon opening, nutritional characteristics and fiber digestibility were determined at a commercial lab (Rock River Lab, Watertown, WI). Statistical analysis was performed using a completely randomized designs. Treatment had no effect ($P > 0.05$) on the content of the following characteristics, which averaged (%) CP (16.9), ADICP (0.61), fat (3.54), aNDF (55.9), lignin (2.04), starch (0.17), sugar (1.73), NFC (11), ash (14), total tract NDF digestibility (49.2), or NDF K_d (4.25%/h). Treatment C (31.4%) had a lower ($P < 0.05$) DM content compared with treatment D (33%) but did not differ ($P > 0.05$) from treatments A (31.3%) or B (31.8%). The digestibility of NDF was lower ($P < 0.05$) for treatments C (52.8%) and D (52.5%) compared with that of treatments A (54.1) and B (57.5%). The content of uNDF240 was higher ($P < 0.05$) for treatment D (13.2%) compared with treatment B (12%) but it was similar ($P > 0.05$) to treatments A (13%) and C (12.7%). Silage that was inoculated and kept in anaerobic storage conditions resulted in lower uNDF240 and may help explain the numerically higher NDF digestibility observed. Aerobic stress (treatments C and D) during the ensiling period decreased fiber digestibility. Inoculating silage that was aerobically stressed resulted in DM content higher compared with that of silage kept under aerobic conditions but not inoculated. Therefore, it is recommended to inoculate silage to prevent DM content and fiber digestibility losses in case of aerobic exposure during the storage period.

Key Words: silage, inoculation, fiber digestibility

0675 Effect of homolactic bacteria inoculation and aerobic stress during ensiling on the fermentation characteristics, dry matter recovery, and aerobic stability of spring triticale. L. C. Solórzano*[1], L. L. Solórzano[2], A. A. Rodriguez[1], and J. A. Teisberg[3], *[1]University of Puerto Rico, Mayagüez, [2]Lankin, Fitchburg, WI, [3]Nurealm, LLC, Hutisford, WI.*

On farm silage storage is often aerobically stressed due to slow ensiling, improper chop length, and packing or poor covering. The effect of homolactic bacteria inoculation (HBI; supplying >9.1 × 10^{10} cfu/g containing *Lactobacillus plantarum*, *Enterococcus faecium*, *Lactococcus lactis*, *Pediococcus pentosaceus*, and *Pediococcus acidilactici*) and aerobic stress during ensiling on fresh whole plant spring triticale (x Triticosecale spp.) was evaluated. Triticale was fermented for 120 d at a temperature of 20 to 23°C using 3-L capacity PVC mini-silos fitted with two-way mechanics to vent gas. Sixteen mini-silos were filled with about 2 kg of the crop at about 35% DM and 5.2% soluble carbohydrates (DM basis). Four treatments were A) no HBI with gas vent closed, B) HBI with gas vent closed, C) no HBI with gas vent open during the ensiling period, and D) HBI with gas vent open during the ensiling period. Upon opening, DM recovery and fermentation characteristics were determined at a commercial lab (Rock River Lab, Watertown, WI). Aerobic stability (AS) was determined by monitoring temperature at 6 h intervals during 7 d. Statistical analysis for fermentation characteristics and DM recovery was performed using a completely randomized design (CRD). Statistical analysis for AS data was performed as a CRD with 4 treatments by 29 time point factorial arrangement of treatments. Treatment B increased ($P < 0.05$) the content of lactic acid (5.33%) and total VFA (9.19%) compared with treatments A (3.71 and 8.18%, respectively), C (3.57 and 8.59%, respectively), and D (3.78 and 8.37%, respectively). Treatment B decreased ($P < 0.05$) pH (4.87) and acetic acid (3.56%) compared with treatments A (5.07 and 4.20%, respectively), C (5.07 and 4.65%, respectively), and D (4.96 and 4.31%, respectively). Treatment C (66%) had lower ($P < 0.05$) DM recovery compared with treatments A (88.6%), B (79.6%), or D (87.1%). Silage that was inoculated and aerobically stressed (treatment D) yielded an additional 24% DM recovery compared with noninoculated silage that was aerobically stressed (treatment C). All silages, regardless of treatment, were

aerobically stable and averaged 18.7°C. Inoculating triticale silage improved the DM recovery when the silo was aerobically stressed to levels comparable to that of anaerobic silages. Inoculating silage stored in anaerobic conditions improved fermentation characteristics. Therefore, it is recommended that silages be inoculated as protection against aerobic stresses due to suboptimal management, whether controllable or not.

Key Words: silage, aerobic stress, inoculation

0676 Effects of inoculant application on chemical composition, fermentation indices, and microbial counts of corn silage.

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This study was performed to determine the effect of inoculant application on chemical composition, fermentation indices, and microbial counts of corn silage and changes of microbes after the silo was opened. Two corn hybrids (Kwangpyeonok [KP] and Pioneer1543 [PI]) were harvested at 29.7 and 29.7% of DM, respectively. The harvested corn forage was chopped to 4 to 6 cm lengths and treated with 2 inoculants at the ratio of 1.2×10^5 cfu/g of *Lactobacillus plantarum* (LP) and 1.2×10^5 cfu/g of *Lactobacillus buchneri* (LB) on a fresh-weight basis. Treatments had a 2 × 2 factorial arrangement with three replications. The chopped corn forage (10 kg) was ensiled in a 20-L mini-silo for 100 d. After the silo was opened, a sample (5 kg) was collected for analyses of chemical compositions, fermentation indices, and microbial counts. The remained silage was stored in a mini-silo under aerobic condition and subsampled on 1, 2, 4, and 8 d of opening the silo to analyze the microbial counts. Data were analyzed with a model including hybrid, inoculant, and the interaction using the GLM procedure of SAS. The KP silage had higher ($P < 0.05$) DM (28.4 vs. 26.7%), crude ash (6.85 vs. 5.96%), in vitro DMD (71.4 vs. 64.3%), and in vitroNDFD (50.2 vs. 45.2%) but lower CP (8.62 vs. 9.61%) and ADF (25.9 vs. 27.1%). The LP silage had higher ($P < 0.05$) CP (9.24 vs. 8.99%) than LB silage. The PI silage had higher ($P < 0.05$) ammonia N (0.11 vs. 0.09%) and acetate (1.00 vs. 0.88%) and lactate-to-acetate ratio (4.22 vs. 3.51) than KP silage. The LP silage had higher ($P < 0.05$) lactate (3.12 vs. 2.07%) but lower acetate (0.76 vs. 1.12%). The LP silage had higher ($P < 0.05$) lactic acid bacteria (6.15 vs. 4.50 log10 cfu/g) and yeast (6.08 vs. 5.21 log10 cfu/g), whereas mold was not detected. During aerobic exposure, PI silage had higher ($P < 0.05$) mold count than KP silage. The counts of LAB, yeast, and mold were lower ($P < 0.05$) in silages treated with LB than in silages treated with LP. Therefore, the KP hybrid with LB application could improve the silage quality not only in the front end phase but also in the feedout phase to the farmers.

Key Words: corn silage, fermentation indices, inoculant

0677 Impact of temperature after defrosting on fermentation of high-moisture corn.

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Late harvest of high-moisture corn (HMC) into late fall and winter months during 2014/2015 raised concerns among northern Wisconsin dairy farmers about fermentation of frozen HMC. Although silage maintains fermentation capacity on defrosting, low temperature may inhibit fermentation. Therefore, the objective of the present study was to evaluate the effect of temperature on fermentation profile of defrosted HMC stored frozen for a longer period. An unfermented HMC sample obtained from the University of Wisconsin – Madison Agricultural Research Station (Arlington, WI) on October 2013 was immediately frozen and stored at −20°C until March 2015. Sample was defrosted, homogenized, and divided into 33 subsamples of 250 g each. Three subsamples were randomly selected as fresh samples whereas the remaining 30 subsamples were vacuum-sealed in plastic bags and randomly assigned to 10 treatments (3 reps per treatment). Treatments were mini-silos fermenting in the dark either in a warm (at room temperature 20°C; WR) or cold (in the refrigerator set for 3°C; CD) temperature and allowed to ferment for 1, 3, 7, 14 or 28 d. All samples were analyzed for DM, fermentation profile, and ammonia N (% DM). Data were analyzed using Proc Mixed of SAS with the fixed effects of temperature, ensiling time, and their interaction. Content of DM was slightly greater for CD than for WR ($P = 0.01$; 71.5 vs. 71.1%, respectively). A temperature × ensiling time interaction was observed ($P < 0.001$) for pH, ammonia N, lactate, acetate, ethanol, and total acid concentrations. All parameters followed a similar pattern with gradual reduction in pH (6.27, 5.40, 4.97, 4.93, and 4.72, respectively) or increases in ammonia N (0.00, 0.01, 0.01, 0.02, and 0.02% of DM, respectively), lactate (0.12, 0.24, 0.39, 0.45, and 0.43% of DM, respectively), acetate (0.00, 0.11, 0.15, 0.17, and 0.19% of DM, respectively), ethanol (0.00, 0.09, 0.17, 0.20, and 0.20% of DM, respectively), and total acid (0.12, 0.35, 0.54, 0.68, and 0.72% of DM, respectively) concentrations as fermentation progressed from 1 to 28 d in WR. In contrast, except for a difference in pH for 28 d compared with 1 d (6.41 vs. 6.48, respectively) of fermentation, ensiling time did not affect other fermentation parameters in CD. These findings suggest that although HMC maintains fermentation capacity on defrosting

even after frozen for a prolonged period in storage, fermentation will not occur until warm temperature is reached. Future research is warranted to elucidate at which temperature fermentation progresses normally.

Key Words: high-moisture corn, fermentation

0678 The effect of two microbial inoculants on the aerobic stability of high-moisture corn. S. A. Polukis*, M. L. Smith, R. M. Savage, E. Benjamim da Silva, A. E. Laubach, A. M. Gray, and L. Kung Jr., *University of Delaware, Newark*.

The objective of this study was to evaluate the effect of two microbial inoculants on the fermentation characteristics and aerobic stability of high-moisture corn (HMC). High-moisture corn (71% DM) was 1) untreated (control) or 2) treated with *Lactobacillus hilgardii* (LH) (600,000 cfu/g of fresh material), 3) treated with *Lactobacillus buchneri* 40788 (600,000 cfu/g), or 4) treated with *L. hilgardii* + *L. buchneri* 40788 (LH+LB) (300,000 cfu/g). Inoculants were supplied by Lallemand Animal Nutrition, Milwaukee, WI. Five individually replicated lab silos (7.5 L) for each treatment were packed (packing density of 669 kg DM/m^3) and ensiled for 10, 30, and 92 d between 21 and 23°C. Data were analyzed using the Fit Model in JMP (SAS Inst. Inc., Cary, NC) as a 4 × 3 factorial arrangement of treatments with the main effects of treatment, day, and their interaction. The numbers of lactic acid bacteria were greater for LH (8.91 log cfu/g) than the control (8.41 log cfu/g) at 30 d, whereas all inoculated treatments had higher numbers (7.91 to 8.03 log cfu/g) than the control (7.18 log cfu/g) at 92 d ($P < 0.01$). At 10 d, all treated HMC had lower numbers of yeasts (3.53 to 4.18 log cfu/g) than the control (5.68 log cfu/g). The same occurred at 30 d (<2.00 to 2.26 vs. 5.18 log cfu/g) ($P < 0.01$). At 92 d, LH (4.30 log cfu/g) was numerically lower than the control (4.91 log cfu/g) and LH+LB and LB (both < 2.00 log cfu/g) had lower numbers of yeasts ($P < 0.01$). There were lower ($P < 0.01$) concentrations of lactic acid for treated HMC compared with the control at both 30 (0.74 to 0.80 vs. 1.04%) and 92 d (0.68 to 1.15 vs. 1.45%). All treated HMC had higher ($P < 0.01$) concentrations of acetic acid than the control at 30 (0.47 to 0.57 vs. 0.13%) and 92 d (0.98 to 1.16 vs. 0.23%). Concentrations of ethanol for treated HMC were lower ($P < 0.01$) than the control at 92 d (0.39 to 0.48 vs. 0.73%). All inoculated HMC were more ($P < 0.01$) aerobically stable than the control at 10 (42 to 56 vs. 22 h), 30 (>250 vs. 31 h), and 92 d (>250 vs. 49 h). The inoculants used in this study altered the fermentation characteristics and improved the aerobic stability of HMC.

Key Words: aerobic stability, *Lactobacillus buchneri*, *Lactobacillus hilgardii*

0679 Investigating the relationship between corn silage fiber digestibility and rainfall, growing degree days, and soil type. S. A. Flis*[1], T. P. Tylutki[2], and P. Sirois[1], [1]*Dairy One, Ithaca, NY,* [2]*AMTS LLC, Cortland, NY*.

The relationship of rainfall, growing degree days (GDD), and soil type on aNDFom and aNDFom digestibility (aNDFdom) measured at 30, 120, and 240 h was evaluated on corn silage harvested in New York in the fall of 2015. Five fresh corn silage samples were taken from four different fields at three different farms in New York during the 2015 harvest (n = 60). Samples were analyzed for DM, aNDFom, aNDFdom30, aNDFdom120, aNDFdom240, and K at a commercial laboratory. Farms are located in Saratoga County, NY; Cayuga County, NY; and Livingston County, NY. Farm records of daily rainfall, daily temperature, GDD50, planting dates, corn hybrid, harvest dates, soil type, and nutrient applications from manure and fertilizer were collected from each farm. Data was analyzed using JMP by correlation and regression. Total rainfall (planting to harvest) and cumulative GDD50 were correlated to decreased aNDFdom30 ($r = -0.44$, $P < 0.001$) and aNDFdom240 ($r = -0.27$, $P < 0.05$). As aNDFom increased, the aNDFdom120 ($r = -0.41$, $P < 0.01$) and aNDFdom240 ($r = -0.38$, $P < 0.01$) decreased. Both aNDFdom240 ($r = -0.62$, $P < 0.001$) and aNDFdom30 ($r = -0.66$, $P < 0.001$) decreased with increased rainfall in July. August rainfall had a negative effect on aNDFom120 ($r = -0.61$, $P < 0.001$). Temperature effect (cumulative GDD) on aNDFdom30 begins with the temperatures the plant is exposed to in May ($r = -0.68$, $P < 0.001$). This effect was greater in June ($r = -0.72$, $P < 0.001$). Stepwise regression analysis found that 53% of the variation in aNDFom30 was explained by May and June GDD and May rainfall. There was a strong relationship of soil type to aNDFdom30, aNDFom120, and aNDF0m240, where soils more prone to being wet had lower digestibility ($r = -0.56$ to -0.78, $P < 0.001$). This small sample size did not allow for investigation of the relationships of aNDFdom digestibility to hybrid. Rainfall, GDD, temperature, and soil type were all found to effect aNDFdom digestibility times. Higher cumulative rainfall or rainfall in specific months decreased aNDFdom digestibility. Additional data relating aNDFom digestibility to environmental and soil characteristics could result in improved water management systems and potentially altering timing for planting and harvest.

Key Words: fiber digestibility, corn silage, rainfall

0680 Forage yield and quality of four maize cultivars sown in single and double rows. M. A. Ramirez*, *Universidad Nacional Autonoma de Mexico, FMVZ, Mexico, City, Mexico*.

Corn silage is an important component in feedlot and dairy rations. The aim of the study was to determine forage yield

and quality of four maize cultivars sown in single and double rows. Cultivars were two hybrids, Gladiator and Fog, and two natives, Red and White; single rows were 80 cm apart and double rows were a pair of rows 40 cm apart with 80 cm separation between pairs of rows. Seeding rate was 80,000 plants ha^{-1}. Experimental design was a completely random with four replicates, the experimental unit was a 4.8- by 3-m plot, and treatments were in a 4 × 2 factorial arrangement. Harvest was at one-half milk line stage. Variables measured were forage yield on DM basis and CP, NDF, and ADF contents. The cultivar × sowing method interaction did not influence ($P > 0.05$) forage yield and quality measures. There was a trend ($P = 0.10$) for native cultivars to show higher forage yield than the hybrids (25.4 vs. 21.4 t/ha, respectively), whereas double-row sowing tended ($P = 0.19$) to yield 12% more forage than single-row sowing (24.7 vs. 22.2 t/ha, respectively). Cultivar determined ($P < 0.05$) CP content; native Red showed the highest content, 9.7%, whereas hybrid Fog showed the lowest, 8.8%. Cultivar and sowing method did not influence ($P > 0.05$) NDF content; the overall mean was 66.5%. There was a trend ($P = 0.09$) for the hybrids to show a lower ADF content than natives (36.1 vs. 38.7%, respectively). The conclusion was that maize cultivar and sowing method could be important factors in forage yield and quality.

Key Words: maize, forage yield, forage quality

0681 Evaluation of genetic diversity of *Lactobacillus plantarum* isolated from alfalfa silage using the BOX-polymerase chain reaction.

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The objective of this study was to evaluate the genetic diversity of isolates of *Lactobacillus plantarum* obtained from wilted and nonwilted alfalfa silage. Alfalfa was harvested at 50 d of regrowth and wilted for 6 h. Alfalfa was chopped into particles of 1.5 cm, packed in plastic bags of 25 by 35 cm, and sealed under vacuum. Lactic acid bacteria (LAB) were isolated from samples of fresh alfalfa plants without wilting, fresh forage (Day 0) wilted for 6 h, and its both nonwilted and wilted silages in different fermentation periods (1, 3, 7, 14, 28, and 56 d). The DNA of the strains of LAB was extracted by using a commercial kit (Wizard Genomic DNA Purification kit; Promega). The sequences of the 16S rRNA gene were amplified by PCR using the primers P027F and 1492R. The sequences of the isolates were compared with those available in the GenBank database and aligned using the BLASTn algorithm (basic local alignment search tool) for nucleotides. Of the 138 isolates identified, 58 were *L. plantarum*; therefore, the BOX-PCR was used to evaluate the diversity of these isolates using the primer BOX-A1. The PCR products were separated on 1.6% agarose gel at 60 V for approximately 2 h. The fingerprint of BOX-PCR was documented using the image display system (Kasvi, K33-312). Ten well-defined banding patterns of polymorphism were obtained between the evaluated isolates, with the same distributed in 10 distinct clades. In each clade, *L. plantarum* was considered to be present when clones showed a percent similarity equal to or greater than 90%. Only three *L. plantarum* strains presented no clones with a percentage of less than 90% similarity. No pattern of days of fermentation was observed and no wilting effect on the grouping of the isolates in the clades was observed. Supported by Fapemig, CNPq, and INCT-CA.

Key Words: 16S ribosomal ribonucleic acid, molecular characterization, primer box

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0682 Volatile organic compounds in sugarcane silage treated with chemical and microbial additives.

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This study aimed to evaluate the production of volatile organic compounds in sugarcane silage treated with different additives. The treatments were sugarcane silage without additive (control) and sugarcane silage with *Lactobacillus buchneri* (LB), *Lactobacillus plantarum* and *Pediococcus pentosaceus* (LPPA), *L. plantarum* and *Propionibacterium acidipropionici* (LPPA), 5 g kg^{-1} CaO (SS5CaO), 10 g kg^{-1} CaO (SS10CaO), 5 g kg^{-1} urea (SS5urea), and 10 g kg^{-1}urea (SS10urea). The contents of ethyl acetate, ethyl lactate, ethanol, and other organic acids were determined at the University of Berlin, Germany. Fifty grams of silage were weighed into glass beakers and 200 mL of distilled water and 1 mL of toluene were added to each beaker and mixed with a glass stirrer in a chemical fume hood. The beakers were immediately sealed with Parafilm and stored in a refrigerator (4°C) overnight. The next day, the solution was carefully mixed by swirling each beaker and the silage extract was obtained by filtration through a Whatman No. 54 filter paper. The extract was further filtered through a microfilter and analyzed for fermentation end products using HPLC and special GC techniques. A lower acetone concentration was verified ($P = 0.001$) for the treatment SS10urea, which did not differ for treatments LB, SS5CaO, SS10CaO, and SS5urea. In relation to methanol ($P = 0.001$), a lower concentration was also verified for the treatment SS10urea but did not differ for treatments SS, LPPP, LPPA, and SS5CaO. The propanol ($P = 0.001$) presented lower concentrations for the treatments SS5urea and SS10urea but did not differ for the treatments LPPP and LPPA. Butanol was only detected in the treatment SS10CaO ($P = 0.001$), whereas only for the treatments SS5CaO, SS10CaO, and LB was the presence of 1,2-propanediol ($P = 0.001$) observed, with the lowest concentration associated with LB. A lower concentration of ethanol was observed for

the treatment SS5CaO and SS10CaO and a greater concentration was observed for LB, but the values did not differ among LPPA, LPPP, and SS treatments. The silages treated with CaO presented lower ethyl esters and ethanol and there was a correlation between ethyl acetate + ethyl lactate and ethanol contents. The ensilage conditions strongly affect the concentrations of acids that are produced during the fermentation process, although in the present experiment, low concentrations of these acids were obtained, thereby indicating that the ensilage was satisfactorily performed. However, more research is needed to understand the role of these compounds in silages.

Key Words: ethanol, ethyl acetate, ethyl lactate

0683 Meta-analysis of the effect of homolactic and facultative heterolactic bacteria inoculation on silage quality: I – Fermentation profile.

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Homolactic and facultative heterolactic acid bacteria (HAB) inoculants enhance silage fermentation by rapid production of lactic acid, which decreases the pH and reduces DM and nutrient losses. Data from 120 peer-reviewed papers were summarized to evaluate the effects of inoculation with HAB on silage fermentation profile. The effects were analyzed by comparing raw mean differences between inoculant and control treatment means that had been weighted by inverse variance using random models. Heterogeneity sources evaluated by meta-regression included crop species, application rate ($<10^4$, 10^5 to 10^6 or $>10^7$ cfu/g, representing 3.7, 93.6 and 2.7% of studies, respectively), HAB species, and silo type (laboratory or farm-scale) as covariates. Inoculation did not affect the pH of corn/sorghum silages ($P = 0.34$, $n = 59$) but reduced the pH ($P < 0.05$) of temperate grasses (−0.17; $n = 60$), tropical grasses (−0.17; $n = 17$), sugarcane (−0.03; $n = 28$), alfalfa (−0.30; $n = 8$), other legumes (−0.25; $n = 29$), and other crops (−0.26; $n = 17$). Inoculation increased lactate (0.97% DM; $P < 0.01$, $n = 249$) and reduced butyrate (−0.05% DM; $P < 0.01$, $n = 56$) but did not affect propionate ($P = 0.61$, $n = 109$). Inoculation did not affect acetate in alfalfa silages ($P = 0.15$, $n = 9$) but reduced acetate in corn/sorghum (−0.10% DM; $P < 0.01$, $n = 57$), temperate grasses (−0.30% DM; $P < 0.01$, $n = 71$), tropical grasses (−0.16% DM; $P = 0.03$, $n = 19$), sugarcane (−0.34% DM; $P < 0.01$, $n = 26$), other legumes (−0.47% DM; $P < 0.01$, $n = 24$), and other crops (−0.11% DM; $P < 0.01$, $n = 12$). Inoculation did not affect NH_3–N (% total nitrogen) concentration in corn/sorghum ($P = 0.63$, $n = 22$) or sugarcane ($P = 0.33$, $n = 5$) but reduced it ($P < 0.01$) in temperate grasses (−2.17% N; $n = 49$), tropical grasses (−1.78% N; $n = 9$), alfalfa (−1.47% N; $n = 6$), other legumes (−1.77% N; $n = 18$), and other crops (−1.36% N; $n = 9$). Inoculation with HAB did not improve the fermentation of corn/sorghum silages or sugarcane silage but markedly improved those of grasses, legumes, and other crop silages independent of the HAB species.

Key Words: ammonia, forage conservation, organic acids

0684 The effects of air and heat stress on the aerobic stability of silage treated with a chemical additive.

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The chemical additive Safesil (active ingredients: sodium benzoate, potassium sorbate, and sodium nitrite; Salinity, Sweden) was evaluated for its effects on the fermentation and aerobic stability of corn silage. Whole plant corn samples were harvested at 40% DM, chopped, processed, and treated with 1) no additive (control), 2) Safesil (2 L/t), or 3) Safesil (3 L/t). Silos (7.5 L; forage density of 224 kg of DM/m^3) from each treatment were stored at either 22 ± 2 or 30 ± 2°C and subjected to no air stress or a 2-h weekly air stress. After 100 d of ensiling, 5 replicate silos were opened for each treatment. Data were analyzed by ANOVA as a 3 × 2 × 2 factorial arrangement of treatments with main factors of additive, storage temperature, air stress, and their interactions. Silages were analyzed for numbers of yeasts, fermentation end products, and aerobic stability. Both application rates of Safesil resulted in silages with lower numbers of yeasts ($P < 0.01$) compared with control silage (3.96 vs. <2.00 log cfu/g). Silos that were stressed with air also had higher ($P < 0.01$) yeast counts compared with silos without air stress (3.21 vs. <2.00 log cfu/g). Treatment with Safesil at both 2 and 3 L/t lowered ($P = 0.01$) the concentration of ethanol in both unstressed and air stressed silos (0.52 to 0.70%) compared with control silages (1.27 to 1.47%). When silos were stored at 22°C, treatment with Safesil at 2 and 3 L/t increased ($P < 0.01$) aerobic stability in unstressed silos (185 and 236 h, respectively) compared with unstressed control silos (72 h). When silos were stored at 30°C, only treatment with Safesil at 3 L/t improved ($P < 0.01$) aerobic stability in silos that were both not stressed (168 h) and stressed (225 h) compared with control silos that were not stressed (79 h) and stressed (44 h). Air-stressed silos treated with Safesil 3 at L/t and stored at 30°C (225 h) had greater ($P < 0.01$) aerobic stability compared with stressed silos treated with Safesil at 3 L/t and stored at 22°C (95 h). The use of Safesil has the potential to improve aerobic stability of corn silage

in warm climates even with decreased silo integrity.

Key Words: corn silage, aerobic stability, sodium benzoate

0685 Effects of chemical additives on fermentation characteristics of high-moisture alfalfa silage.

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Alfalfa is sometimes harvested with a high moisture content that increases the chances for undesirable fermentations. The objective of these experiments were to determine the effectiveness of Safesil (SF; active ingredients: 10% potassium sorbate, 20% sodium benzoate, and 5% sodium nitrite) and Safesil Challenge (SC; active ingredients: 7.5% potassium sorbate, 15% sodium benzoate, and 10% sodium nitrite) from Salinity, Sweden, on improving the fermentation of high-moisture alfalfa silage. Alfalfa was directly chopped at 23% DM and used in two experiments. In Experiment 1, we evaluated the effect of SF on the characteristics of early fermentation. Four individual 1-kg replicates of untreated alfalfa or alfalfa treated with 4 L/t of SF were ensiled in vacuumed and heat-sealed, nylon–polyethylene bags for 1, 2, 4, and 7 d. Data were analyzed as a 2 × 4 factorial arrangement of treatments, with main factors of treatment, days of ensiling, and their interaction. In Experiment 2, the long term effects of SF or SC with and without air stress during storage were determined. Replicated silos (7.5 L) were packed (density of 224 kg of DM/m^3) with the same forage described above and were untreated or treated with SF (3 and 4 L/t) or SC (2 and 3 L/t). Half of the silos were submitted to a 2-h weekly air stress. Data were analyzed by ANOVA as a 2 × 5 factorial arrangement of treatments with main factors of air stress, treatment, and their interaction. In Experiment 1, pH decreased and acids and ethanol similarly increased for untreated and treated silages as ensiling progressed. Compared with untreated silage, treated silages had fewer yeasts ($P < 0.01$) at 4 d of ensiling (4.52 vs. 2.96 log cfu/g) and less enterobacteria after 1 d (6.79 vs. 5.81 log cfu/g). Ethanol concentration was numerically lower for treated silages at all time points. In Experiment 2, for silos submitted to air stress, the DM recovery after 100 d was higher ($P = 0.04$) for SF- and SC-treated silage than for untreated silage. After 100 d, numbers of yeasts and molds were less than 2.00 log cfu/g for all treatments. These experiments showed that Safesil can quickly reduce harmful microorganisms, such as yeasts and enterobacteria, in high-moisture alfalfa and that Safesil and Safesil Challenge can improve DM recovery in silage submitted to air stress.

Key Words: alfalfa, silage, Safesil

FORAGES AND PASTURES SYMPOSIUM: GREENHOUSE GAS EMISSIONS IN PASTURE-BASED DAIRY AND BEEF CATTLE SYSTEMS

0686 Comprehensive national assessment on the sustainability of beef production.

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To develop better scientific understanding of the sustainability of beef in the United States, a national assessment is being conducted by the National Cattlemen's Beef Association, a contractor to the beef checkoff. This includes a life cycle assessment (LCA) of greenhouse gas emissions along with other environmental, social, and economic impacts. Assessments are being made for representative cattle operations in each of seven geographic regions to form the national total. Producer surveys and visits are used to characterize region-specific production systems, and the information gathered provides a basis for system simulation and a farm-gate LCA. Assessments have been completed for the central plains and midwestern regions and are in progress for the western and eastern regions of the country. Results thus far show farm-gate carbon footprints of representative production systems vary from 16 to 28 kg CO_2e/kg of carcass weight (CW) with a mean around 20 kg CO_2e/kg CW. The cow–calf operation is the source of 67 to 77% of this footprint and stocker operations contribute up to 18% of the footprint. Therefore, depending on whether cattle are backgrounded on pasture or in a feedlot, the grassland-based portion of the system can contribute 67 to 85% of the farm-gate carbon footprint of finished beef cattle. Enteric methane emission is the source of about 60% of the total greenhouse gas emissions from cow–calf and stocker operations and 35% of that from feedlot finishing operations. Nitrous oxide emissions contribute about 20% of the carbon footprint of grazing cattle. Considering post-farm gate sources (harvest, retail, restaurant, and consumer), the full carbon footprint is about 45 kg CO_2e/kg of consumed beef. Of this total, 58 to 73% can be attributed to emissions from grazing cattle and the inputs required to maintain them. A similar result is found for environmental impacts such as total reactive nitrogen loss, where 50 to 70% of the farm-gate footprint is attributed to grazing cattle. Therefore, to make substantial reductions in the environmental impacts of beef production, our analysis to this point indicates that mitigation strategies are needed to reduce greenhouse gas and nitrogen emissions from grassland systems. This provides a major challenge for beef cattle research because practical technologies or strategies for reducing these emissions are

essentially unknown.

Key Words: beef, cattle, carbon footprint

0687 Screening for forages and foraging managements that reduce nitrogen excretion and methane emissions while maintaining or increasing animal production. P. Gregorini*, P. C. Beukes, and A. J. Romera, *DairyNZ Ltd., Hamilton, New Zealand*.

Farmers face complex decisions at the time to feed animals, trying to achieve their production goals while contemplating social and environmental constraints. Our purpose was facilitating such decision-making for pastoral dairy farmers, aiming to reduce urinary N (UN) and methane (CH_4) emissions while maintaining or increasing milk production (MP). There are a considerable number of forages the farmers can choose from and combine. First, we used three grasses, three legumes, and two herbs combined in 72 mixed swards. Then, 50 feeds (forages and grains) were systematically combined in different proportions producing 11,526 binary diets. Swards and binary diets were screened, using an a posteriori approach and a Pareto front (PF) analysis of model (Molly-DairyNZ) outputs. The objective was identifying combinations with the best possible compromise (i.e., frontier) between UN, CH_4, and MP. All PF solutions are considered optimal and equally good. Using MP and low UN as objective functions, PF included seven optimal swards, with fescue, alfalfa, and plantain as key species. Adding CH_4 emissions as objective function increased the number to 23. For binary diets, the MP–UN frontier included 10, 14, 12, and 50 for nonlactating and early, mid, and late lactation periods, respectively, with cereals and beets featuring strongly. Using the same objective functions but including ryegrass as dietary base, PF included 2, 4, 8, and 4 diets for those periods. These results suggest that from a wide range of diverse diets, farmers could choose from a handful of mixed swards and binary diets to reduce UN while maintaining or increasing production. If the criterion is maintaining pasture-based systems, there are fewer suitable options. Reducing UN will simply require dilution of N supplied by pasture by either supplementing low-N forages or strategic foraging managements. The results also indicate that reducing UN may imply increments in CH_4 emission and vice versa, that is, pollution swapping. Although there is no perfect sward or diet that optimizes all the objectives at once, there are feeding options to offset pollution swapping, if the current diet is not in the frontier. Ultimately, it is up to the farmers to choose the best options, according to their farming context.

Key Words: forages, ruminant nutrition, environmental footprint

0688 Outcomes and future directions from the National Livestock Methane Program in Australia. T. M. Davison*, *Meat and Livestock Australia, Brisbane, Australia*.

The National Livestock Methane Program (NLMP) was a collaborative and coordinated research effort run by Meat and Livestock Australia. The investment in methane research was initiated by a federal government program, filling the Research Gap. This overall initiative also included other national programs of work in soil carbon, nitrous oxide, and manure management. The program aims were to provide Australian livestock producers with practical strategies and tools to help them increase productivity and profitability and at the same time lower methane emissions. The NLMP was a $33.5 million investment over 3 yr and consisted of 17 projects in 5 themes of work: 1) forages, 2) supplements, 3) beef genetics, 4) rumen microbiology, and 5) measurement. Three overarching themes linked the program of work within NLMP. First, to develop a greater understanding of the underlying mechanisms in the production and control of methanogenesis; second, to identify methods or farming practices that might apply to the federal government Carbon Farming Initiative (a scheme that offers income opportunities for carbon abatement), and third, communication products for use by partners. A variety of outcomes included knowledge of the relationship between productivity and methane emissions, identification of methane abatement from various forages, the role of supplements such as red algae and grape marc, the role of wheat in dairy diets, identification of potential plant bioactives, new bacterial species, and knowledge of rumen methane pathways. A national needs and gaps analysis that included a marginal abatement cost curve analysis was conducted to determined future priorities for research based on a range of investment criteria.

Key Words: methane research, forages, supplements, carbon schemes

0689 Greenhouse gas emissions and mitigation in the West African subregion: Challenges and opportunities. C. Antwi*, *Kwame Nkrumah University of Science & Technology, Kumasi, Ghana*.

Animal agriculture contributes to about 18% of the global greenhouse gasses (GHG), of which 3% is generated by all ruminants in sub-Saharan Africa. The methane emissions from these ruminants represent about 12% of the GE intake, which could otherwise be used as energy for maintenance. In an attempt, therefore, to reduce emissions, researchers in the West African subregion have initiated profiling GHG emissions of feed resources and selection feed with less methane emission potential. Some common feedstuffs in the subregion were assayed for their methane production using either the in vitro systems or hand-held methane analyzer. In vitro assessment of shea nut (*Butyrospermum parkii*) for methane

production indicated that including 10% of shea nut cake in finishing feedlot *Bos taurus* diets reduced 24-h in vitro methane production by approximately 20% without any significant reduction in total and individual VFA production. Methane output was also reduced during in vitro ruminal fermentation of *Brachiaria ruziziensis* when the in vitro mixture was supplemented with 20% of leaves of the browse plant *Securinega virosa*. Different fractions of Napier grass were evaluated in Ghana for methane production using a hand-held methane analyzer. The stem fraction was 2.5 times higher than that of the leaves, and as the grass advanced in age, the methane production increased. Emissions directly associated with animal production have globally increased partly because of the high demand for animal products. It is envisaged that emission intensity from animal agriculture in the West African subregion will increase due to the nature of feed they feed on. In an attempt to reduce emissions from animals, scientists adopt in vitro method of screening and selection of feed for ruminants. This, however, fails to estimate emission per feed intake, making it impossible to advance the best practices that result in GHG mitigation without any adverse effect on animal productivity. Although the global research alliance suggests to its member countries, of which Ghana is one, to focus on activities that reduce emissions intensity of livestock while increasing productivity, little is seen in terms of investment in developing research activities that reduces emissions. Several agro-byproducts including palm kennel cake and other cakes of leguminous crop exist in the subregion. Owing to their high lipids content, when supplemented to the high fibrous diet consumed by ruminants, it is certain that not only will methane emissions be reduced but that productivity will also increase.

Key Words: methane, mitigation, Africa

0690 Effects of native and tame grassland species reintroduction on carbon sequestration potential on the Canadian Prairies. A. D. Iwaasa*, B. McConkey, and H. Wang, *Agriculture and Agri-Food Canada, Swift Current, SK, Canada*.

Rising concentration of carbon dioxide in the atmosphere has prompted interest in implementing improved grassland management practices that could lead to a net accumulation of carbon in grassland soils. Converting cropland into native or tame perennial grasslands may result in substantial increase in soil C sequestration. Two studies were started in southern Saskatchewan where semiarid cropland was converted to perennial grasslands: Study 1 (2000–2014) seeded two different native pasture mixes (Simple, 7 species, and Diverse, 12 species) and Study 2 (2006–2011) seeded four different pasture types (meadow bromegrass + alfalfa [A], native grass mix [NG], NG + A, and NG + native legume). The objective of the studies was to determine the change in soil organic carbon (SOC) levels as affected by type of forage pasture mix and form of disturbance (grazing and nongrazing). In Study 1, the disturbance treatments were continuous, rotational, and nongrazing and the stocking rates were 0.8 and 1.9 animal unit (AU) ha^{-1}, respectively. In Study 2, continuous grazing occurred and the stocking rate ranged from 2.0 to 4.0 AU ha^{-1} depending on which pasture treatment was used. All pastures were grazed to a utilization rate of 50 to 60%. Soil samples from each pasture were collected from three locations and at each location, a five radial (star pattern) sampling pattern occurred. From each of the five microsites, core samples were taken at five depths (0–7.5, 7.5–15, 15–30, 30–45, and 45–60 cm). Soil sampling for study 1 occurred in 2000, 2004, 2008, 2011, and 2014, whereas in study 2, it occurred in 2008 and 2011. In study 1, no SOC level (0–15 cm) differences were observed between disturbance and pasture mix combinations and interaction after 14 production years. Soil organic C levels were affected by year ($P < 0.0001$), which was expected with the different environmental conditions experienced among the different soil sampling years. In study 2, no SOC level (0–15 cm) differences were observed for interaction or main effects after three production years. Our studies did not support our hypothesis that a more diverse native mix (higher species richness) and tame grass + alfalfa would have higher SOC level than other treatments. Detecting small SOC change is difficult due to spatial heterogeneity in initial SOC, soil texture, bulk density, and plant productivity. Using our results, we develop criteria for measurement systems to detect changes design to detect SOC change.

Key Words: grazing, soil organic carbon, native and tame forages

GENOMICS SYMPOSIUM: TRANSLATIONAL GENOMICS TO IMPROVE FERTILITY OF ANIMALS

0691 Translational genomics for improving sow reproductive longevity. D. C. Ciobanu*[1], S. D. Kachman[1], S. Olson[1], M. L. Spangler[1], M. D. Trenhaile[1], H. Wijesena[1], P. S. Miller[1], J. J. Riethoven[1], C. A. Lents[2], J. F. Thorson[2], R. Massey[3], and T. J. Safranski[3], *[1]University of Nebraska – Lincoln, Lincoln, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [3]University of Missouri, Columbia*.

Approximately 50% of sows are culled annually with more than one-third due to poor fertility. Age at puberty, the earliest prebreeding indicator of reproductive longevity, can be measured early in life and has a moderate heritability. Selection for age at puberty is challenging due to labor-intensive phenotyping. Genomic selection for this trait would be a more viable option because it could increase accuracy and selection response. This study aims to identify DNA markers that

will predict, at weaning, gilts with early age at puberty and superior reproductive longevity. Our hypothesis is that genetic sources that affect age at puberty also explain variation in sow reproductive longevity. To test the hypothesis, data and tissues from a UNL resource population (n > 1,700 gilts) were integrated with genomewide association analyses, genome/RNA sequencing, and polymorphism discovery to uncover DNA variants that could predict age at puberty and reproductive longevity. A BeadArray panel of 56,424 SNP explained 25.2% of the phenotypic variation in age at puberty in a training set (n = 820). In an evaluation data set consisting of subsequent batches of similar genetics (n = 412), we compared a model based on all SNP from major 1-Mb windows with one based on SNP with the largest estimated effect. The model based on all SNP from the major windows explained more of the phenotypic variance compared with the model based on large effect SNP (12.3 to 36.8% vs. 6.5 to 23.7%). One major pleiotropic region included AVPR1A, for which the favorable genotype was associated with higher probability of the gilts to produce the first parity compared with the other genotypes (P < 0.05). Genome sequencing of 20 sires using Proton technology provided sources of genetic variation outside the limited capability of the BeadArray. Sequencing reads averaged 165 bp with a depth that varied from 16.2x to 29.7x. A substantial proportion (38%) of the total SNP discovered (140,000) were located in known genes. Transcriptome profile was evaluated by RNA sequencing of the microdissected arcuate nucleus (ARC) in pre-/postpubertal gilts (n = 12) subjected to different dietary treatments. Using a combination of Tophat and local Bowtie, the majority of the reads were aligned to the reference genome/transcriptome (>93%). This integrated knowledge accompanied by economic modeling will be evaluated in commercial populations to understand and improve expression of puberty and sow reproductive potential through genomic selection. This project is supported by Agriculture and Food Research Initiative Competitive Grant number 2013-68004-20370 from the USDA–National Institute of Food and Agriculture. The USDA is an equal opportunity provider and employer.

Key Words: age at puberty, genomic selection, reproductive longevity.

0692 Detection and selection against early embryonic lethals in United States beef breeds. J. F. Taylor*[1], R. D. Schnabel[1], B. Simpson[2], J. E. Decker[1], M. Rolf[3], B. P. Kinghorn[4], A. Van Eenennaam[5], M. D. MacNeil[6], D. S. Brown[1], M. F. Smith[1], and D. J. Patterson[1], *[1]University of Missouri, Columbia, [2]GeneSeek, a Neogen Company, Lincoln, NE, [3]Oklahoma State University, Stillwater, [4]University of New England, Armidale, Australia, [5]University of California, Davis, [6]Delta G, Miles City, MT.*

More than 3,000 bovine genomes have now been sequenced worldwide, and much of the variation within the genome of cattle has been discovered. Many variants likely to have functional effects due to their locations within annotated coding regions have been identified. However, the lack of complete annotation leads to our inability to identify variants that lie within regulatory regions, and furthermore, the phenotypic effects caused by coding variants are not well understood. Among these are the class of loss of function variants within genes that are essential for life—a gene set that is largely conserved in identity among mammals. Based on marker haplotype analyses performed primarily in dairy breeds, we postulate that several lethal variants segregate within most cattle breeds and that these variants tend to be breed specific in their identity. To identify these variants, we have designed the first generation of a bovine functional assay, the GGP-F250, to contain 34,000 common variants present on many of the genotyping assays currently used by the cattle industry and 199,000 predicted genic functional variants. The assay is publicly available from GeneSeek. These variants were discovered by analyzing whole genome sequence data for 297 cattle from 17 breeds and RNA-seq data for 159 animals and were confirmed using data from the 1000 Bull Genomes Project and dbSNP. We have genotyped 18,300 animals with this assay representing Holstein and 9 U.S. beef breeds including over 11,000 Angus animals, and these data are being used to fine map QTL underlying susceptibility to respiratory disease and feed efficiency. Data from Angus are being used to sequentially test each putative functional variant for a deficiency of homozygotes and fully penetrant lethals will manifest with a complete lack of homozygotes. Candidate lethal alleles will be migrated to assays commonly used in the beef industry such as the GGP-LD and GGP-HD platforms to genotype hundreds of thousands of animals and validate the lack of homozygotes. Mate selection software is being developed as part of the USDA National Institute of Food and Agriculture grant number 2013-68004-20364 “Identification and management of alleles impairing heifer fertility while optimizing genetic gain in Angus cattle” project to assist breeders with mating decisions based on each animal’s carrier status for defects and embryonic lethals.

Key Words: GGP-F250, fertility, embryonic lethal

-693 Genomic selection for improved fertility of dairy cows with emphasis on cyclicity and pregnancy.

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The overall goal of this ongoing integrated project (research, extension, and education) is to make use of advanced genomic technologies to improve dairy cattle fertility, with emphasis on cyclicity and pregnancy. The specific aims are 1) development of a fertility database with genotypes and phenotypes based on objective and direct measures of fertility in Holstein dairy cows, 2) identification of genome regions associated with fertility traits and use of this information on prediction models that can be applied in selection of dairy cattle for improved fertility, 3) development and implementation of a comprehensive extension program on best management and genomic selection practices to improve fertility of dairy herds, and 4) development of an education component targeting the general public as well as students in animal and veterinary sciences. In this presentation we will describe the development and outcomes on Specific Aim 1 as well as some preliminary analyses and results related to Specific Aim 2. A total of 12,000 Holsteins cows from 7 states (New York, Minnesota, Wisconsin, Texas, California, Florida, and Ohio), comprising 2 to 3 farms per state, were enrolled at calving and monitored weekly until pregnancy. Main events were uterine health, metabolic disorders, cyclicity, estrus, pregnancy per AI, and pregnancy loss, together with milk yield until 305 DIM. A reproductive index, calculating the predicted probability of pregnancy at first AI after calving, was generated using a logistic regression model that included cow-level variables such as diseases incidence, anovulation, BCS, and milk yield. Within each farm, cows were stratified as pregnant on d 60 after the first AI (high-fertility population) and as nonpregnant on d 60 after 2 AI (low-fertility population). A selective genotyping approach was implemented using the reproductive index developed, with selected cows from the high-fertility pregnant (850 cows) and the low-fertility nonpregnant (1,750 cows) groups. Preliminary analyses of the phenotypic data have been implemented, including the estimation of genetic parameters of cyclicity and other fertility indicators as well as the impact of postpartum diseases on lactation curves. Heritability estimates ranged from 0.03 to 0.12 for the various traits, and many factors influencing the lactation curve have been detected. The next step of the project will include multitrait and network analyses of the fertility indicators as well as genomewide association and gene-set enrichment analyses for detection of genomic regions and sets of genes affecting fertility traits in dairy cattle.

Key Words: genomics, fertility, dairy

0694 Improving fertility of dairy cattle using translational genomics.

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Selection for higher milk production in United States dairy cattle has been very successful during the past 50 yr; however, today's lactating dairy cows exhibit a high incidence of subfertility and infertility with a national pregnancy rate of only 15%. An integrated approach is being used to improve reproductive performance and profitability of dairy cattle using recent advances in animal genomics and improved understanding of fertility. The overarching hypothesis is that lactating cow fertility can be increased through genetic selection for maternal fertility in heifers and cows and use of sires with high daughter pregnancy rate (DPR), resulting in a significant, sustainable, and profitable increase in overall herd fertility. Objectives are to 1) identify genomic loci associated with fertility in dairy heifers and cows, 2) identify functional SNP associated with DPR and early embryo development, (3) evaluate the efficiency and profitability of increasing fertility in dairy cattle using genetic selection tools, and 4) engage in technology transfer regarding novel approaches for improving fertility using genetic selection tools to dairy farmers, dairy farm personnel, and their advisors in English and Spanish using DAIReXNET and extension road shows. Each objective involves an integrated team of scientists working in animal reproduction, genomics, breeding, and extension toward a common goal. The expected outcome and impact of meeting our goal is increased sustainability, profitability and international competitiveness of the U.S. dairy industry. This project was supported by Agriculture and Food Research Initiative Competitive Grant number 2013-68004-20365 from the USDA

National Institute of Food and Agriculture.

Key Words: dairy cattle, fertility, genomics

ADSA–ASAS NORTHEAST SECTION GRADUATE STUDENT ORAL COMPETITION

0695 Survival and growth of *Listeria monocytogenes* on queso fresco cheese stored under modified atmospheres. S. R. Barnes* and D. J. D'Amico, *University of Connecticut, Storrs*.

Cheese varieties characterized by high moisture and low acidity, such as queso fresco (QF), have been shown to support the growth of *Listeria monocytogenes* to very high levels during refrigerated storage. In addition to improving quality and extending shelf life, modified atmosphere packaging (MAP) has been used to control the growth of pathogenic microorganisms in various foods. The objective of this research was to determine the effect of five MAP conditions on the survival and growth of *L. monocytogenes* as postprocessing contaminants on QF during refrigerated storage at 7°C. To test the hypothesis that MAP affects *L. monocytogenes* growth on QF during storage when compared with conventional methods of packaging (i.e., vacuum), 25-g samples of QF were surface inoculated with an eight-strain cocktail of *L. monocytogenes* to achieve 4 log cfu/g. Following microbial attachment, individual cheeses were placed in 75-µm high barrier pouches (nylon/ethylene vinyl alcohol/polyethylene), packaged under one of seven conditions (air, vacuum, 100% carbon dioxide [CO_2], 70% CO_2/30% nitrogen [N_2], 50% CO_2/50% N_2, 30% CO_2/70% N_2, or 100% N_2), and stored at 7°C. Samples were removed weekly through 28 d of storage for enumeration of *L. monocytogenes*. Data were analyzed using one-way ANOVA. Analyses identified overall effects of time and packaging treatment on the change in *L. monocytogenes* counts over 28 d ($P < 0.001$). *Listeria monocytogenes* populations increased rapidly on cheese packaged under air, vacuum, and 100% N_2, with counts significantly differing ($P < 0.001$) from the initial inoculum by Day 7. Changes in counts over time and counts on individual days did not differ between these treatments, with means exceeding 7 log cfu/g on Day 14 and stabilizing at >8 log cfu/g through Day 28. Treatments that incorporated CO_2 at any percentage significantly limited pathogen growth over time compared with treatments without CO_2, including air and vacuum controls ($P < 0.001$). Although pathogen growth was limited, the change in counts over 28 d in CO_2 treatments was significant ($P < 0.05$), reaching a mean of 5.0 log cfu/g. Pathogen growth during storage did not significantly differ between treatments with varying percentages of CO_2. These data demonstrate that vacuum packaging and conditions containing 100% N_2 do not impede the growth of *L. monocytogenes* on QF. However, packaging under anaerobic modified atmospheres containing CO_2 may be a promising control for limiting *L. monocytogenes* growth on QF and other high-moisture, low-acid cheeses during cold storage.

Key Words: packaging, *Listeria monocytogenes*, cheese

0696 The effects of poor maternal nutrition on dam and offspring inflammatory status throughout gestation. A. K. Jones*, S. M. Pillai, M. L. Hoffman, K. K. McFadden, K. E. Govoni, S. A. Zinn, and S. A. Reed, *Department of Animal Science, University of Connecticut, Storrs*.

We hypothesized that poor maternal nutrition during gestation exaggerates the inflammatory status of ewes throughout gestation and that this would be reflected in the immune profile of offspring during late gestation and at parturition. Pregnant western white-faced ewes ($n = 78$) were individually housed and fed 100 (CON), 60 (RES), or 140% (OVER) of NRC requirements for TDN beginning at d 30.2 ± 0.2 of gestation. Whole blood was collected from a subset of ewes at d 24.0 ± 0.9 and 135.0 ± 0.3 of gestation ($n = 4$ ewes per diet per day) and from 3 to 4 offspring per diet euthanized at d 135 of gestation or within 24 h of parturition. Whole blood RNA was isolated, and expression of 84 genes mediating inflammation was profiled using a real-time PCR array. Data were analyzed using PROC MIXED in SAS for main effects and interaction of diet and day of gestation for ewes and main effect of maternal diet for offspring with the PDIFF option for mean comparisons. In ewes, regardless of diet, relative to d 24, *interleukin* (*IL*) *17β*; receptors for *IL1*, *IL6*, *IL8*, *IL10α*, and *IL10β*; *colony stimulating factor* (*CSF*) *2*; *CSF3*; *tumor necrosis factor superfamily member* (*TNFSF*) *13*; *TNFSF13β*; *chemokine ligand 17*; *chemokine receptor 1*; *vascular endothelial growth factor A*; and *platelet factor 4* increased 3.8-, 1.7-, 2.1-, 2.4-, 1.5-, 1.3-, 1.9-, 2.0-, 1.6-, 1.9-, 3.7-, 1.7-, 1.7-, and 2.5-fold at d 135 of gestation, respectively ($P \leq 0.05$). In contrast, *chemokine ligand 10* decreased 4.1-fold at d 135 relative to d 24 in ewes, regardless of diet ($P = 0.02$). In OVER ewes, *TNFSF4* decreased 1.5-fold compared with CON ewes ($P \leq 0.05$). *Interleukin 1 receptor antagonist* (*IL1RN*) increased 1.8-fold in RES ewes at d 135 compared with CON ewes at d 24 ($P \leq 0.04$). In offspring, *chemokine ligand 22* increased 2.8-fold in OVER ewes compared with CON ewes at d 135 ($P \leq 0.05$). At parturition, *interferon γ* decreased 3.0- and 3.8-fold in OVER and RES ewes, respectively, compared with CON ewes ($P \leq 0.006$). In conclusion, inflammatory progression is characteristic of advancing gestation and the increased expression of *IL1RN*, an antagonist of *IL1α* and *IL1β*, in RES ewes at d 135 may be a protective mechanism suppressing proinflammatory signaling. The inflammatory profile of offspring was altered by poor maternal nutrition, which may negatively affect growth and health if persistent postnatally, thereby reducing offspring productivity.

Key Words: inflammation, maternal nutrition, sheep

0697 Effects of poor maternal nutrition during gestation on offspring prenatal muscle growth.

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Poor maternal nutrition during gestation can negatively affect offspring muscle development, thereby reducing production efficiency. We previously observed that cross-sectional area (CSA) of semitendinosus muscle fibers from offspring of ewes exposed to restricted feeding or overfeeding during gestation were increased at birth and reduced at 3 mo of age. Although the negative effects of poor maternal nutrition persist into postnatal growth, it is not well known when during gestation poor maternal diet affects offspring muscle growth. We hypothesized that restricted feeding and overfeeding ewes during gestation would alter fetal muscle fiber CSA during gestation. To test this hypothesis, 78 pregnant western white-faced ewes were individually housed and fed 100 (control fed, $n = 25$), 60 (restricted fed; $n = 27$), or 140% (overfed; $n = 26$) of NRC requirements for TDN beginning at d 30.2 ± 0.2 of gestation. For CSA analysis, a subset of ewes was euthanized at d 45 ($n = 20$) or 135 ($n = 19$) of gestation and offspring were collected ($n = 10$ to 14 per treatment per time point). Offspring from control-fed, restricted-fed, and overfed ewes are referred to as CON, RES, and OVER, respectively. From offspring, longissimus dorsi and semitendinosus muscles were excised, weighed, and frozen in optimal cutting medium. Muscle sections were cryosectioned and immunostained with wheat germ agglutinin. Images ($n = 5$ per offspring) of muscle cross-sections were taken and CSA were determined using ImageJ software. The CSA data were analyzed using the MIXED procedure of SAS, with maternal diet as the main effect. No differences ($P \geq 0.53$) due to maternal diet were observed for the BW of offspring or weight of semitendinosus or longissimus dorsi (as percent of BW) at d 45 or 135. At d 45, longissimus dorsi CSA tended to be smaller in RES and OVER compared with CON (CON: 228.8 ± 19.0 μm^2; RES: 171.0 ± 18.1 μm^2; OVER: 183.0 ± 16.1 μm^2; $P \leq 0.07$); however, no effect of maternal diet was observed for CSA of longissimus dorsi at d 135 ($P = 0.48$). There was no effect of maternal diet on CSA of semitendinosus ($P \geq 0.40$) at either time point. In conclusion, during the period of primary myogenesis (approximately d 45 of gestation) and within 15 d of the beginning of dietary treatment, poor maternal nutrition, both restricted feeding and overfeeding, during gestation caused a reduction in offspring longissimus dorsi CSA.

Key Words: maternal nutrition, muscle, sheep

0698 Effects of citral and linalool on blood neutrophil toxicity and oxidative response in dairy cows.

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Alternative therapies to controlling and treating mastitis are being pursued to reduce potential antibacterial resistance. Certain bioactive phytochemicals extracted from plants, such as citral and linalool, have demonstrated antimicrobial activity and may serve as acceptable alternatives for conventional mastitis treatments. It is unknown how these phytochemicals may interact with bovine polymorphonuclear cells (PMN), the predominant cell type recruited during mastitis. The objective of this study was to evaluate the effects of citral and linalool on cytotoxicity and the oxidative response of bovine blood PMN in vitro. Blood was sampled from four healthy, primiparous Holstein dairy cows in mid lactation (DIM > 90). Polymorphonuclear cells were isolated and incubated for 2 h with various concentrations of citral (0, 0.1, 0.2, 0.4, 0.8 and 10 μL/mL) and linalool (0, 0.1, 1.2, 2.4, and 10 μL/mL). Cytotoxicity was measured by nonradioactive, colorimetric assay to quantify lactate dehydrogenase production. Oxidative burst response for the PMN was measured by relative chemiluminescence of reactive oxidative species production after exposure to 1.6 μg/mL phorbol 12-myristate-13-acetate in addition to citral or linalool during incubation. Data were analyzed by ANOVA using the MIXED procedure of SAS 9.2. Each phytochemical was separately analyzed. Differences among treatments were determined using the PDIFF statements and significance was declared at $P \leq 0.05$. Citral concentrations of 0.8 and 10 μL/mL increased PMNL cytotoxicity to 33.0 and 68.3%, respectively ($P < 0.01$), relative to the control. Oxidative burst response increased at 0.01 and 0.02 μL/mL concentrations of citral, whereas 0.4 and 0.8 μL/mL concentrations decreased oxidative burst ($P < 0.01$). Linalool concentrations equal to or less than 2.4 μL/mL did not alter PMN cytotoxicity relative to the control and 10 μL/mL increased cytotoxicity to 81.2% ($P < 0.01$). Oxidative response of PMN increased for 1.2, 2.4, and 10 μL/mL concentrations of linalool ($P = 0.02$). In summary, citral and linalool do affect in vitro bovine blood PMN cytotoxicity and oxidative burst response. Concentrations less than 0.4 μL/mL of citral and 2.4 μL/mL of linalool were nontoxic to bovine blood PMN and concentrations between 0.1 to 0.2 μL/mL citral and 1.2 to 10 μL/mL linalool increased oxidative burst response. The use of citral and linalool as an alternative therapy for mastitis is promising as they may not interfere with the immune response during mastitis.

Key Words: mastitis, polymorphonuclear cell, alternative therapy

0699 In vitro screening of the anthelmintic efficacy of birdsfoot trefoil commercial varieties and cultivars against ovine *Haemonchus contortus*.

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Some forages containing condensed tannins (CT), also called proanthocyanidins (PAC), suppress gastrointestinal nematode (GIN) infections in small ruminants. The objective of this study was to investigate the anthelmintic potential of 51 commercial varieties and cultivars of birdsfoot trefoil (BFT) against *Haemonchus contortus*. The antiparasitic activity of BFT proanthocyanidin extract (BFT-PAC) and BFT aqueous extract (BFT-AqE) was tested using the following in vitro assays: 1) egg hatching and viability of L1 *H. contortus* larvae and 2) exsheathment of L3 *H. contortus* larvae. Birdsfoot trefoil powder of each variety or cultivar was analyzed for CT content (mg/g) by the 4-(dimethylamino)cinnamaldehyde method. Birdsfoot trefoil proanthocyanidin extract was prepared by isolating PAC extract from the BFT powder using solid-phase chromatography. Birdsfoot trefoil aqueous extract was prepared by soaking BFT powder in water at room temperature for 24 h. The plant matter was then removed, leaving an aqueous extract. 1) For in vitro egg hatch and viability of L1 larvae, *H. contortus* eggs were isolated from fresh feces and exposed to varying concentrations of BFT extracts for 24 h. The percentage of hatched eggs and L1 larval mortality (based on motility) were determined. 2) For in vitro exsheathment, 2,000 *H. contortus* L3 larvae were incubated in varying concentrations of BFT extracts for 24 h followed by exsheathment using CO_2. The percentage of exsheathed larvae (based on absence of sheath) was determined. Condensed tannin content ranged between 1.5 and 63.8 mg/g across 51 varieties and cultivars. Inhibition of egg hatch and larval mortality was observed with incubation in BFT-AqE; however, the concentration at which this inhibition and mortality was most effective varied among varieties and cultivars: at 3 mg/mL, percent inhibition of egg hatch and L1 mortality spanned between 0 and 100% across 51 varieties and cultivars tested. Results for incubation in BFT-PAC and results for exsheathment are pending. Preliminary results indicate that commercial varieties and cultivars of BFT-AqE inhibited egg hatch and increased larval mortality, but the degree of inhibition and mortality varied. Additional results testing BFT-PAC and testing exsheathment will provide further information about the anthelmintic efficacy of commercial varieties and cultivars of BFT for small ruminant GIN control.

Key Words: small ruminant, sheep, condensed tannin

ADSA DAIRY FOODS GRADUATE STUDENT ORAL COMPETITION

0700 Anti-obesity and antidiabetic properties of lactoferrin are independent of calorie intake.

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Whey proteins provide multiple health benefits to humans including promotion of weight loss and improving diabetic control. However, the bioactive components of whey that produce such benefits and the underlying mechanisms of action are poorly understood. Our objectives were to determine the effects of whey, and its components lactalbumin and lactoferrin, on 1) energy balance, body composition, glucose tolerance, and gut hormones and 2) key regulatory markers of glucose and lipid metabolism in liver and skeletal muscle of diet-induced obese (DIO) rats. The DIO rats were randomized to receive one of 5 isocaloric dietary treatments (n = 8/group; 40% fat and 4.63 kcal/g)—control (CON; 15% protein), whey (WH), lactalbumin (LA), lactoferrin (LF), and pair-fed WH to LF (PF)—for approximately 8 wk. The high-protein diets contained 15% added whey or its components. Food intake, meal patterns, energy expenditure, body composition, glucose tolerance, plasma hormone, and hepatic and muscle mRNA abundance were measured. Data were analyzed by linear mixed models, ANOVA, or ANCOVA. We found that 1) compared with CON, WH, LA, and LF reduced food intake, with LF producing a greater and sustained reduction of intake; 2) the hypophagia is partly due to reduced meal size and/or frequency, increased peptide YY mediated satiety, and decreased diet preference; 3) LF produced greater reductions in BW and fat mass, enhancement in energy expenditure, and improvement in glucose tolerance than PF; 4) LA decreased BW and fat mass, increased energy expenditure, and improved glucose tolerance compared with CON; 5) LA and LF decreased plasma concentrations of insulin and leptin relative to CON; and 6) LA increased the mRNA abundance of GLUT2, glucokinase, glycogen synthase, and carnitine palmitoyltransferase-1 and decreased fatty acid synthase and pyruvate dehydrogenase, whereas LF increased glucokinase and glucose-6-phosphate dehydrogenase and decreased phosphofructokinase and fatty acid synthase in the liver and both LA and LF increased muscle pyruvate dehydrogenase compared with CON. Together we demonstrate that the improvement in energy balance, lipid metabolism, and glucose tolerance by lactoferrin are beyond its hypophagic effects. Our findings have important implications for developing lactalbumin- and lactoferrin-based functional foods and nutraceuticals for weight loss and diabetic control. Funding by ALMA, AI-Bio, and Alberta Milk.

Key Words: diabetes, lactalbumin, lactoferrin, obesity, whey

0701 Effect of milk protein intake and casein:whey ratio in breakfast meals on postprandial glucose, satiety ratings, and subsequent meal intake. B. Kung*[1], S. Paré[1], A. J. Tucker[1], G. H. Anderson[2], A. J. Wright[1], and H. D. Goff[1], *[1]University of Guelph, Guelph, ON, Canada, [2]University of Toronto, Toronto, ON, Canada*.

Novel satiating dairy-based breakfast products have potential to reduce the risk of developing and improve management of type 2 diabetes and obesity. Whey and casein proteins may induce different physiological effects on blood glucose, induction of satiation, and satiety. Whey proteins have been associated with acute satiation, compared with the prolonged feelings of satiety from casein. The purpose of this work is to investigate the impact of breakfast meal milk casein:whey ratio and protein concentration on postprandial blood glucose, appetite ratings, and subsequent food intake. In a randomized, controlled, double-blinded study, healthy young adults ($n = 32$; 16 m/f, 23.4 ± 3.1 yr, and 22.2 ± 2.5 kg/m^2 BMI) consumed milk (250 mL) with normal (80:20) or modified (40:60) casein:whey protein ratio at normal (3.1%) or high (9.3%) protein concentration, or water (control), along with 2 servings of breakfast cereal. Following an overnight fast and up to 120 min following the breakfast meal, participants had their plasma glucose concentrations determined from fingerprick samples, completed a series of scale ratings to assess satiety, and consumed a weighed ad libitum pizza lunch. Repeated measures ANOVA followed by Tukey–Kramer's post hoc testing was performed. Incremental area under the curve (AUC) glucose values showed significant attenuations in postprandial plasma glucose concentration for all milk treatments, relative to control ($P < 0.05$). Also, the high-protein treatments (9.3%) had significantly attenuated glucose concentrations compared with those with lower-protein treatments (3.1%). However, there was no effect of casein:whey protein ratio on blood glucose. Treatments were not associated with differences in total AUC for individual scale ratings of Hunger, Desire to Eat, Fullness, and Prospective Consumption. Nor were differences observed in mean appetite score ($P = 0.86$) or subsequent lunch intake ($P = 0.06$). Therefore, because consumption of high-protein milk treatments with breakfast cereal was associated with the lowest plasma postprandial glucose concentration, new high-protein dairy breakfast products should be considered for product development. (Supported by a contribution from the Dairy Research Cluster Initiative.)

Key Words: appetite, dairy protein, glycemia

Table 0701.

Table 1 Overview of results after the breakfast meal (0-120 min)

	Control	9.3% MP (40:60)	9.3% MP (80:20)	3.1% MP (40:60)	3.1% MP (80:20)	P-value Treatment
Glycemia incremental area under the curve (mmol*min/L)						
Glucose[1]	258.87 ± 16.99^{a}	142.96 ± 12.310^{b}	149.62 ± 10.39^{bc}	190.16±13.01^{cd}	211.37±13.93^{d}	P<0.0001
Satiety total area under the curve (mm*min)						
Hunger[2]	4157.53 ± 329.13	4344.64 ± 367.96	4163.40 ± 336.05	4439.98 ± 382.84	4349.77 ± 366.12	NS
Desire to Eat[2]	4294.73 ± 373.50	4480.81 ± 369.78	4280.74 ± 401.08	4449.84 ± 383.79	4473.75 ± 363.70	NS
Fullness[2]	6537.63 ± 415.05	6643.59 ± 388.72	6645.71 ± 389.67	6578.09 ± 367.86	6316.38 ± 373.93	NS
Prospective Consumption[2]	4726.44 ± 404.97	4699.44 ± 394.74	4841.44 ± 456.54	5050.73 ± 434.38	4914.95 ± 430.24	NS
Mean Appetite[2,3]	4676.81 ± 340.62	4768.38 ± 366.94	4711.98 ± 379.70	4898.19 ± 364.14	4850.13 ± 365.03	NS
Food Intake						
Grams (g)[2]	314.4 ± 24.3	285.4 ± 25.3	301.7 ± 26.6	311.7 ± 23.5	302.4 ± 23.5	NS
Energy (kcal)[2]	699.7 ± 54.0	634.1 ± 56.2	668.5 ± 58.2	692.7 ± 52.3	672.0 ± 52.3	NS

All Values are ± S.E.M. n=32. NS (not significant) and MP (milk protein).
[1]Data was analyzed by treatment incremental area under the curve interaction by general linear model ANOVA (Proc Mixed) and significance was assessed using Tukey's post hoc, means in the same row with different superscripts a, b, c, d, are significantly different.
[2]Data were analyzed treatment×time×sex interaction by 3-factor ANOVA (Proc Mixed) and significance was assessed using Tukey's post hoc, means in the same row with different superscripts a, b, c, d, are significantly different.
[3]Mean appetite derived from an average of each satiety measurement.

0702 Evaluation of modified stainless steel surfaces targeted to reduce biofilm formation by common dairy related sporeformers. S. Jindal*[1], S. Anand[1], J. K. Amamcharla[2], and L. Metzger[1], *[1]South Dakota State University, Brookings, [2]Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan*.

Development of bacterial biofilms on stainless steel (SS) surface of dairy equipment such as plate heat exchangers pose a great threat to the quality of milk and other dairy products, as the biofilm-embedded bacteria can survive thermal processing to a greater extent. Many of these are sporeformers that also form heat-resistant spores, leading to a long-term persistent contamination. Biofilms also offer cleaning challenges, as they are generally resistant to regular cleaning protocols. The main objective of this study was to evaluate different surface modifications (AMC 18, Durasan, Lindgren, and Magnaplate) of stainless steel for their resistance to biofilm formation. It was hypothesized that these coated surfaces would promote a lower deposit build-up and bacterial adhesion. Challenge studies, using vegetative cells of common dairy-related

aerobic sporeformers, namely *Geobacillus stearothermophilus* (ATCC 15952), *Bacillus licheniformis* (ATCC 6634), and *Bacillus sporothermodurans* (DSM 10599), were conducted to study the biofilm formation on the modified and native SS coupons under static conditions. Standard enumeration techniques were used to culture biofilm-embedded bacteria. The adherence of these organisms was observed to be influenced by surface energy and hydrophobicity but exhibited no relationship with surface roughness. Statistical analysis of the number of adhered cells of *G. stearothermophilus* to different native and modified SS surfaces, after 72 h of incubation, revealed significant differences in counts. Lindgren was observed to be most resistant to bacterial attachment (average 3.15 log cfu/cm^2), in comparison to the native SS surface that recorded a higher average bacterial adhesion of 5.11 logs. Similar results were obtained with *B. licheniformis* and *B. sporothermodurans*, the latter showing least attachment. Scanning electron microscopy provided the visual evidence of the extent of biofilm development and bacterial attachment on the surface of modified and native SS surfaces. In conclusion, Lindgren coating, being the most resistant to biofilm development, could potentially help in reducing the bacterial cross-contamination of milk and dairy products during processing.

Key Words: biofilms, sporeformers, surface modification

0703 Gelation properties of micellar casein concentrate when recombined with cream. Y. Lu*, D. J. McMahon, and A. H. Vollmer, *Western Dairy Center, Utah State University, Logan*.

Skim milk can be concentrated using microfiltration and evaporation to produce a highly concentrated micellar casein concentrate (HC-MCC), containing approximately 20% casein with approximately 70% of serum proteins removed during diafiltration. Understanding the gelation properties of HC-MCC and when mixed with cream to form a recombined concentrated milk (RCM) is important for using RCM for cheese manufacture. After concentration, HC-MCC forms a gel when cooled. Heating above the cold gelation temperature (up to 50°C) can break up the gel so that the individual casein micelles are solubilized. When examined using transmission electron microscopy, cold-gelled HC-MCC was observed to form a close-packed gel, which probably occurs when kinetic energy of the casein micelles is sufficiently reduced to inhibit their mobility in relation to adjacent casein micelles. Similar observations of cold gelation were made when HC-MCC was mixed with cream in casein to fat ratios of 0.8 or 1.2 as would be used for the manufacture of cheddar or part skim mozzarella cheese. At pH 6.6, an RCM with high protein can gel at cheese-making temperatures, whereas with 12% or less casein, it does not gel above 12°C. In micrograghs of cold-gelled RCM, casein micelles were less closely packed together and were partially dissociated. It appears that the protein strands that have been partially released from the casein micelles still entangle, restrict the mobility of each other, and form a fine stranded gel network. To understand challenges related to cheese making using an RCM that contains 4 times the level of casein than normally found in milk, its coagulation properties (rennet coagulation time and curd firmness) were studied using a rheometer. Reducing rennet amount can lengthen coagulation time of RCM but it does not affect curd firmness or firming rate. Decreased coagulation temperature can lengthen coagulation time and slow curd firming rate, but it also increases initial viscosity of RCM. Lowering pH of RCM to pH 6.0 did not solve the problem of curd firming being too rapid. Microstructure of RCM and its rennet coagulum indicated that the increased curd firmness probably results from the highly interlinked and longer protein strands in RCM curd. Overall, RCM with a casein level of 11 to 12% has potential for use in cheese making, provided its higher viscosity compared with milk and its fast curd firming rate can be overcome. Reducing rennet amount can be used to slow coagulation and curd firming.

Key Words: rheology, microstructure, casein micelle

0704 Thermal stability of microfiltered and ultrafiltered retentates. I. R. T. Renhe*[1] and M. Corredig[1,2], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Gay Lea Foods, Guelph, ON, Canada*.

Membrane filtration technologies are widespread unit operations in the dairy industry and are often used to obtain ingredients of tailored processing functionalities. The objective of this work was to better understand the effect of partial removal of whey proteins by microfiltration (MF) on the heat stability of the retentates. Control retentates were obtained using ultrafiltration (UF). Pasteurized milk was microfiltered (80 kDa polysulfone membrane) or ultrafiltered (30 kDa cellulose membrane) in a plate and frame membrane system to reach two and four times concentration (based on volume reduction). Concentrates showed no differences in pH, casein micelle size, or minerals in the serum phase, before heating, as diafiltration was not used in this study. The reduced amount of whey protein in the MF retentates caused a significant increase in the heat stability of the retentates, compared with UF retentates. This difference was not due to ionic composition differences or to pH. Heat coagulation time decreased with protein concentration but significantly increased in MF retentates, containing less whey proteins than the corresponding UF controls. In 2x concentrates, retentates prepared with MF, containing 20% less whey proteins than UF control, showed an increase in the heat coagulation time of about 11 min. 4xMF retentates contained 17 ± 3 mg/mL of whey proteins, about 40% less whey proteins than the 4xUF control retentates. A 4x concentrate prepared by MF showed heat stability statistically similar to that of a 2xUF concentrates, with a heat coagulation time of about 38 min. The turbidity parameter

1/l*, measured by diffusing wave spectroscopy, increased after heating, with the UF retentates showing a higher value than the MF retentates, at the same protein concentration. In addition, 4xMF concentrates showed a 1/l* value comparable to that of 2xUF concentrates. In conclusion, this work demonstrated that partial removal of whey proteins by MF could be used as a means to increase heat stability of milk concentrates.

Key Words: heat coagulation time, milk concentrate, whey protein

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0705 Effect of milk protein composition on in vivo gastric digestion of a model infant formula.

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The objective of this work was to determine the effect of protein composition and, in particular, the presence of whey proteins or b-casein, on the digestion behavior of a model infant formula. An in vivo piglet model was used, as this is an established model for human infants' digestion. Three formulas optimized for piglets were prepared with the same concentration of protein and same caloric content. One formula contained only whey proteins (WP) and two others contained a casein-to-WP ratio of 40:60 but differed in the amount of β-cas. To obtain modified protein ratios, microfiltration (using polyethersulfone membrane with 80 KDa of molecular weight cut-off) was conducted on skimmed milk at either 7 or 22°C. Retentates and permeates were combined with additional whey protein and other ingredients, and after heating, the formulas were used to feed 24 piglets. The piglets were housed and fed from age 3 to 21 d, and animal behavior and health conditions were investigated. The study was performed in two blocks, sacrificing the animals after 60 and 120 min from the last meal. Gastric digesta samples were collected and studied for physicochemical properties. The tests were performed on fresh samples in less than 10 min after euthanizing. There were no differences in the properties of the curd, within a treatment, between the two blocks. All curds showed a shear-thinning behavior, with a significantly higher viscosity and a higher modulus for curds obtained from casein/WP formula, compared with the curds from WP formula. Confocal microscopy showed structures with larger voids in WP digestates, compared with those from cas/WP formula, which showed a higher density throughout the matrix. Despite differences in physicochemical properties, a pH range of 4.4 to 5.8 was measured for the gastric contents, with no significant difference observed between diets or with time of digestion. There were also clear differences in animal growth between treatments. Casein/WP formulas were shown to improve growth performance, with approximately 50% higher average daily growth and increased feed efficiency, compared with the WP formula. The results bring significant advances to our understanding of the importance of different protein ratios on the digestion of dairy matrices.

Key Words: digestion, infant formula, milk proteins

0706 Differences in high-density polyethylene milk packaging performance under light-emitting diode and fluorescent retail storage.

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The purpose of this study was to determine how commercial and designed packaging performed in the conditions of a retail dairy case with fluorescent and light-emitting diode (LED) lighting. Commercial retail cases in the Tennessee and Virginia area and the retail case used in this study were tested for light intensity (lux) within various locations on the shelf units with a hand-held light meter. Freshly processed milk (2%) was filled in high-density polyethylene (HDPE) packages with varying light protective additives (LPA). Treatments included yellow, low titanium dioxide (TiO_2; 1.3%) and high (4.9%) TiO_2; controls included translucent HDPE (0% TiO_2; light exposed [LE]) and translucent HDPE with foil overwrap (light protected [LP]). All packages were stored for 4, 8, 16, 24, 48, and 72 h under fluorescent and LED light. Riboflavin (Rb) retention and thiobarbituric reactive substances (TBARS) were measured (2 replications) as indicators of initiation and secondary oxidation products. Means were compared using ANOVA and Tukey's HSD ($\alpha = 0.05$). The polymer conducting electronic nose (eNose) analyzed headspace volatiles for milk quality for all packages under light treatments for 8 and 24 h (canonical distribution $\alpha = 0.05$) for one replication. Commercial retail cases varied from 50 to 4,700 lux, with fluorescent light having a greater variability than LED lights. The retail case used in this study fell within the light intensity range of commercial retail cases. Mean light intensity within fluorescent (1,617 ± 505 lux) and LED (929 ± 97 lux) cases were significantly different, but this difference did not affect Rb and TBARS analysis based on analysis of covariance. Light protected performed most effectively under both lights whereas LE provided inadequate protection ($P < 0.05$). Milk in yellow and high TiO_2 packages retained the highest concentration of Rb (61 and 55% retention, respectively) among LPA packages under LED through 72 h. Under fluorescent light, interactions with package and light were different from LED, suggesting light spectra and light transmittance interactions occur between light source and LPA packaging. Milk stored in the two lighting conditions each had unique volatile chemistry based on (eNose) canonical distribution. Under fluorescent light, eNose effectively separated controls from LPA packages but not under LED light, suggesting that LED does not have as much effect on volatile profile as does fluorescent light. High-density polyethylene packaging with pigments performs better under LED lights than under fluorescent lights at low lux conditions. Effective packaging should protect milk

quality regardless of light and intensity.

Key Words: light-emitting diode, milk, packaging

0707 Efficient removal of spores from skim milk using microfiltration: Spore size and surface property considerations. E. R. Griep*, Y. Cheng, and C. I. Moraru, *Cornell University, Ithaca, NY*.

Presence of spores in milk can cause numerous quality and shelf-life issues for dairy products. Microfiltration (MF) using a 1.4-µm pore size can effectively remove vegetative bacterial cells from milk and is used in commercial applications. However, this pore size may be not be equally effective in spore removal. The objective of this study was to determine the effectiveness of MF using 1.4- and 1.2-µm pore sizes for removing spores of *Bacillus licheniformis* (BL) and *Geobacillus* spp. (GEO) from skim milk. Cell size of both spores and vegetative cells was evaluated by scanning electron microscopy, surface charge by zeta potential analysis, and surface hydrophobicity by contact angle measurements, in triplicate. Commercially pasteurized skim milk was inoculated in a sterilized feed tank with a spore suspension, at about 10^6 spores/mL, and then treated by MF (in triplicate) using ceramic Isoflux membranes at 6°C, cross-flow velocity of 4.1 m/s, and transmembrane pressure between 69 and 74 kPa. Total aerobic plate count and spore count of the permeate were conducted. An unpaired *t* test was used to determine significant differences between samples at a $P < 0.05$ significance level. Vegetative cell length ranged between 2.40 and 3.82 µm and the width ranged between 0.39 and 0.64 µm. Spores were shorter and wider, averaging 1.39 to 1.58 µm in length and 0.63 to 0.88 µm in width, therefore having a higher probability to pass through a 1.4-µm membrane. Indeed, for BL (1.39-µm length × 0.63-µm width) an average spore reduction of only 2.17 log was achieved by 1.4-µm pore size. For the 1.2-µm membrane, a 4.57 log reduction was achieved. For GEO spores, their larger spore size (1.58-µm length by 0.81-µm width) allowed a practically complete removal using both pore sizes (spore counts in permeate below the detection limit). The surface properties of BL and GEO indicated that they may interact differently with the membrane. Both spore species and the ceramic membrane had negative surface charge at the milk pH, indicating slight electrostatic repulsion between them. *Geobacillus* spp. spores were hydrophilic, whereas BL spores were slightly hydrophobic; the ceramic membrane surface changes from hydrophilic (in unfouled state) to hydrophobic after adsorption of caseins during MF. Consequently, BL spores may experience slight attractive force to the membrane through hydrophobic interactions, which will facilitate their passage through the membrane. A good understanding of all factors that affect the removal of spores using MF can lead to the production of milk with lower spore count, higher quality, and increased shelf life.

Key Words: microfiltration, skim milk, spore removal

ADSA DAIRY FOODS GRADUATE STUDENT POSTER COMPETITION

0708 Unit operations before and during spray drying influence the flavor of milk protein concentrate and whole milk powder. C. Park* and M. Drake, *Southeast Dairy Foods Research Center, North Carolina State University, Raleigh*.

Flavor is a limiting factor in the application and shelf life of dried dairy ingredients. Many off-flavors are caused during ingredient manufacture, which carry through into ingredient applications and decrease consumer acceptance. The objective of this research was to investigate the effect of spray drying parameters on the flavor of milk protein concentrate (MPC) and whole milk powder (WMP). Liquid MPC70 was produced from pasteurized skim milk by ultrafiltration/diafiltration to 19% solids (wt/wt) and evaporated to 32% solids (wt/wt). Spray drying was performed with varying inlet temperature (160, 210, or 260°C) and feed solids concentration (12, 22, or 32%). Whole milk powder was produced from standardized pasteurized whole milk that was evaporated to 50% solids (wt/wt), homogenized in two stages with varying pressures (0/0, 55.1/13.8, 110/27.6, or 165/41.4 bar), and spray dried. Whole milk powder was evaluated at 0, 3, and 6 mo storage at 22°C. Sensory properties were evaluated by descriptive sensory analysis and volatile compounds were evaluated by headspace extraction (SPME) with gas chromatography mass spectrometry. Fat globule size in condensed whole milk and particle size of powders were measured by laser diffraction. Surface free fat of WMP was measured by solvent extraction. Furosine in MPC70 was analyzed by UPLC-MS. Spray drying of MPC70 at 160°C increased cardboard flavor and volatile lipid oxidation products and decreased sweet aromatic flavor and furosine concentration compared with 210 or 260°C ($P < 0.05$). Solids concentration during drying had no effect on furosine concentration ($P > 0.05$). Decreasing feed solids concentration decreased sweet aromatic flavor and increased cardboard flavor and volatile lipid oxidation products ($P < 0.05$). Increased homogenization pressure decreased cardboard flavor, volatile lipid oxidation compound concentrations, fat globule size in condensed milk, and surface free fat in WMP ($P < 0.05$). Surface free fat in powders increased cardboard flavor and lipid oxidation. These results indicate that off-flavors are decreased with increasing feed solids concentration and inlet temperature in MPC70 and with increased homogenization pressures in WMP. To decrease off-flavor intensities in WMP and MPC70, manufacturers should evaluate these parameters during ingredient manufacture.

Key Words: milk proteins, whole milk powder, unit operations

0709 The effect of bleaching agents on the degradation of vitamins and carotenoids in WPC80.

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Previous research has demonstrated that chemical or enzymatic bleaching impact flavor and functionality of whey proteins. The role of bleaching on vitamin and carotenoid degradation is unknown. The objective of this study was to determine the effects of bleaching with hydrogen peroxide (HP), benzoyl peroxide (BP), or native lactoperoxidase (LP) on vitamin and carotenoid degradation. The role of an alternative colorant on whey protein vitamin profile was also evaluated. Colored cheddar whey (15 mL/454 L milk) was manufactured, pasteurized, and fat separated and then assigned to 250 ppm HP, 25 ppm BP, or 20 ppm HP (LP system) at 50°C for 1 h. An unbleached control (Con) as well as whey from cheese milk with an alternative colorant (AltC) were also included. The Con and AltC were also heated to 50°C for 1 h. Wheys were concentrated to 80% protein by ultrafiltration and spray dried. The experiment was replicated in triplicate. Vitamin, norbixin, and carotenoid contents were determined by HPLC and volatiles by gas chromatography mass spectrometry. A trained panel documented sensory properties of the rehydrated WPC80. Volatile compound and sensory results were consistent with previous studies on bleached and unbleached whey proteins. WPC80 that were chemically or enzymatically bleached had decreased retinol, β-carotene, ascorbic acid, α-carotene, thiamine, lutein, and α-tocopherol ($P < 0.05$) compared with Con WPC80 or AltC WPC80. Benzoyl peroxide WPC80 contained less of these compounds than HP or LP WPC80 ($P < 0.05$). Riboflavin, pantothenic acid, pyridoxine, and nicotinic acid concentrations were not impacted by bleaching ($P > 0.05$). Alternative colorant WPC80 contained 6% more β-carotene than Con WPC80 ($P < 0.05$). Bleaching to remove norbixin decreases fat soluble vitamin and carotenoid concentrations in the final spray dried whey protein.

Key Words: bleaching, vitamin degradation, alternative colorant

0710 Characterization of flavor and functional properties of liquid and dried WPC 80, WPI, MPC 85, and micellar casein concentrates.

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Traditionally most protein ingredients are sold as a powder due to its ease to transport and longer shelf life. Many high-protein powder ingredients such as MPC 85 and micellar casein concentrate (MCC) have poor rehydration properties (e.g., solubility), which might be a limiting factor for using these ingredients in end applications. Previous research suggested that the spray drying may have some adverse effects on flavor and functional properties of dried ingredients. Moreover, spray drying is the costly unit operation in the manufacture of protein ingredients. Considering this, manufacturers of dried protein ingredients are considering an option to manufacture liquid retentate, which will not only save the cost of spray drying but may provide improved flavor and functional properties. The objective of this study was to determine what effect, if any, spray drying has on the flavor and functionality of high-protein ingredients. Liquid and dried protein ingredients (WPC 80, WPI, MPC 80, and MCC) were manufactured from the same lot of milk at the North Carolina State University pilot plant. These ingredients were characterized using native PAGE, particle size, and calcium activity, and functionality differences were evaluated by measurement of foam stability, protein solubility, and heat stability. Protein solubility was measured at pH 7 before and after centrifugation by micro-bicinchoninic acid assay (micro-BCA), and heat stability by heating at 90°C for 0, 10, 20, and 30 min followed by micro-BCA and turbidity loss. Flavor was evaluated by descriptive analysis, and volatile compound analysis was conducted by GC–MS to identify key flavor differences between the liquid and spray dried protein ingredients. No differences were detected in solubility and heat stability between liquids and powders ($P > 0.05$). WPC 80 (liquid or spray dried) did not produce a foam; powder WPI produced a more stable foam as opposed to the liquid, but with milk proteins, the liquids produced a more stable foam ($P < 0.05$). This result is likely due to the particle size difference between liquid and powder being much greater in milk proteins compared with whey proteins ($P < 0.05$). All powders had higher aroma intensity and cooked flavors compared with liquids ($P < 0.05$). Powder proteins also had low but distinct cardboard flavor concurrent with higher volatile aldehydes compared with liquids. An understanding of how spray drying effects both flavor and functionality will help producers better use the ingredients they have available to them.

Key Words: milk proteins, whey proteins, flavor, functionality

0711 Effect of milk protein concentrate (MPC 80) quality on susceptibility to fouling during thermal processing.

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Milk protein concentrate (MPC) is incorporated into wide range of dairy beverages to improve the functional, nutritional,

and sensory properties. Various factors such as drying conditions, composition, storage, and dissolution conditions affect the overall functional characteristics of MPC. To be used for its intended purpose, it is essential to study the functional properties such as solubility, dissolution, and fouling characteristics of MPC. Fouling of the stainless steel (SS) surfaces during thermal processing of milk is a major problem in the dairy industry. It is important to understand the composition and structure of the fouling layer to minimize the fouling of the processing equipment. The objective of the present study was to understand the effect of MPC solubility on its susceptibility to initiate fouling on SS surfaces during thermal processing. Milk protein concentrate powder with 80% protein content was obtained from a commercial manufacturer, divided into two lots. To create powders with different solubility characteristics, the first lot was stored at 25°C and the second lot at 40°C for 2 wk. Immediately after the storage, the powder solubility characteristics were monitored using focus beam reflectance measurement technique and solubility index. As expected, the MPC stored at 40°C showed the slow dispersion rate of particles when compared with the powder stored at 25°C, indicating poor solubility characteristics. Fouling characteristics were studied using a custom-build benchtop heat exchanger (bPHE). The bPHE was designed to accommodate two SS coupons with 1″ by 1″ dimensions. The MPC was reconstituted to 10% (wt/wt) solution and pumped for 2 h through bPHE to an average outlet temperature of 71.9°C. Subsequently, the SS coupons were removed from the bPHE and fouled layer was characterized using weight of fouling, scanning electron microscopy, confocal laser scanning microscopy, energy dispersive X-ray spectroscopy, and SDS-PAGE. The average foulant accumulated over the SS coupons by the poor quality powder (stored 40°C) and the good quality (stored at 25°C) powder was 0.171 ± 0.031 and 0.093 ± 0.019 g, respectively. Storing the powders at 40°C significantly ($P < 0.05$) increased the amount of fouling on SS coupons. Microscopic investigations revealed the heterogeneity of the fouling layer with the discrete distribution of lipids and proteins with uniform calcium distribution. Therefore, the study will be helpful in designing effective strategies to reduce fouling during processing of high-protein dairy beverages.

Key Words: fouling, milk protein concentrate, plate heat exchanger

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0712 Oxygen barrier and light interference packaging properties for controlling light-induced oxidation in milk. H. Potts*, S. Duncan, M. L. Johnson, S. F. O'Keefe, J. E. Marcy, and K. Mallikarjunan, *Virginia Tech, Blacksburg*.

A recent shift to more energy efficient light-emitting diode (LED) lights in retail dairy cases has occurred, but the effects of LED light on fluid milk in retail conditions are not known. Our objective was to determine the efficacy of polyethylene terephthalate (PET) packaging at preventing light-induced oxidation in 2% milk under LED and fluorescent retail light. Light interference effects were studied in combination with the oxygen barrier effects of PET. The extent of oxidation in 2% milk packaged in PET bottles (2 L; average wall thickness: 0.33 mm; treatments: clear with UV barrier and 2.1, 4.0, and 6.6% titanium dioxide [TiO_2]) under fluorescent and LED retail light up to 72 h was studied. Two control packages (clear PET = full light exposure and PET wrapped with foil and plastic = no light exposure) were used for comparison, creating a total of six packaging experimental treatments. Chemical measures of oxidation ($\alpha = 0.05$; ANOVA) included formation of secondary lipid oxidation products, riboflavin degradation, and headspace volatiles analysis by an electronic nose. Volatile analysis compared electronic nose smell-prints by canonical discrimination analysis. Sensory evaluation of milk (triangle test, 3 replications) compared milk from experimental packages to light-protected control milk for similarity ($\beta = 0.05$) and to light-exposed control milk for differences ($\alpha = 0.05$). Polyethylene terephthalate with 6.6% TiO_2 was an effective package for protecting fluid milk sensory quality for up to 8 h under LED light (936 ± 136 lux) but only for 4 h under fluorescent light (1,447 ± 1,072 lux). Polyethylene terephthalate with 4% or less TiO_2 could not effectively protect milk flavor from light-induced changes through 4 h fluorescent or LED light exposure. Milk stored in PET packages retained 0.90 mg/L or higher riboflavin content over 72 h retail light exposure. Electronic nose technology differentiated ($P < 0.05$) volatile profiles among fresh milk with no light exposure and milk that remained under retail lights for 8 h or more, indirectly supporting the changes in sensory quality. The results conclude that LED light is less detrimental to milk quality than fluorescent light and higher levels of TiO_2 in PET packages were more effective at preventing light-induced oxidation in 2% milk.

Key Words: milk, oxidation, sensory

0713 Use of fluorescence-based Amaltheys analyzer for studying effect of pH and heat on whey protein interactions in reconstituted milk protein concentrate. K. Sajith Babu*, Z. Liu, and J. K. Amamcharla, *Food Science Institute, Animal Sciences and Industry, Kansas State University, Manhattan*.

Milk protein concentrates (MPC) are complete proteins that contain both casein and whey proteins in the same ratio as in milk. In comparison with skim milk powder or whole milk powder, MPC are higher in protein and lower in lactose and minerals. The objective of our study was to use fluorescence-based Amaltheys analyzer to study the effect of pH and heat on whey protein interactions in reconstituted milk protein concentrate. MPC85 from two different lots of same manufacturer was reconstituted into 5% solution and the pH values were adjusted between 5.5 and 7 and heated (70, 80, and 90°C) up to 20 min. The level of whey protein denaturation

and protein associations were examined for each milk sample. The level of native whey protein in the no-heat and heat-treated milk samples were determined using native PAGE. The whey protein nitrogen index (WPNI) and the FAST (fluorescence of advanced Maillard products and soluble tryptophan) index were measured by fluorescence-based Amaltheys analyzer (Spectralys Innovation, Romainville, France) and was compared with the native PAGE results. The results based on the WPNI, gives an indirect indication of the denaturation and aggregation of whey proteins. The level of denatured whey proteins was significantly dependent on the pH and thermal treatment, with high levels of interactions at pH 5.5 and low levels of changes at pH 7. Reconstituted MPC85 with no heat treatment (WPNI 1.84 ± 0.01 mg WPN·g^{-1} powder at pH 7 and WPNI 1.69 ± 0.01 mg WPN·g^{-1} powder at pH 5.5, respectively) retained most of the whey proteins in the native state. In contrast, the reconstituted MPC85 at 90°C for 20 min (WPNI 0.44 ± 0.01 mg WPN·g^{-1} powder at pH 7 and WPNI 0.21 ± 0.01 mg WPN·g^{-1} powder at pH 5.5) contained a comparatively small proportion of native whey proteins, although some α-lactalbumin was still present (shown in native PAGE). The degree of denaturation of β-lactoglobulin appeared to be crucial and could be related to the WPNI and FAST index. The amount of whey protein interactions increased with increase in temperature and decrease of pH. The results in this study indicate that the changes in whey protein induced by the heat treatment of reconstituted milk protein concentrate were affected by pH and thermal treatment time, and the Amaltheys analyzer was found to be a simple and rapid instrument for studying these interactions.

Key Words: milk protein concentrate, whey protein nitrogen index, protein denaturation and aggregation

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0714 Use of ozonated water in removing *Bacillus cereus* biofilms from the dairy membranes.

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Fouling of dairy membranes is a major problem and leads to biofilm development. This causes reduction in membrane performance and leads to premature replacement of membranes. Ozone is a potent bactericidal agent used in diverse applications. The objective of this study evaluates the efficiency of ozonated water on removal of biofilms from dairy processing membranes. To generate aqueous ozone, an ozone generator system supplied by CleanCore Technologies Inc. (Omaha, NE) was used. The system consists of six ozone generators connected to an injector that mixes ozone with water. It also houses a dissolved ozone monitor and oxidation–reduction potential sensor. The half-life of ozone in ozonated water was evaluated using a factorial design with pH (2, 4, and 7) and temperature (5, 10, and 20°C) as independent factors with two replications. Reduction in ozone concentration in ozonated water was monitored at regular intervals until the final concentration dropped below 1.0 ppm. First order rate constants (k) were calculated using a first order decay model and ozone half-life was then calculated. Temperature and pH and their interaction significantly ($P < 0.05$) affected half-life. Maximum ozone half-life was achieved with pH 4 solution at 10°C, with an average half-life of 478 min; therefore, these conditions were used to evaluate biofilm removal from dairy membranes. Ultrafiltration of skim milk was performed in a bench-top plate and frame system. Flat sheet polyethersulfone (PES) membranes (Hannifin Corp., Oxnard, CA) were fouled during 5x ultrafiltration of pasteurized skim milk. Fouled PES membranes were submerged in Luria broth inoculated with *Bacillus cereus* (ATCC 10987) and incubated for 48 h at 37°C to promote biofilm formation. Biofouled membranes were installed in the plate and frame system and exposed to ozonated water for 6 min in recirculation mode. Subsequently, residual biofilm was removed by scraping a 6.45 cm^2 of the membrane, transferred into 10 mL of 0.1% peptone water, and vortexed. Serial dilutions were plated onto mannitol egg yolk polymyxin agar, and plates were incubated at 37°C for 24 to quantify viable *B. cereus* populations, which were compared with corresponding population levels on nontreated control membranes. The *B. cereus* biofilms grown on fouled PES dairy membranes and treated with ozonated water under the described conditions were reduced by an average of 1.0 log cfu/cm^2. Data suggests ozonated water has potential as an effective and environmentally friendly means for removing biofilms from dairy membrane systems.

Key Words: ozonated water, ultrafiltration membranes, biofilms

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0715 Development of a benchtop method to polymerize lactose to soluble fiber.

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Twin-screw extrusion is used to polymerize lactose and glucose to an oligosaccharide, polylactose. However, previous research in our lab demonstrated that the lactose in permeate and acid whey could not be polymerized using our standard method. There is a lack of understanding for what inhibits the polymerization reaction; the citric acid content and extruder feed rate have been researched, yet chemical properties such as moisture and mineral contents have not. The objective of this study was to develop a benchtop method for polymerization using a CEM Mars 6 microwave reaction system so that inhibition factors could be identified before scaling up to the extruder. A heating profile needed to be established that

would consistently polymerize a blend of citric acid (6%), glucose (20%), and lactose (74%). Seven-gram samples of the sugar acid blends were added to 8 Teflon MarsXpress vessels. The set temperature, ramp time, and hold time were varied to melt the powder blend and achieve polymerization, without reaching decomposition. All vessels were continuously monitored for temperature during the reaction via an infrared thermometer. The reacted samples were cooled and dissolved in water, passed through ion-exchange resins, and then separated and detected by HPLC-ELSD. An initial heating profile with a 5-min ramp time to a 180°C target temperature imitated extrusion conditions known to result in polymerization. Even though polymerization was observed with this heating profile, the reactants did not reach the target temperature and temperature variability between vessels occurred. These challenges led to modifications of the heating profile including an increase in the ramp time (15 min) and a reduction in the temperature (140°C). Uneven heating was still a challenge so the formula was modified by adding a small amount of water (<1% wt/wt) to increase dipole rotation due to the microwave energy. The inclusion of a polar solvent resulted in consistent, even heating. Product resulting from the lower-temperature, longer-time heating profile demonstrated successful polymerization. The elevated pressure in the microwave reaction system, when compared with the open extrusion system, allowed for polymerization at a lower temperature. This benchtop polymerization method allows for experimentation of numerous formulas and the identification of inhibitors. Understanding these factors for permeate or acid whey will allow for polymerization into a value added ingredient, soluble fiber.

Key Words: lactose, polymerization, microwave

0716 Effect of microencapsulated iron salts on cheddar cheese divalent cation balance and composition.

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Milk is considered an important source of macro- and micronutrients but naturally low in iron content. Cheese and other dairy products had been fortified with iron with low success due to negative changes in composition and organoleptic attributes. There is limited information about using microencapsulation of iron compounds in dairy products. Minerals have the ability to displace one another in any system; consequently, it is expected that encapsulation will avoid divalent cation displacement within the cheese matrix. The objective of this study was to analyze divalent cation balance in fortified cheddar cheese with microencapsulated ferrous sulfate. Furthermore, proximate analysis was done to provide more information about any compositional changes after fortification. Cheddar cheese was manufactured using standard cheddar cheese procedures a total of three times. Cheddar cheese was fortified with either large microencapsulated ferrous sulfate (LMFS; 0.9536 g microencapsulated ferrous sulfate/kg cheese and 700–1,000 μm diameter) or small microencapsulated ferrous sulfate (SMFS; 1.7801 g microencapsulated ferrous sulfate/kg cheese and 220 to 422 μm diameter). Iron treatment was incorporated to cheddar cheese processing in the salting step but omitted for the control. After 90 d of aging, calcium, iron, magnesium, and zinc content were analyzed using atomic absorption spectroscopy and percent recoveries were calculated. Moisture, ash, fat, and protein analysis were done using AOAC methods. All collected data was analyzed using one-way ANOVA and Tukey's HSD test ($P = 0.05$). Iron content for all treatments were significantly different ($P < 0.05$): approximately 0.030 mg Fe/g cheese for the control, 0.134 mg Fe/g cheese for LMFS, and 0.174 mg Fe/g cheese for SMFS. Results showed 81.3% iron recovery for LMFS and 90.0% iron recovery for SMFS. Proximate analysis and magnesium, zinc, and calcium content were not significantly different when comparing fortified cheeses with the control. Overall, microencapsulated ferrous sulfate caused no major changes in terms of cheddar cheese composition and successfully increased iron content. Microencapsulated ferrous sulfate with smaller diameter showed slightly better results for iron retention in cheddar cheese. The proposed fortified cheddar cheese can help increase total iron intake for children, pregnant women, vegetarians, and those whose diets are likely to be deficient in iron by providing at least 5 mg Fe (30% RDA) per serving.

Key Words: fortification, cheese, minerals

ADSA PRODUCTION DIVISION GRADUATE STUDENT ORAL COMPETITION: MS

0717 Rumen development in Holstein calves.

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Feed intake in calves is very important for future production and health, but there are many issues that can influence starter intake such as weather, rumen development, and overall calf health. The objectives of this study were to observe the interaction of starter grain intake and rumen development. Data from 122 Holstein bull and heifer calves were collected from age 2 to 69 d, time of exit from hutch including fecal scores (1–3), DMI, medication, and milk intake. Daily starter grain samples were pooled by week and analyzed for nutrient content by Analab (Agriking, Fulton, IL). Blood samples were collected from a subset of 38 calves and analyzed for glucose (mg/dL) and β-hydroxybutyrate (BHBA; mmol/L) levels with Precision Extra (Abbott Diabetes Care, Inc., Alameda, CA) blood meters. At 1, 6, and 9 wk, blood samples were also analyzed using a VetScan Large Animal Profile rotor (Abaxis Inc., Union City, CA). The rotor tested for albumin (ALB), alkaline phosphatase (ALP), aspartate aminotransferase (AST),

calcium (Ca), creatine kinase (CK), γ glutamyl transferase (GGT), phosphorus (P), magnesium (Mg), total protein (TP), and urea nitrogen (BUN). The Abaxis blood parameters indicate immune status and, indirectly, liver function (ALB, Glob, TP, and GGT), liver and bone function (ALP, Ca, P, and Mg), liver and kidney function (AST and BUN) and muscle damage (CK). Weekly outcomes, average DMI, average milk intake, and blood parameters were analyzed using the MIXED procedure of SAS with repeated measured by calf, hutch, and gender as fixed effects and the random variable week. Hutch and gender were not significant but week was significant for all comparisons. Alkaline phosphatase and Ca were all elevated whereas AST, TP, and Glob were lower than expected values. Blood urea nitrogen and CK were within the expected range for adult cows and steadily increased over the experimental period. Total protein ($P < 0.064$), AST ($P < 0.0001$), Glob ($P < 0.0076$), BHBA ($P < 0.0001$), and BUN ($P < 0.013$) increased with increasing DMI. Glucose ($P < 0.0001$), however, decreased with increasing DMI. Increases in these parameters also show changes as the rumen develops. Therefore, starter grain intake is an important factor for rumen development in a Holstein calf.

Key Words: blood parameters, calves, rumen development

0718 Milk fat secretion in lactating dairy cattle is influenced by soybean particle size and fatty acid profile. K. A. Weld* and L. E. Armentano, *University of Wisconsin – Madison, Madison*.

It is well established in the literature that when feeding free vegetable oils, oleic acid has a smaller negative effect on milk fat secretion than does linoleic acid. The objectives of these experiments were to analyze the effects of oleic and linoleic acid fed as part of full fat soybeans and to analyze the interaction between soybean particle size and fatty acid profile. Trial 1 used 63 cows (28 primiparous and 35 multiparous; 111 ± 20 d in milk [DIM]). Cows were housed in a common pen with 32 electronic feed gates and fed conventional or high-oleic (Plenish) whole raw beans for 3 wk following a covariate adjustment period. The second trial used 20 cows (10 primiparous and 10 multiparous; 88 ± 10 DIM) in a tie stall barn, using two complementary 5 × 5 Latin squares per parity. Raw Plenish or conventional beans, either ground (GP and GC) or whole (WP and WC), formed 4 iso-fat diets in a 2 × 2 factorial, plus a fifth treatment was a low-fat diet without soybeans. Diets were 55% forage and isonitrogenous and contained 2.9 to 3.9% added ether extract from soybeans (15.5–18.7% soybeans, DM basis). In trial 1, there was a parity × diet interaction ($P < 0.10$); there were no diet effects with primiparous cows ($P > 0.10$), but for multiparous cows, feeding Plenish beans increased milk fat yield ($P < 0.05$). In trial 2, when there was a significant interaction ($P < 0.10$) between bean type and particle size, we tested GP vs. GC and WP vs. WC. If the interaction was not significant ($P > 0.10$), the main effects of bean type and particle size were tested. There was a significant interaction between bean type and particle size for both milk fat yield and concentration ($P < 0.05$). GP resulted in greater milk fat yield and concentration than GC ($P < 0.05$), whereas there was no difference between WP and WC ($P > 0.10$). Diet affected milk yield with the Plenish diets resulting in lower milk yield ($P < 0.05$). In both trials, the increase in milk fat yield was due to an increase in 18-carbon milk fatty acids ($P < 0.05$) and there was not a difference in short-chain fatty acid yield ($P > 0.10$). Plenish high-oleic soybeans result in moderately increased milk fat compared with conventional soybeans, and this difference is greater when soybeans are fed ground rather than whole.

Key Words: linoleic, oleic, soybeans

Table 0718.

Variable	Trial 1			Trial 2					
	Conventional Multiparous	Plenish Multiparous	SE	Low Fat	Ground Conventional	Ground Plenish	Whole Conventional	Whole Plenish	SE
DMI (kg/d)	26.5	26.8	0.9	26.5	26.3	26.3	26.7	26.6	0.6
Milk (kg/d)	45.1	45.0	1.2	48.0	48.8	47.2	48.5	46.8	1.0
Protein (%)	3.05	3.06	0.05	3.18	3.09	3.18	3.08	3.13	0.04
Protein (kg/d)	1.36	1.40	0.06	1.51	1.50	1.49	1.49	1.40	0.03
Fat (%)	3.84	4.07	0.10	3.25	3.09	3.50	3.40	3.53	0.16
Fat (kg/d)	1.70	1.84	0.06	1.54	1.49	1.64	1.64	1.63	0.08

0719 Effects of heat stress and dietary zinc source on mammary tight junction of lactating dairy cows. X. Weng*[1], A. P. A. Monteiro[1], J. Guo[1], J. K. Bernard[1], J. DeFrain[2], and S. Tao[1], *[1]University of Georgia, Tifton, [2]Zinpro Corporation, Eden Prairie, MN*.

Dietary Zn has been shown to alter gut integrity in monogastrics under heat stress. However, the effect of Zn on mammary tight junction (MTJ) integrity in heat-stressed lactating dairy

cows has not been studied. Seventy-two multiparous lactating Holstein cows (2.9 ± 1.1 parity and 99.7 ± 55.5 d in milk) were randomly assigned to 4 treatments with a 2 × 2 factorial arrangement to study the effect of environment and Zn source on performance and MTJ integrity (n = 18/treatment). Treatments included two environments, cooled (CL) or not cooled (NC), and two Zn sources, 75 ppm supplemental Zn as ZnCl (IOZ) or 35 ppm ZnCl + 40 ppm Zn–methionine complex (ZMC). The experiment was divided into baseline and environmental challenge phases, 84 d each. During the baseline phase, all cows were cooled (fans and misters over the freestall and feeding areas; average temperature–humidity index = 73) and fed respective dietary treatments, whereas during the environmental challenge phase, NC cows were not cooled (average temperature–humidity index = 78). Feed intake was measured daily. Milk yield was recorded at each milking (3x/d) and composition was analyzed weekly. Vaginal temperature was measured every 5 min for 4 d/wk. Milk and plasma samples were collected weekly for analyses of milk BSA and plasma lactose. Deprivation of cooling decreased DMI ($P < 0.01$). Energy-corrected milk yield decreased ($P < 0.01$) for NC cows relative to CL cows (24.5 vs. 34.1 kg/d). An interaction between environment and Zn source ($P = 0.04$) occurred for milk fat percent as CL cows fed ZMC had lower milk fat percent relative to other groups. Relative to CL cows, NC cows had lower milk lactose and solids-not-fat percent ($P = 0.05$) but higher concentration of milk urea nitrogen ($P < 0.01$). Vaginal temperature was higher ($P < 0.01$) in NC cows relative to CL cows (39.9 vs. 39.0°C). Plasma lactose was similar between treatments at the start of the baseline phase but increased in cows fed IOZ and was unchanged in cows fed ZMC throughout the baseline phase (Zn source × day, $P = 0.06$). Relative to CL cows, plasma lactose tended to increase in NC cows over time (environment × day, $P = 0.09$), indicating increased MTJ permeability, and feeding ZMC tended to decrease plasma lactose during the environmental challenge phase relative to IOZ ($P = 0.11$). In conclusion, removing active cooling impairs lactation performance and feeding a portion of dietary Zn as ZMC improves the integrity of MTJ as evidenced by the decreased permeability of lactose through MTJ.

Key Words: heat stress, mammary tight junction, zinc

0720 Effects of feeding forage and concentrate, separately or as a total mixed ration, on ruminal methane emission, fermentation characteristics, and total tract digestibility. B. Rajaraman*[1], A. Selvaraj[2], C. H. Lee[2], and K. H. Kim[1,2], *[1]Graduate School of International Agricultural Technology, Seoul National University, Pyeongchang, the Republic of Korea, [2]Green Bio Science and Technology, Seoul National University, Pyeongchang, the Republic of Korea*.

Very little research is available on the advantages of feeding systems, specifically how forage and concentrate feeding, separately (SF) or as a total mixed ration (TMR), affects methane production from enteric fermentation of ruminant. Three experiments were performed at three different levels of daily feed intake (1.8, 2.1, and 2.6% of BW) to investigate methane production from the different feeding systems by using a quadruplicated 2 × 2 crossover design. Each experiment was conducted using eight male Holsteins with BW ranging from 230 to 570 kg. Animals were provided either SF or TMR containing 73% concentrate and 27% forage, with the same ratio of same ingredients and grasses, twice a day. Animals fed SF received the forage first for 30 to 40 min and then received the concentrate. In experiment 2, the ruminal fermentation characteristics (1.5, 3.0, and 4.5 h after morning feeding) and indirect total tract digestibilities were evaluated based on rumen fluid and fecal grab samples, respectively. Animals fed TMR in experiment 1 and 2 emitted significantly more methane (169.9 vs. 140.1 ± 6.9 L/d [$P < 0.05$] and 138.4 vs. 114.19 ± 4.2 L/d [$P < 0.01$], respectively) and lost more methane energy (7.1 vs. 5.6 ± 0.4% [$P = 0.01$] and 4.0 vs. 3.4 ± 0.2% [$P < 0.01$], respectively) compared with those fed SF. No differences ($P > 0.1$) were observed in methane emissions and methane energy losses for animals fed diets at 2.6% of BW in experiment 3, although those fed TMR emitted slightly more methane than those fed SF. Cattle that received SF exhibited significantly lower ($P < 0.05$) ruminal pH and higher ($P < 0.05$) ammonia N concentration, total VFA, and individual VFA production compared with those fed a TMR at 4.5 h after feeding. A significantly ($P < 0.05$) lower acetate:propionate ratio (2.2 vs. 2.6) in those fed SF reflected the shift in hydrogen transfer toward the formation of more propionate than in those fed TMR. Significantly higher levels of isobutyrate and isovalerate ($P < 0.05$) were observed in those fed SF compared with those fed TMR. The total tract digestibilities of CP, NDF, and OM were not affected by the feeding system. Overall, these results indicate that, compared with TMR, SF significantly reduces methane emission from ruminants and increases VFA production without affecting the total tract digestion.

Key Words: methane, rumen, separate feeding

0721 The effect of dietary fats on fatty acid composition, gene expression, and vitamins status in preruminant calves. C. Y. Tsai*, W. I. Loucks, C. M. Scholte, K. C. Ramsey, M. E. Doumit, and P. Rezamand, *University of Idaho, Moscow*.

Dietary saturated (SFA) and unsaturated fat (UFA) alters fatty acid composition of various tissues, serum, and lipid-soluble vitamins. The objective was to examine the effect of dietary SFA and UFA on adipose, liver, serum, polymorphonuclear (PMN) and peripheral blood mononuclear cells' (PBMC) fatty acid profiles, selected gene expression of inflammatory mediators, and their relation with vitamin content in preruminant calves. Twelve Holstein male calves were randomly assigned to two treatments. Starting at 3 d of age, 6 calves on SFA received 120 mL palm oil/d and 6 calves on UFA received 80 mL flaxseed oil plus 40 mL CLA. After 50 d, all animals were euthanized and samples were obtained. Gas chromatography was used to analyze fatty acid composition. High-performance liquid chromatography was used to analyze α-tocopherol and retinol in liver tissues as well as α-tocopherol, retinol, and β-carotene in serum. Liver and adipose tissue were analyzed for relative gene expression of interleukin (IL)-1β, IL-6, IL-8, IL-10, IL-12, interferon-γ, peroxisome proliferator-activated receptor-γ, TNF-α, retinol binding protein-4, and NF-κB. The PBMC were examined for gene expression of IL-1β, IL-6, TNF-α, and intercellular adhesion molecule-1; PMN were analyzed for expression of caspase-1, IL-8 receptor, and L-selectin (L-SEL). Data were analyzed using the PROC TTEST of SAS with significance declared at $P \leq 0.05$. The UFA had greater α-linolenic acid (α-LA) compared with SFA calves in (NEFA, neutral lipids [NL], and phospholipids [PL]) fractions of liver, adipose, and serum as well as PBMC and PMN. The higher content of α-LA in calves fed UFA resulted in greater EPA in all three lipid fractions of serum as well as NL and PL fractions of adipose tissue. In addition, PBMC and PMN had higher EPA in UFA calves. The UFA group, however, had lower γ-linolenic acid compared with SFA calves in all three fractions of liver as well as NL and PL fractions of serum. Dietary UFA also increased total PUFA in three lipid fractions of serum and adipose. The lipid-soluble vitamins content in serum was reduced by dietary UFA. Moreover, L-SEL expression was upregulated in calves receiving UFA. This may indicate that UFA supplementation elevated the substrate of PUFA biosynthesis but possibly degraded the lipid soluble vitamins to protect these fatty acids from oxidation. This may influence the migration of PMN from the blood to tissues, affecting overall inflammatory responses.

Key Words: calves, fatty acid composition, gene expression

0722 Effect of OmniGen-AF and heat stress during the dry period on subsequent performance of cows. T. F. Fabris*[1], J. Laporta[1], F. N. Correa[1], Y. M. Torres[1], D. J. Kirk[2], D. J. McLean[2], J. D. Chapman[2], and G. E. Dahl[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Phibro Animal Health Corp., Quincy, IL*.

Heat stress in dairy cows during the dry period impairs milk production in the next lactation. Feeding OmniGen-AF (OG) to lactating cows during heat stress increases DMI and lowers respiration rate (RR) and rectal temperature (RT), but effects in dry cows are not known. We hypothesized that OG supplementation before, during, and after the dry period (approximately 160 d) would overcome the effects of heat stress and improve performance. Treatment groups were heat stress (HT; only shade; $n = 17$), heat stress with OmniGen-AF (HTOG; 56 g/d; $n = 19$), cooling (CL; shade, fans, and sprinklers; $n = 16$), and cooling with OmniGen-AF (CLOG; $n = 11$). Cows were randomly assigned to treatments based on previous mature equivalent milk production. Cows were dried off 45 d before expected calving and after parturition; cows were kept under the same cooling system and management until 60 DIM. Cooling cows during the dry period reduced RT (38.8 vs. 39.0 for CL vs. HT, respectively; $P < 0.01$) and RR (44 vs. 73 for CL vs. HT, respectively; $P < 0.01$). Respiration rate was also decreased by OG supplementation (56 vs. 61 for OG vs. non-OG, respectively; $P < 0.01$). There was an interaction between OG supplementation and HT ($P < 0.1$); HTOG cows had lower RT compared with HT cows. During the dry period, OG reduced DMI relative to non-OG cows ($P < 0.1$). Calf birth weight was greater in calves from CL cows (CL vs. HT; $P < 0.01$). In cows, no differences in hematocrit, total protein, and BCS among treatments were detected. Cows on CLOG had higher BW (kg) at parturition (CLOG, 794.9 kg; CL, 746.8 kg; HTOG, 762.9 kg; and HT, 720 kg). Gestation length was approximately 4 d longer for CL cows compared with HT cows ($P < 0.01$). Cows on CLOG, CL, and HTOG treatments produced more milk (5.2 ± 1.9, 4.8 ± 1.6, and 4.6 ± 1.4 kg/d, respectively) than HT cows (35.9 ± 1.5 kg/d). Body weight after parturition and DMI were evaluated up to 60 DIM and averaged DMI 19.4 ± 0.7 kg/d, with no differences observed among treatments. These results confirm that exposure of dry cows to heat stress negatively impacts milk production in the subsequent lactation. Active cooling of dry cows and OG supplementation can reduce the negative effects of heat stress in the dry period.

Key Words: cooling systems, heat stress, OmniGen-AF

0723 Feed efficiency is associated with reproductive performance in dairy cows. E. M. Bart*[1], M. D. Hanigan[2], D. M. Spurlock[3], M. J. VandeHaar[4], and R. R. Cockrum[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Virginia Tech, Blacksburg, [3]Iowa State University, Ames, [4]Michigan State University, East Lansing*.

For residual feed intake (RFI) to be used as an alternative measure of feed efficiency in the dairy industry, it must not be unfavorably correlated with fertility. Previous research in beef cattle, sheep, and pigs suggests that reproduction is impacted by RFI status. Therefore, the objective of this study was to determine the phenotypic relationship between RFI and reproductive performance in dairy cows. Feed, milk, and health data were collected on 1,513 Holstein cows in various stages of production at Virginia Tech and Iowa State University for 84 d. Daily measurements of DMI, milk yield, weekly milk composition, and monthly BW were used to calculate RFI. Cows with lower RFI were identified as more feed efficient. Four measures of reproductive performance were examined: number of services (NS; n = 1,037), previous days dry (DD; n = 760), days open (DO; n = 716), and days to first calving (DFC; n = 472). Correlation and ANOVA analyses with ad hoc comparisons using a Tukey adjustment were performed in R. For the ANOVA, cows were categorized into top 5% (high RFI; n = 50), middle 5% (medium RFI; n = 50), and bottom 5% (low RFI; n = 50). Correlations were calculated between reproductive measures and RFI. There was a weak positive phenotypic correlation (r_p = 0.18 ± 0.04, P < 0.01) between NS and DO with RFI, suggesting that feed-efficient cows may require fewer services to become pregnant and shorter periods to become bred. There was also a weak negative phenotypic correlation (r_p = −0.14 ± 0.04, P < 0.01) between DFC and RFI, suggesting increased days for feed-efficient cows to produce their first calf. Medium-RFI cows had greater DD (P = 0.046; 109.5 ± 13.9) compared with high-RFI cows (63.3 ± 11.7), but neither differed ($P \geq 0.12$) from low-RFI cows. High-RFI cows had increased NS (P = 0.016; 4.80 ± 0.54 services) compared with low-RFI cows (3.05 ± 0.33 services), but neither differed ($P \geq 0.14$) from medium-RFI cows. Low-RFI cows had lower DO ($P \leq 0.05$; 83.61 ± 10.4 d) than both medium- (126.0 ± 14.3 d) and high-RFI cows (115.9 ± 10.4 d). Therefore, feed-efficient cows had decreased NS and DO. Overall, results suggested that selection for RFI will not unfavorably impact reproduction in dairy cows.

Key Words: feed efficiency, reproductive performance, residual feed intake

0724 Use of 1,25(OH)2 vitamin D_3 to maintain postpartum blood calcium and improve immune function in dairy cows. A. Vieira Neto*, I. A. Peixoto, F. R. Lopes Jr., R. Zimpel, C. Lopera, L. D. P. Sinedino, K. N. Galvão, C. D. Nelson, and J. E. P. Santos, *University of Florida, Gainesville*.

Objectives were to determine the effects of a slow-release injectable formulation of 1,25-dihydroxyvitamin D_3 (calcitriol) on mineral metabolism and measures of immune function in recently calved Holstein cows. Cows were blocked by parity (2 vs. >2) and calving sequence and, within each block, randomly assigned to subcutaneously receive 300 µg of calcitriol (DHVD; n = 25) or vehicle (CON; n = 25) within 6 h of calving. Blood and urine were sampled before treatment application, 12 h later, and on d 1, 2, 3, 5, 7, 9, 12, and 15 postpartum. Samples were analyzed for total (tCa) and ionized Ca (iCa), magnesium (Mg), phosphorus (P), calcitriol, NEFA, β-hydroxybutyrate (BHBA), glucose, serotonin (5-HT) and crosslaps (CTX-1). Neutrophil function was evaluated in the first week postpartum. Intake of DM and production performance was evaluated for the first 42 d postpartum. Data were analyzed by ANOVA with mixed models using the MIXED procedure of SAS. DHVD increased (P < 0.01) concentrations of calcitriol within 4 h of application from 24 to 420 pg/mL, which returned to baseline within 3 d. Blood iCa and tCa took 12 and 24 h, respectively, to increase after treatment with vitamin D compared with CON. Concentrations of iCa (CON = 1.05 vs. DHVD = 1.18 mM), tCa (CON = 2.11 vs. DHVD = 2.35 mM), and P (CON = 1.51 vs. DHVD = 2.06 mM) remained elevated (P < 0.01) in DHVD until 3, 5, and 7 d postpartum, respectively. Concentration of Mg (CON = 0.76 vs. DHVD = 0.67 mM) was less (P < 0.01) in DHVD cows until 5 d postpartum. DHVD cows excreted more urinary Ca (CON = 0.6 vs. DHVD = 1.7 g/d; P < 0.01) and Mg (CON = 3.6 vs. DHVD = 5.5 g/d; P = 0.02) in the first 5 and 1 d postpartum, respectively. Concentrations of glucose, NEFA, BHBA, 5-HT, and CTX-1 in plasma did not differ between treatments. DHVD improved neutrophil function compared with CON. Relative to a reference cow, the percentage of neutrophils with oxidative burst activity (CON = 80.0 vs. DHVD = 101.0%; P = 0.03), the mean fluorescence intensity (MFI) for oxidative burst (CON = 96.0 vs. DHVD = 105.0%; P = 0.09), and the MFI for phagocytosis (CON = 94.0 vs. DHVD = 110.0%; P = 0.03) were all greater for DHVD than CON cows. Intake of DM and yields of milk and milk components did not differ between treatments. Administration of 300 µg of calcitriol at calving was safe and effective in increasing plasma concentrations of calcitriol, iCa, tCa, and P for the first few days after treatment and improved measures of innate immune function in early lactation Holstein cows.

Key Words: calcitriol, hypocalcemia, transition period

0725 Effect of 2,4-thiazolidinedione treatment in the inflammatory response to induced subclinical mastitis in dairy goats receiving adequate vitamin supplementation. F. Rosa*[1], M. Moridi[2], J. S. Osorio[1], J. Lohakare[1], S. Filley[1], J. L. Belveal[1], J. J. Bruton[1], E. Trevisi[3], C. Estill[1], and M. Bionaz[1], *[1]Department of Animal and Rangeland Sciences, Oregon State University, Corvallis, [2]University of Guilan, Rasht, Iran (Islamic Republic of), [3]Università Cattolica del Sacro Cuore, Piacenza, Italy*.

Mastitis is one of the most costly diseases for the dairy industry. A prior experiment in our laboratory indicated a positive role of 2,4-thiazolidinedione (TZD), a peroxisome proliferator-activated receptor γ (PPARγ) agonist, on the inflammatory response after induced subclinical mastitis in dairy goats fed hay without supplements. Despite this, lack of effect on expression of targets genes in adipose tissue and mammary cells and in vitro data suggested the possibility that TZD did not activate PPARg due to an insufficient activation of its obligate heterodimer nuclear receptor RXR by 9-*cis*-retinoic, a metabolite of vitamin A. This study investigated the hypothesis that continuous activation of PPARγ by TZD in goats supplemented with adequate amount of vitamin A can improve inflammatory response to subclinical mastitis in lactating dairy goats. To test this, 12 Saanen multiparous goats in mid lactation received a diet that met NRC requirements, including vitamin A. Does received a daily intrajugular injection of either TZD (n = 6) or saline (CTRL; n = 6). Following 14 d of treatments, all goats received an intramammary infusion (IMI) of *Streptococcus uberis* to induce subclinical mastitis in the right half with the left half used as control. Metabolic, inflammation, and oxidative-status profiling in blood including 19 parameters was performed. Milk yield and SCC and rectal temperature were assessed. Data were analyzed by GLIMMIX of SAS with treatment (TRT) and time and TRT × time interaction as main effects and goat as random effect. For milk and SCC, mammary half was also included in the main effect (including interactions). Significance was declared at Tukey's corrected $P < 0.05$. Milk yield and SCC were not affected by TZD administration. However, the udder receiving IMI had greater SCC. In blood within 2 d from IMI, ceruloplasmin, haptoglobin, and glucose were increased whereas Zn was decreased. At 3 d after IMI, AST/GOT, gGT, and bilirubin decreased, whereas by 6 to 11 d after IMI, urea, protein, albumin, globulin, NEFA, and creatinine increased. All these data confirmed successful induction of subclinical mastitis. There was a tendency for TZD to have a higher globulin and lower BHBA compared with CTRL and a tendency for a higher increase in haptoglobin after IMI (TRT × time, $P = 0.06$) with a quick recovery, indicating a stronger response of the liver to inflammation. No other parameters measured were affected by TZD treatment. Our findings indicate that addition of TZD has mild effect on inflammatory response in animals receiving adequate amount of vitamin A.

Key Words: immune response, mastitis, 2,4-thiazolidinedione

0726 Effect of increasing milk feeding frequency of an elevated plane of nutrition on glucose and insulin kinetics in male Holstein calves both before and after weaning. J. A. R. MacPherson*[1], J. Haisan[1], S. J. Meale[2], S. I. Pletts[1], and M. Steele[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]UMR Herbivores, INRA, Vetagro Sup, Saint-Genès-Champanelle, France*.

The objective of this study was to investigate how feeding elevated levels of milk replacer before weaning, at different feeding frequencies, could influence glucose and insulin kinetics both before and after weaning. Ten male Holstein calves (42.2 kg ± 1.8 birth weight) were randomly assigned to 2 treatments whereby calves were offered 8 L of milk replacer (150 g/L; 26% CP and 18% CF) per day in two (2x) or four feedings (4x) via an automated feeding system. Calves were gradually stepped down by 1 L/d from wk 7 until weaning on wk 8 (0 L). Postprandial blood samples were collected on wk 4 and 7 via jugular catheters during the 1000-h meal every 30 min up to 240 min after feeding. A glucose tolerance test was conducted on wk 4, 7, and 10 via the jugular catheter the day following the postprandial measurements, with 540 mg glucose/kg $BW^{0.75}$ infused after a 12-h feed restriction. Statistics were determined using SAS PROC MIXED and any data not normally distributed was logarithmically transformed. Postprandial glucose area under the curve over 240 min (AUC_{240}) tended ($P = 0.06$) to differ between treatments overall (2x: 383.51 ± 60.08 mmol/L; 4x: 246.68 ± 64.2 mmol/L) but both treatments were able to adequately control glycemia. Postprandial insulin AUC_{240} differed ($P = 0.01$) by treatment with 2x calves (13,808 ± 3,136 μU/mL) having higher insulin concentrations compared with 4x calves (4,716 ± 3,250 μU/mL), and both treatments demonstrated a decrease in insulin AUC_{240} ($P < 0.01$) with increasing age (wk 4: 14,287 ± 2,818 μU/mL; wk 7: 4,237 ± 2,686 μU/mL), which can most likely be attributed to meal size relative to calf BW. Additionally, there was no effect observed for any of the measurements (time to maximum concentration, maximum concentration, AUC_{240}, basal concentration, or change in concentration) for the glucose tolerance test between treatments or across ages, suggesting that feeding frequency in this study had no effect on insulin sensitivity. These findings suggest that feeding 8 L/d at a frequency of 2x or 4x are both viable feeding methods that do not compromise insulin sensitivity.

Key Words: calf, feeding frequency, insulin sensitivity

0727 Repeatability of residual feed intake across dietary forage concentration. M. J. Carrasquillo-Mangual*, E. Liu, and M. J. VandeHaar, *Michigan State University, East Lansing*.

Residual feed intake (RFI) has received considerable attention as a possible breeding goal in the near future. For RFI to be useful as a breeding goal, it should be repeatable for cows under different types of diets. Our objective for this study was to determine the repeatability of RFI across two levels of dietary forage NDF. Holstein cows in mid lactation were studied in winter (n = 32) and summer (n = 32). The study followed a crossover design with 2 treatment periods of 31 (winter) and 28 d (summer). Cows were milked twice daily and fed treatment diets once daily. Treatments were a high-forage–low-starch diet (HF; 36% NDF and 19% starch) and a low-forage–high-starch diet (LF; 26% NDF and 32% starch). Forage composed 70% of the DM in the HF and 47% in the LF. Dry matter intake and milk yield were recorded daily. Body weight was measured 3x weekly and milk composition was measured for 4 consecutive milkings each week. Body condition score was measured at the beginning and end of each experimental period. Statistical analysis was performed using the GLM procedure (SAS 9.4). An RFI value was obtained for each cow under each treatment; cows were ranked using SD of the RFI value as HRFI (greater than +0.5 SD), MRFI (±0.5 SD) or LRFI (less than −0.5 SD). A group rank was established for all cows under each treatment diet. The HF decreased DMI by 2.5 kg/d and milk yield by 3 kg/d when compared with the LF. Body weight changed by 0.4 kg/d on the LF but 0.2 kg/d on the HF. Fat yield, BW, and BCS were not altered by treatments. The decrease in DMI as well as the difference in energetic density of the diet could explain the differences observed in production performance as there was no significant difference in energy partitioned toward milk production. The RFI ranking was relatively repeatable (r = 0.44). Of all animals, 48% maintained their group ranking across treatments whereas 47% changed ranking by 1 group. Only 5% moved in the ranking from the HRFI to the LRFI group or vice versa. In conclusion, although intake, production, and energy partitioning were significantly altered by dietary treatments, RFI was relatively repeatable across these diets. Therefore, genomic breeding values of RFI estimated from cows fed a high-starch diet should still be useful when animals are fed more forage and less starch.

Key Words: dairy cow, residual feed intake

ADSA PRODUCTION DIVISION GRADUATE STUDENT ORAL COMPETITION: PHD

0728 Effects of supplementing rumen-protected methionine on lactational performance of Holstein dairy cows during early and mid lactation. M. A. Fagundes*[1], S. A. Blaser[2], S. Y. Yang[2], J. S. Eun[1,2], and J. O. Moon[3], *[1]School of Veterinary Medicine, Utah State University, Logan, [2]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [3]CJ CheilJedang Research Institute of Biotechnology, Suwon, the Republic of Korea*.

Supplementing rumen-protected methionine (RPMet) has been shown to maintain milk and milk protein yields when dietary MP is decreased by 5% due to its direct impacts on milk protein synthesis in the mammary gland. The present study investigated production responses of lactating dairy cows to RPMet supplementation in suboptimal protein (SOPD; 15.5% CP) and normal protein diet (NPD; 16.5% CP). Eight lactating dairy cows (53 d in milk, on average) were blocked by parity and days in milk, and the experiment was performed in a duplicate 4 × 4 Latin square design. Within each square, cows were randomly assigned to a sequence of 4 diets during each of the four 21-d periods (14 d of treatment adaptation and 7 d of data collection and sampling). A 2 × 2 factorial arrangement was used; SOPD or NPD was combined without or with RPMet: SOPD without RPMet, SOPD with RPMet (S+Met), NPD without RPMet, and NPD with RPMet (N+Met). An experimental RPMet product from CJ CheilJedang (Suwon, the Republic of Korea) was supplemented in the S+Met and the N+Met at 30 g/cow per day. Supplementation of RPMet did not affect DMI (25.4 kg/d) and milk yield (40.6 kg/d). Supplementing RPMet resulted in a similar milk true protein concentration (2.80%) with a numerical increase in milk protein yield at 3.6%. In contrast, supplementing RPMet increased milk fat concentration (P = 0.02) and yield (P = 0.03) and 3.5% fat-corrected milk (FCM) yield (P = 0.05) and tended to increase energy-corrected milk (ECM) yield (P = 0.06) regardless of CP level. In addition, trends were observed for increased 3.5% FCM yield/DMI (P = 0.09) and ECM yield/DMI (P = 0.10), and the positive effects were greater under NPD than SOPD, resulting in trends toward interaction between CP and RPMet (P = 0.06). Overall results in the current study suggest that supplementing RPMet in SOPD and NPD improved milk fat concentration, possibly due to increases in apolipoprotein and phospholipid syntheses in the liver, leading to an increase in fatty acid supply to the mammary gland via very-low-density lipoproteins.

Key Words: feed efficiency, lactational performance, rumen-protected methionine

0729 Effect of dextrose and purified starch at two levels of rumen degradable protein on lactation performance and enteric methane emission in dairy cows. F. Sun*, M. J. Aguerre, and M. A. Wattiaux, *University of Wisconsin-Madison, Madison*.

The objective of this study was to evaluate the effect of source of nonfiber carbohydrate (NFC) at two levels of rumen degradable protein (RDP) in the diet on lactation performance and enteric methane (CH_4) emission. In addition, hourly CH_4 emission rate relative to time of feeding was studied. Eighteen Holstein cows (mean ± SD; 148 ± 10 d in milk and 644 ± 41 kg BW) housed in a tie-stall barn were used in a split plot study. Cows were randomly assigned to either (DM basis) 11 (11-RDP) or 9% RDP (9-RDP) diets as whole plot. To lower diet RDP, soybean meal was partially replaced with expeller soybean meal and blood meal. Subplot treatments, which were allocated in three 3 × 3 Latin squares (28-d period) were (DM basis) 10% dextrose (DX), 5% dextrose and 5% purified starch (DX-ST), and 10% purified starch (ST). Cows were fed a total mixed ration with 61% forage and 39% concentrate, with approximately 16.5% CP and 45.5% NFC, once daily and milked twice daily. During wk 3 of each period, enteric CH_4 emission was measured at 1, 2.5, 4, 5.5, 10, 11.5, 13, 14.5, 16, 17.5, and 22.5 h after feeding, over a 4-d interval with GreenFeed (C-lock Inc., SD). The SAS mixed procedure with Tukey option was used to analyze the data. There was no NFC × RDP interaction ($P > 0.05$), and therefore, main effects are presented in table below. Cows fed 9-RDP had greater yield of fat–protein corrected milk (FPCM), milk (37.4 vs. 34.8 kg/d), milk fat (1.57 vs. 1.44 kg/d), and lactose (1.80 vs. 1.63 kg/d) compared with cows fed 11-RDP. Cows fed ST had lower DMI, greater feed efficiency (FPCM/DMI), and lower enteric CH_4 emission than cows fed DX and DX-ST. The hourly CH_4 emission rate was lower for the 22.5-h sampling time compared with all others (15.9 ± 2.8 vs. 20.1 ± 4.9 g/h). Dietary treatments did not influence CH_4/DMI (20.0 ± 3.5 g/kg) or CH_4/FPCM (13.1 ± 2.6 g/kg). In conclusion, the level of RDP did not influence the responses to the source of NFC in the diet. Compared with dextrose as a source of NFC, starch reduced DMI, increased feed efficiency, and reduced daily CH_4 emission.

Key Words: feed efficiency, greenhouse gas, nonfiber carbohydrate

0730 Influence of mixed cropping of corn and soybean with different seeding rates on forage yield, quality, and nutrient yield grown under organic condition. I. P. Acharya*[1], X. Gu[2], and D. P. Casper[1], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Deparment of Plant Science, South Dakota State University, Brookings*.

A field plot study was laid out using a randomized complete block design with three replicates to evaluate two organic corn hybrids (MC 5300 [N] and MasterGraze [MG]) with two soybeans (Viking 2265 [R] and Vining [V]) at four seeding rates (R1 = 65:35, R2 = 55:45, R3 = 45:55, and R4 = 35:65 of corn:soybean) in terms of forage yield, nutrient yields, and quality. Forage was hand harvested 101 (MG corn with both soybeans) and 116 d (N corn with both soybeans) after planting during 2015 season, inoculated, packed into buckets, weighed, and ensiled for 90 d. Buckets were then reweighed and opened and forage samples were collected and analyzed for nutrient composition. The main effect of corn for DM yield (DMY) was greater ($P < 0.05$) for N compared with MG (27.73 and 19.90 T/ha for N and MG, respectively), whereas the main effect of soybean for DMY was similar ($P > 0.05$; 23.77 and 23.86 T/ha for R and V, respectively). Main effect of seeding rate on DMY was higher ($P < 0.05$) for R1 and R2 compared with R3 and R4 (25.38, 24.48, 21.81, and 23.59 T/ha for R1, R2, R3, and R4, respectively). Yields of digestible DM (DDM; 19.55 and 13.67 T/ha) and CP (2.40 and 2.12 T/ha) were greater ($P < 0.05$) for N corn compared with MG corn, similar ($P > 0.05$) for both soybean (DDM: 16.65 and 16.57 T/ha and CP: 2.33 and 2.19 T/ha for R and V, respectively) and higher ($P < 0.05$) DDM for R1 and R2 compared with R3 and R4 (17.70, 17.08,15.13, and 16.54 T/ha for R1, R2, R3, and R4, respectively). Yield of starch (7.78 and 2.45 T/ha for N and MG) and 30-h NDF digestibility (NDFD30; 44.47 and 52.49% for N and MG) for main effect of corn were different ($P < 0.05$), whereas they were similar ($P > 0.05$) for the main effect of soybean (starch yield: 5.25 and 4.98 T/ha and NDFD30: 48.58 and 48.38% for R and V, respectively). The combination of N corn with either R or V soybean at the ratio of R1 or R2 resulted in the greatest yield of DM, DDM, and starch. A forage blend produced through mixed cropping of corn and soybeans holds a great potential for increasing the forage and nutrient yields to meet the nutrient requirements of lactating dairy cows.

Key Words: corn, forage, soybean

0731 Association between circulating progesterone during the luteal phase and estrous activity detected by automated activity monitoring in dairy cattle. J. Denis-Robichaud*[1], S. J. LeBlanc[1], A. Jones-Bitton[1], and R. L. A. Cerri[2], *[1]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [2]Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada*.

The objective of this study was to evaluate the association between circulating progesterone (P4) concentration during the luteal phase (LP) and estrous activity detected by automated activity monitoring. The hypothesis was that a shortened LP would decrease the intensity of estrus expression. A total of 48 cows at the UBC Dairy Center were assigned to one of two treatments: a short (n = 23) or a normal P4 (n = 25) LP. The short LP was achieved by injecting 25 mg of prostaglandin F2α at d 7 of the cycle; normal LP cows were not treated. Ultrasound of the reproductive tract was performed at Day 0, 2, 5, 7, 9, and 11 of the cycle and then daily until ovulation to identify and measure the dominant follicle. Blood samples were taken on the same days to measure serum P4. Cows were equipped with two activity monitoring devices: Heatime HR System (SCR, Israel) and SmartDairy (BouMatic, United States). The peak activity score (Heatime), peak of relative activity (%; SmartDairy) and duration of the estrus (both systems) following the LP were recorded. Linear regression models were used to calculate marginal means (least squares means ± SEM). As expected, P4 at d 14 of the cycle differed between the short and normal LP (2.9 ± 0.4 vs. 7.6 ± 0.4 ng/mL, respectively; $P < 0.01$). The number of estrus events detected was not different between treatment groups for Heatime (short: n = 15; normal: n = 20; P = 0.25) or for SmartDairy (short: n = 15; normal: n = 16; P = 0.93). Using the Heatime system, the peak activity score differed between the short and normal LP groups (73.3 ± 4.0 vs. 84.3 ± 3.5; P = 0.05) and the duration of estrus tended to differ (10.8 ± 1.0 vs. 13.1 ± 0.9 h; P = 0.09). Using the SmartDairy system, neither the peak activity (434 ± 39 vs. 465 ± 38%; P = 0.57) nor the duration of estrus (8.0 ± 1.2 vs. 10.0 ± 1.2 h; P = 0.25) differed. There was no difference in serum P4 concentration (0.89 ± 0.14 vs. 0.95 ± 0.13 ng/mL; P = 0.75) or in ovulatory follicle size (18.7 ± 1.4 vs. 18.1 ± 1.4 mm; P = 0.78) on the day of estrus. The number of cows that ovulated was not different between short and normal LP groups (short: n = 14; normal: n = 18; P = 0.41). The shortened LP moderately reduced the intensity of estrus expression but did not affect ovulatory follicle size or ovulation. Decreased LP duration or peak circulating concentration of P4 may reduce the intensity of estrus-related activity.

Key Words: automated activity monitoring system, estrus detection, luteal phase

0732 Effect of prepartum physical activity on behavior and immune competence of dairy cows. R. A. Black*, G. M. Pighetti, and P. D. Krawczel, *University of Tennessee, Knoxville*.

The objective was to determine the effect of prepartum exercise, pasture turnout, or total confinement on activity and immune competence of dairy cows. Sixty pregnant, nonlactating cows were assigned to control (19 Holstein and 1 Jersey × Holstein), exercise (19 Holstein and 1 Jersey × Holstein), or pasture (20 Holstein) treatments using rolling enrollment from Jan. to Nov. 2015 at dry-off. Cows were balanced by parity (1.8 ± 0.9), projected ME fat-corrected milk yield (13,831 ± 2,028 kg/lactation), and projected due date. Cows were housed in a naturally ventilated, 4-row deep-bedded sand freestall barn at the University of Tennessee's Research Unit (Walland, TN). Cows were moved to a maternity pen with a rubber mattress to calve. Fitted 3 d before dry-off, accelerometers determined lying time (h/d), lying bouts (number/d), lying bout duration (min/bout), and steps (number/d) at 1-min intervals. Data were averaged by four periods relative to actual calving date: −58 to −15 d (FO), −14 to −1 d (CU), d 0 (CA), and 1 to 14 d (PP). Exercise was done on five consecutive days per week for 1.4 ± 0.1 h/d (targeted 1.5 h/d), at a pace of 1.88 ± 0.58 km/h. Pasture turnout occurred on a grassy paddock five consecutive days per week for 1.8 ± 0.3 h/d (targeted 1.5 h/d). Control cows remained in the home pen throughout the dry period. Blood was sampled on d −3 and 42, relative to dry-off, to assess immune competence via ROS generation using PMA. A mixed model determined the effects of treatment, period, and treatment × period on daily lying behavior and steps and the effect of treatment, day, PMA level, and their interactions on ROS generation. Cow within treatment was the random variable. Exercise cows lay down less frequently at CA (11.6 ± 1.0 bouts/d) compared with control cows (14.6 ± 0.9 bouts/d; P = 0.03). However, lying bout duration and lying time did not differ among treatments at CA ($P > 0.31$). Exercise cows were more active at FO, CU, and CA (2,895.4 ± 107.6, 2,614 ± 125.2, and 2,824.6 ± 224.4 steps/d, respectively) than control (1,788.8 ± 103.9, 1,840.8 ± 120.7, and 1,969.3 ± 216.2 steps/d) and pasture (2,132.0 ± 103.6, 1,951.6 ± 120.9, and 2.234.9 ± 216.3 steps/d; $P < 0.01$). ROS production was not affected (P = 0.63). Exercised cows took more steps but had fewer lying bouts around calving, suggesting more comfort during calving. Furthermore, physical activity did not alter immune competence. Prepartum exercise may be a viable management strategy to improve calving performance.

Key Words: dairy cow, immune competence, physical activity

0733 Associations between preventive hoof trimming, activity, and resting behaviors. G. Stoddard*[1] and G. Cramer[2], *[1]University of Minnesota Twin-Cities, Saint Paul, [2]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, St. Paul*.

Hoof trimming is a commonly recommend practice to prevent lameness, one of the dairy industry's biggest animal well-being and economic issues. Unfortunately, limited scientific data exists to support our current hoof trimming (HT) practices and what affects HT has on cow behavior. The objective of this research is to determine the association between HT of non-lame cows and activity and resting behaviors. A convenience sample of farms from the United Kingdom and Canada were recruited to participate. Selection criteria required that farms used free-stall housing, have a regular hoof trimming schedule, and use either Afi PedoPlus or AfiACT2 (Afimilk, Ltd.) pedometers. Activity, milk yield, resting time, and resting bout information was collected daily at the time of milking. Hoof trimming data was collected from on farm records. The association between activity, resting behaviors, and HT was evaluated by comparing the averages of the behavior parameter at different time points before and after HT. Time periods evaluated included 1 to 10 d before HT; day of HT; and 2 to 3, 4 to 7, and 8 to 10 d after HT. Models were created using linear regression with behavior as the outcome variable and including the fixed effects of farm, lactation number, milk yield, and days in milk. Time period was forced into each model and a robust SE was used to account for repeated measures. A total of 1,393 cows were used in the analysis with average days in milk, lactation, and milk yield being 182, 1.9, and 33.6 kg/d, respectively. Activity and resting bouts were associated with every time period except for on the day after HT. Resting time was positively associated with all time periods after HT. Resting time increased from 21 to 27 min/d between 1 and 10 d after HT. Activity between 2 and 10 d after HT decreased by a minimum of 20 steps/h and reached a maximum decrease of 27 steps/h. Resting bouts increased from 0.2 to 0.4 bouts between 2 and 10 d after HT. These results show that the HT process is associated with changes in activity, resting time, and resting bouts of the cow during the 10 d following HT. This indicates that there is an adjustment phase either due to the actual HT or due to the disruption of the cow's daily routine during the HT process.

Key Words: activity, hoof trimming, rest

0734 Enhanced preweaning nutrition increases mammary gland development without negatively affecting tissue composition in Holstein heifer calves. A. J. Geiger*[1], R. M. Akers[1], and C. L. M. Parsons[2], *[1]Virginia Tech, Blacksburg, [2]Virginia Polytechnic Institute and State University, Blacksburg*.

We have reported that enhanced feeding of prepubertal Holstein heifer calves increased mass of mammary parenchyma (PAR; 7.9x) and mammary fat pad (MFP; 5.3x). Our objective was to measure fat, protein, and DNA content of PAR and MFP in restricted- and enhanced-fed calves with or without estrogen. For 8 wk, 36 Holstein heifer calves received 1) a control milk replacer (MR) fed at 454 g powder/d (R; 20% CP and 20% fat) or 2) an enhanced MR fed at 1,135 g powder/d (E; 28% CP and 25% fat). At weaning a subset of calves were sacrificed (n = 6/diet). Remaining calves received E_2 implants and were sacrificed at wk 10. Treatments were 1) R, 2) R + E_2 (R-E2), 3) E, and 4) E + E_2 (E-E2). At sacrifice, udder haves were removed and snap frozen. Dissected MFP and PAR were analyzed for fat, protein, and DNA (Daniels et al., 2009). At weaning, E-fed calves had greater MFP protein (2.11 vs. 0.46 g; $P < 0.01$), DNA (22.1 vs. 4.5 mg; $P < 0.01$) and fat (116 vs. 3.3 g; $P < 0.01$). R-fed calves had increased MFP protein concentration (15.6 vs. 12.2 mg/g; $P < 0.01$), but MFP DNA concentration was not different. E-fed calves had increased PAR total protein (1.36 vs. 0.20 mg; $P < 0.01$) and DNA (20.4 vs. 2.7 mg; $P < 0.01$). After estrogen administration, E-E2 calves had more MFP total protein ($P < 0.01$) and fat ($P < 0.01$) and greater fat concentration ($P < 0.01$) than all other treatments. Calves fed E-E2 had greater MFP total DNA than R and R-E2 calves ($P < 0.01$) but not E-fed calves. In addition, E-E2 calves had greater PAR total protein ($P < 0.01$) and DNA ($P < 0.01$) compared with all other treatments. Even further, E-E2 calves had increased total PAR fat compared with R-E2 calves ($P < 0.02$) and R-fed calves had decreased PAR fat content compared with all other treatments ($P < 0.01$). Results reinforce that composition of MFP is nutrient responsive. Moreover, data indicate that the impact of an enhanced diet on PAR tissue composition is likely positive, but more research is needed to determine if observed results would correlate to altered future milk yield.

Key Words: mammary gland, milk replacer, parenchyma

0735 Effects of fuels derived from starch digestion on feeding behavior of cows in the postpartum period. L. B. Gualdron-Duarte* and M. S. Allen, *Michigan State University, East Lansing*.

Absorbed fuels from the digestion of starch include propionic acid (P) produced by ruminal fermentation and glucose (G) from intestinal digestion that is partially metabolized to lactic

acid (L). Our objective was to evaluate effects of these fuels on DMI and feeding behavior of cows in the postpartum period. We hypothesized that effects of these fuels on DMI and ME intake (MEI) are consistent with their ability to stimulate hepatic oxidation. Little or no G is extracted from blood by the liver. Although both L and P are anapleurotic and can stimulate oxidation of acetyl CoA, hepatic extraction of P is greater than L, which depends on cytosolic redox state. Continuous isoenergetic (150 kcal/h) infusions of P, L, or G were abomasally administered to eight rumen-cannulated multiparous Holstein cows (12.4 ± 6.2 DIM) in a duplicate 4 × 4 Latin square design experiment balanced for carryover effects. Treatment sequences were randomly assigned to cows. Treatments were control (C; no infusion) and P (99.5%; 0.41 mol/h), L (88.0%; 0.46 mol/h), and G (99.9%; 0.22 mol/h) infused at 500 mL/h for 22 h/d and providing 3.3 Mcal/d. Feeding behavior was recorded by a computerized data acquisition system. Gross energy digestibility of the diet was determined for each cow and used to calculate MEI from the diet. Total MEI was calculated as the sum of MEI from the diet plus energy from infusions. Data were analyzed by ANOVA; the model included random effects of block, cow within block, and period within block and fixed effects of treatment. Treatments were compared with C by preplanned contrasts. Propionic acid decreased DMI by 24.3% (14.3 vs. 18.9 kg/d; $P < 0.001$) and MEI 13.4% (34.8 vs. 40.2 Mcal/d; $P < 0.04$) compared with C by tending to decrease meal frequency ($P = 0.087$). Lactic acid decreased DMI by 13.8% (16.3 vs. 18.9 kg/d; $P < 0.05$) compared with C by decreasing meal size 19.8% ($P < 0.05$) but did not affect MEI. Glucose infusion did not affect DMI or MEI. Treatment effects on DMI and MEI were consistent with their expected effects on hepatic oxidation. Propionic acid production from highly fermentable diets might reduce energy intake of cows in the PP period.

Key Words: anapleurosis, fresh cows, hepatic oxidation

0736 Fetuin-A: A novel biomarker for lipolysis-induced metabolic stress in transition dairy cows.

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Periparturient cows that experience severe adipose tissue lipolysis are at a higher risk for inflammatory and metabolic diseases. Fetuin-A (FetA) is a glycoprotein that inhibits insulin signaling and enhances inflammatory responses in adipose tissues, which are known to exacerbate lipolytic responses in humans and rodents. However, little is known about its role during lipolysis and its use as a biomarker for metabolic stress and lactation performance in dairy cows. Our objective was to determine the dynamics of serum and adipose FetA concentrations and its association with metabolic markers during negative energy balance (NEB)–induced lipolysis at different stages of lactation. In Experiment 1, 26 multiparous cows were followed through the transition period. Blood samples and subcutaneous adipose tissue were collected at dry-off (DO; −51 ± 3 d), close-up (CU; −14 ± 2 d), and early lactation (EL; 7 ± 0.5 d). In Experiment 2, FetA response to lipolysis was evaluated independently of parturition-associated metabolic challenges using midlactation cows (119–210 DIM) assigned to one of two feeding protocols: ad libitum (AL; $n = 3$; +EB = 3.2 ± 0.66 Mcal/d) or feed restricted (FR; $n = 3$; EB = −13.3 ± 0.5 Mcal/d). Blood and subcutaneous adipose tissue were collected after a 4-d period of feed restriction. FetA was determined by ELISA and western blot. Data were analyzed using a repeated measures mixed model. Serum and adipose FetA concentrations were affected by lactation stage. In Experiment 1, serum FetA concentrations were lower at EL (DO: 1.31 ± 0.06 mg/mL; CU: 1.27 ± 0.09 mg/mL; and EL: 1.14 ± 0.06 mg/mL; $P < 0.05$) when NEFA concentration was greatest (DO: 0.34 ± 0.02 mEq/L; CU: 0.63 ± 0.2 mEq/L; and EL: 1.19 ± 0.14 mEq/L; $P < 0.05$). Unlike in serum, adipose FetA expression decreased at CU (relative band density; DO: 1.5 ± 0.4; CU: 0.2 ± 0.02; EL: and 1.6 ± 0.6; $P < 0.05$). Circulating FetA concentration was higher in overconditioned dry cows (BCS ≥ 3.75; $P < 0.05$) and was positively associated with BCS ($R^2 = 0.24$, $P < 0.0001$) and BCS loss ($R^2 = 0.43$, $P = 0.0005$) during the transition period. Cows with high BCS and increased serum FetA concentrations at DO had lower serum glucose concentrations at EL ($P < 0.05$). In Experiment 2, despite the feed restriction-induced lipolysis (NEFA; FR = 0.47 ± 0.05 mEq/L and AL = 0.09 ± 0.08 mEq/L), neither serum nor adipose FetA concentrations were affected in midlactation cows ($P > 0.05$). These results demonstrate that serum and adipose FetA concentrations during lipolytic states are determined by lactation stage and BCS around parturition. Fetuin-A is a potential novel biomarker for metabolic stress induced by lipolysis during the transition period. Future work will determine the mechanisms by which FetA affects lipolytic and inflammatory responses in adipose tissues of transition dairy cows.

Key Words: adipose, biomarker, lipolysis

0737 The effect of trace mineral source and fiber source on total-tract nutrient digestion.

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Excess rumen soluble Cu and Zn can reduce fiber digestion and alter rumen microbial populations. Substitution of forage with nonforage fiber sources (NFFS) can be economically beneficial, but the reduction in particle size can decrease rumen pH, increase fiber passage rates, and decrease fiber digestion. Eighteen multiparous cows were used in a split-plot replicated Latin square with two 28-d periods to evaluate the effects of Cu, Zn, and Mn source (sulfates or hydroxy;

Micronutrients Inc., Indianapolis, IN) and dietary NDF source (forage diet = 26% NDF vs. NFFS = 36%) on total-tract nutrient digestibility. We hypothesized that hydroxy trace minerals, which are soluble at a lower pH compared with sulfates, would increase digestibility regardless of fiber source. During the entire experiment (56 d), cows remained on the same fiber treatment but the source of supplemental trace mineral was different for each 28-d period so all cows were exposed to both mineral treatments. During each of the two 28-d periods, cows were fed no supplemental Cu, Zn, or Mn for 16 d followed by 12 d of feeding supplemental Cu, Zn, and Mn from either sulfates or hydroxy sources. Basal Cu, Zn, and Mn concentrations for the forage diet were 9, 30, and 38 mg/kg, respectively, whereas basal concentrations were 11, 50, and 47 mg/kg, respectively, for the NFFS diet. Supplemental concentrations of Cu, Zn, and Mn fed were approximately 9, 30, and 30 mg/kg, respectively. No mineral source × fiber interactions were observed for production measures or digestibility. Treatment had no effect ($P \geq 0.38$) on DMI (24.2 kg) or milk production (34.9 kg). Mineral source had no effect on macronutrient intakes ($P \geq 0.63$), but feeding hydroxy Cu, Zn, and Mn increased NDF digestibility (48.5 vs. 46.4%). Cows fed NFFS had decreased DM digestibility (65.9 vs. 70.2%), OM digestibility (67.4 vs. 71.7%), CP digestibility (58.8 vs. 62.1%), and starch intake (4.3 vs. 8.8 kg) and increased starch digestibility (97.5 vs. 96.3%), NDF intake (8.6 vs. 6.0 kg), and NDF digestibility (50.5 vs. 44.4%) compared with cows fed the forage treatment. Digestible OM (DOM) was reduced (62.0 vs. 66.8%) for cows fed NFFS compared with those fed forage, indicating a reduced concentration of DE. Mineral source did not affect DOM ($P = 0.32$). Replacing dietary forage with NFFS reduced dietary energy and although hydroxy minerals increased NDF digestibility, the effect was not great enough to influence DOM.

Key Words: fiber, total-tract nutrient digestion, trace minerals

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0738 Economic value of cooling dry cows across the United States. F. C. Ferreira*[1,2], A. De Vries[2], G. E. Dahl[2], and R. Gennari[2], [1]*Embrapa Gado de Leite, Juiz de Fora, Brazil,* [2]*Department of Animal Sciences, University of Florida, Gainesville*.

Heat stress during the dry period reduces milk yield in the next lactation. Our objectives were to quantify the economic losses due to heat stress of dry cows and to evaluate investment in cooling of dry cows. We used weather data from The National Oceanic and Atmospheric Administration to quantify the average amount of heat stress for the 48 contiguous U.S. states. A heat stress day was declared when the average daily temperature–humidity index was ≥68. A spreadsheet was developed for economic analyses. Assumptions were that 15% of the cows were dry at any time, the dry period length was 46 d, and only cows in parities ≥2 increased milk yield if cooled in the dry period. Milk yield decreased by 0.11 kg/d in the next lactation (305 d) per heat stress day in the dry period based on a review of the literature. Marginal decrease in DMI was 0.4 kg per 1 kg less milk. Marginal value of milk minus feed cost was $0.33/kg. Economic analysis included investment in fans and soakers and use of water and electricity. Building investment was considered separately at a price of $2,500 per stall. On average, a U.S. dairy cow is under heat stress 96 d during the year and loses 271 kg of milk in the subsequent lactation if not cooled when dry. Weighted by the number of cows in each state, annual losses would be $820 million if dry cows were not cooled ($89/cow per year). For the top 3 milk-producing states (California, Wisconsin, and New York) and Florida, the average milk loss in the next lactation was 316, 212, 234, and 726 kg and profit loss/cow per year were $104, $70, $77, and $238, respectively. The average benefit:cost ratio of cooling dry cows in the United States is 2.46 (dry cow building already present) and 1.59 (including building a dry cow barn) in the baseline scenario. For positive net present values, 18 and 27 d are necessary when a building is not built (considering marginal milk prices of $0.33 and $0.22, respectively). If a barn is built, minimum days of heat stress would be 47 and 69, respectively. Other benefits of dry cow cooling, such as increased health and more productive offspring, were not considered. In conclusion, cooling of dry cows was profitable in all 48 states and very profitable in most states.

Key Words: dry cows, economics, heat stress, temperature–humidity index

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0739 Palmitic acid feeding increases hepatic ceramide accumulation and modulates expression of genes responsible for ceramide synthesis in midlactation dairy cows. J. E. Rico*, A. T. Mathews, and J. W. McFadden, *West Virginia University, Morgantown*.

Circulating sphingolipid ceramides are associated with elevated NEFA availability and reduced insulin sensitivity in dairy cows transitioning from gestation to lactation. In monogastrics, palmitic acid (C16:0) can increase hepatic synthesis and lipoprotein secretion of ceramides, lipid mediators that inhibit insulin action in skeletal muscle. Increasing ceramide synthesis by feeding C16:0 may be a means to restore insulin resistance and enhance milk yield during midlactation. Therefore, our objective was to determine whether dietary C16:0 can augment liver and skeletal muscle ceramide concentrations in midlactation dairy cows. Twenty multiparous Holstein cows were enrolled in a study consisting of a 5-d covariate and a 49-d treatment period. Cows were randomly assigned to a sorghum silage–based diet containing no supplemental fat (control; $n = 10$; 138 ± 45 DIM) or C16:0 at 4% of ration DM (PALM; 98% C16:0; $n = 10$; 136 ± 44 DIM). Blood was routinely collected, and liver and skeletal muscle tissue was biopsied at d 47 of treatment. Intravenous glucose

tolerance tests (GTT) were performed at d −1, 21, and 49 relative to start of treatment. Tissue concentrations of sphingolipids were determined using liquid chromatography tandem mass spectrometry. Expression of ceramide synthesis genes was evaluated using real-time PCR. Data were analyzed under the generalized linear model. Pearson correlations were analyzed. The most abundant liver and muscle sphingolipids detected were C24:0-ceramide, C24:0-monohexosylceramide (GlcCer), and C16:0-lactosylceramide (LacCer). Relative to control, PALM increased C24:0-ceramide and total hepatic ceramide levels by 29 and 20%, respectively, at wk 7 ($P < 0.05$); a response not observed in muscle. Similarly, PALM increased hepatic C22:0-, C22:1-, C24:1-, and C26:0-ceramide at wk 7. PALM increased C16:1- and C24:1-GlcCer in liver ($P < 0.05$). Plasma total ceramide and C24:0-ceramide were positively associated with hepatic total ceramide and C24:0-ceramide ($r = 0.63$ and $r = 0.58$, respectively, $P < 0.05$). Hepatic total ceramide and C24:0-ceramide were positively associated with plasma NEFA ($r = 0.63$ and $r = 0.57$, respectively, $P < 0.001$) and negatively associated with NEFA disappearance during GTT ($r = -0.57$ and $r = -0.65$, respectively, $P < 0.001$). Ceramide synthase-6 (CerS6) was the predominant hepatic CerS isoform followed by CerS2 and CerS5. Surprisingly, PALM decreased CerS2 and CerS5 mRNA and sphingomyelinase mRNA by 35, 36, and 62%, respectively ($P < 0.05$). We conclude that feeding midlactation dairy cows C16:0 can increase hepatic ceramide accumulation and generate hepatic ceramide profiles that are similar to circulating ceramide. Our work also demonstrates a possible relationship between hepatic ceramide supply and adipose tissue insulin sensitivity.

Key Words: ceramide, insulin resistance, lactation

0740 Assessment of performance, oxidative stress status, and plasma amino acid profiles in peripartal dairy cows supplemented with rumen-protected methionine or choline and with different liver functionality indices. Z. Zhou*[1], M. Vailati Riboni[1], E. Trevisi[2], D. N. Luchini[3], and J. J. Loor[1], *[1]University of Illinois, Urbana, IL, [2]UniversitaÂ Cattolica del Sacro Cuore, Piacenza, Italy, [3]Adisseo S.A.S., Alpharetta, GA*.

Objectives were to evaluate performance, oxidative stress status, and plasma AA profiles of peripartal dairy cows with different liver functionality indices (LFI). Forty multiparous Holstein cows were randomly assigned to control (CON), no methionine (MET) or choline (CHO), CON+MET, CON+CHO, and CON+MET+CHO treatments. Cows received the same diet (1.52 Mcal/kg DM) from −21 d (close-up) to calving. Cows were on the same diet (1.71 Mcal/kg DM) after calving and continued to receive the same treatments through 30 d. Blood samples were taken at −30, −10, 4, 14, and 28 d relative to calving. Liver samples were harvested at −10, 7, 20, and 30 d relative to calving. Methionine supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow per day. Main effect of LFI was analyzed using PROC MIXED in SAS. The LFI is an index assessing transition cow metabolic health by measuring changes in plasma albumin, cholesterol, and bilirubin. A high LFI (better liver function) is characterized by lower bilirubin and higher cholesterol and albumin, and the opposite is true for low LFI. Cows were ranked retrospectively and assigned to low (L; LFI < 0), medium-low (ML; 0 < LFI < 1.5), medium-high (MH; 1.5 < LFI < 3), and high (H; LFI > 3) groups according to LFI regardless of MET or CHO supplementation. Most (13/20) of the MET cows fell into the MH and H groups, whereas CHO cows were evenly distributed across the 4 LFI groups. Close-up and lactation DMI, milk yield, and protein yield increased ($P < 0.01$) with higher LFI. Compared with L and ML, cows in MH tended ($P = 0.08$) to have greater total and reduced hepatic glutathione concentration. Similarly, compared with L, plasma paraoxonase was greater ($P = 0.04$) in MH and H, suggesting better oxidative stress status in cows with higher LFI. A main effect of LFI was detected for essential AA ($P < 0.01$) and branched-chain AA ($P = 0.04$) concentration due to increased ($P < 0.05$) concentration of methionine, lysine, histidine, arginine, tryptophan, valine, leucine, and isoleucine with higher LFI. Concentrations of serine, asparagine, proline, alanine, tyrosine, citrulline, and ornithine also increased ($P < 0.05$) with higher LFI and contributed to greater ($P < 0.05$) total AA concentration. Overall, results indicate that cows with higher LFI had improved production performance, a reduction in oxidative stress, and a better plasma AA profile.

Key Words: amino acid, liver functionality index, transition cow

ADSA PRODUCTION DIVISION GRADUATE STUDENT POSTER COMPETITION: MS

0741 Effect of intrammamary infusion of chitosan hydrogels on bovine mammary gland involution after drying-off. S. Lanctot*[1], X. Zhao[1], P. Fustier[2], A. Taherian[2], B. Bisakowski[2], and P. Lacasse[3], *[1]Department of Animal Science, McGill University, Montreal, QC, Canada, [2]Food Research and Development Centre, St-Hyacinthe, QC, Canada, [3]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada*.

The transition from lactation to the dry period in dairy cows is a period of high risk for acquiring new intramammary infections. This risk is reduced when the involution of the mammary gland is completed. Accordingly, approaches that accelerate the involution process after drying-off could reduce

the incidence of mastitis. The current study aimed to develop a biological response modifier that could be injected into cow teats to promote immune cell migration and speed up involution. Chitosan is natural polysaccharide derived from chitin, which is able to trigger host innate immunity. We have developed two formulations, using crab or shrimp chitosan, which are liquid at room temperature but form a hydrogel at the body temperature. Each quarter of 7 Holstein cows in late lactation was randomly assigned at drying-off to an intramammary infusion of 2.5 or 5 mL of crab chitosan hydrogel (crab2.5 or crab5), 5 mL of shrimp chitosan (shp5), or 5 mL of saline (control). Milk (mammary secretion) samples of each quarter were collected on d −4, 0 (dry-off), 1, 3, 5, 7, and 10. Milk somatic cell counts (SCC) and concentrations of involution marker such as bovine serum albumin (BSA), lactate dehydrogenase (LDH), and lactoferrin gradually increased ($P < 0.01$) during the first 10 d following the last milking whereas the citrate concentration decreased ($P < 0.01$). Intramammary infusion of chitosan hydrogel (crab5, crab2.5, and shp5) hastened the increase in SCC, BSA, and LDH ($P < 0.01$). The SCC and BSA concentrations for chitosan-treated quarters were greater ($P < 0.01$) than those of milk from control quarters on Days 1, 3, and 5. The LDH concentration was greater ($P < 0.01$) in milk from chitosan-treated quarters than in that of control quarters on Days 1, 3, 5, and 7. Similarly, chitosan induced a faster rise in lactoferrin concentration, which was greater ($P < 0.01$) than that of the control quarters on Days 3 and 5. Milk citrate concentration was unaffected by treatments but the citrate:lactoferrin ratio was lower ($P < 0.05$) in chitosan treated quarters on Days 3 and 5 than that in control quarters. No major differences between source or volume of chitosan were noted for the measured parameters. These results suggest that chitosan hydrogel infusion hastened mammary gland involution, which may reduce the risk of acquiring new intramammary infection during the drying-off period.

Key Words: involution, mastitis, immunity

0742 Mitigation of variability in feeding patterns between competitively fed dairy cows through increased feed delivery frequency. R. E. Crossley*, A. Harlander, and T. J. DeVries, *Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada*.

The objective of this study was to determine if increased frequency of feed delivery can mitigate the effects of feed bunk competition. We hypothesized that at a greater frequency of feed delivery, 1) there will be improved access to feed (i.e., greater feeding time and consumption of more meals per day) and 2) there will be greater consistency in feeding and meal patterns between cows. Sixteen lactating Holstein dairy cows, with an average DIM of 72 ± 35 d and production of 42 ± 6 kg/d at the start of the trial, were categorized by parity as either young (≤second lactation) or mature (≥third lactation) and paired to maximize difference in parity. Pairs were housed 4 at a time and competitively fed at a ratio of 2 cows:1 feed bin. They were exposed, at a pair level, in a crossover design to each of 2 different treatments: 1) lower feed delivery frequency (2x/d) or 2) higher feed delivery frequency (6x/d). Treatments were applied for 10 d, with DMI and feeding behavior (feeding time, feeding rate, and meal patterns) for each cow recorded using an automated feed intake system on d 6 to 10 of each period. Data were summarized by pair and treatment period and analyzed using a general linear mixed model. Dry matter intake (27.1 kg/d), feeding time (180.2 min/d), and feeding rate (0.17 kg DM/min) were unaffected by increased feed delivery frequency ($P \geq 0.22$). There was a tendency for rumination time to increase with higher frequency of feed delivery (low = 520.5 min/d and high = 547 min/d; SE = 11.32, $P = 0.06$). No differences in meal patterns were found between feed delivery frequency treatments ($P \geq 0.20$). However, comparing the young and mature individuals within each treatment pair revealed differences in both feeding and meal patterns. Feeding rate (young = 0.16 kg DM/min and mature = 0.19 kg DM/min; SE = 0.032, $P = 0.02$) and DMI (young = 25.6 kg DM/min and mature = 28.6 kg DM/min; SE = 1.36, $P = 0.04$) were lower for the young cows on both treatments. Meal frequency was greater in young cows (young = 9 meals/d and mature = 7 meals/d; SE = 0.7, $P = 0.03$) and meal size was greater in mature cows (young = 3.2 kg DM/meal and mature = 4.2 kg DM/meal; SE = 0.35, $P < 0.001$) across treatments. These results suggest that for cows fed at a high level of competition, increasing feed delivery frequency from 2x/d to 6x/d did not improve access to feed. However, under these conditions, the relative parity of competitively fed cows had a greater impact on feeding behavior and meal patterns than the frequency of feed delivery.

Key Words: dairy cow, competition, behavior, feed frequency, meal patterns

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0743 Infusion of a serotonin precursor prepartum induces dynamic glucose and fat metabolism gene expression in the livers of multiparous dairy cows during peripartum. A. P. Prichard*[1], S. R. Weaver[2], E. L. Endres[1], M. S. Akins[3], R. M. Bruckmaier[4], and L. L. Hernandez[2], *[1]University of Wisconsin-Madison, Madison, [2]Department of Dairy Science, University of Wisconsin, Madison, [3]Univeristy of Wisconsin, Platteville, [4]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland*.

Nonneuronal serotonin receptors are dynamic in the liver of transition cows and serotonin is known to affect metabolism. Yet the extent to which glucose and fat homeostasis during the transition period are transcriptionally regulated in response to serotonin is unknown. To this end, we intravenously infused multiparous Holstein ($n = 12$) and Jersey ($n = 12$) cows daily with either 1 L of saline (CON; $n = 6$ for Holstein and Jersey)

or 1 mg/kg BW of 5-hydroxytryptophan (5-HTP; n = 6 for Holstein and Jersey). Holsteins were infused for 5.67 ± 0.78 d and Jersey cows for 8.67 ± 1.53 d prepartum, until parturition. A liver biopsy was performed before treatment, on the day following parturition (d 1), and on Day 7 (d 7) of lactation. Ribonucleic acid was extracted from all samples and real-time PCR was performed. Ribonucleic acid expression was analyzed using the delta-delta CT method and statistical analysis was conducted using a two-way ANOVA for time, treatment, and the interaction on gene expression of phosphoenolpyruvate carboxykinase 1 (PCK1), fructose 1-6 bisphosphatase (FBP1), acetyl co-A carboxylase (ACACA), and carnitine palmitoyltransferase 1 (CPT1A). On d 1, PCK1 and FBP1 expression was elevated in the liver of 5-HTP Holsteins relative to CON Holsteins, but not in Jerseys (P = 0.05 for both PCK1 and FBP1 in Holsteins). In Holsteins, FBP1 expression was greatest on d 1 and returned to baseline levels on d 7 (P < 0.0001). In Jerseys, time had a dynamic effect on FBP1 expression but without the dramatic decline to baseline expression seen in Holsteins (P = 0.04). Expression of ACACA was elevated on d 1 in 5-HTP Holsteins compared with CON (P < 0.05). ACACA expression in 5-HTP Jerseys compared with CON Jerseys was highest on d 7 compared with d 1 or baseline (P = 0.03). There was a treatment (P = 0.03) and time (P = 0.009) effect on CPT1A expression in the Holsteins, with 5-HTP Holsteins having higher expression than CON on d 1 and 7 of lactation. In Jerseys, CPT1A expression was higher on d 7 than on d 1 (P < 0.0001), but there was no treatment effect. Given the roles of PCK1 and FBP1 in promoting gluconeogenesis and the dynamic fatty acid metabolism roles of ACACA and CPT1A, serotonin appears to have an effect on regulating energy and fat homeostasis in a breed- and time-dependent manner during the transition period in dairy cattle.

Key Words: serotonin, liver, gene expression

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744 Sire performance and reproductive breeding values are associated with feed efficiency and growth in dairy heifers. C. E. Owens*, *Virginia Polytechnic Institute and State University, Blacksburg*.

Feed costs represent upward of 60% of total inputs in the dairy industry; moreover, poor fertility is the primary factor influencing cow productive life (PL). To improve profitability, producers must begin selecting for metabolic and reproductive efficiency. To do this, the relationship between feed efficiency and growth must be assessed for milk production and fertility measures. Therefore, the objective of this study was to determine the relationship between sire performance predicted transmitting ability (PTA) with progeny feed efficiency (G:F) and ADG. Twelve dairy heifers (1 wk age and 40.41 ± 4.34 kg BW) were randomly administered one of two diets, restricted (R; 20% CP and 20% fat) or enhanced (E; 28% CP and 25% fat), for 8 wks. Heifers were weighed weekly and daily feed intake measurements were collected to determine G:F and ADG. Sire PTA (milk, fat, protein, PL, somatic cell score, daughter pregnancy rate, and heifer conception rate [HCR]) were collected via the Council on Dairy Cattle Breeding. Using PROC CORR in SAS, phenotypic correlations were determined between sire PTA with calf G:F and ADG, regardless of diet and within diet. There was a strong positive phenotypic correlation between heifer G:F and milk PTA (r_p = 0.76, P = 0.007), and ADG tended to have a moderate positive phenotypic correlation with milk PTA (r_p = 0.57, P = 0.068). A suggestive moderate positive phenotypic correlation (r_p = 0.60, $P \leq 0.081$) was determined between G:F with HCR and PL (r_p = 0.55). Within treatment, R heifers had a strong positive phenotypic correlation between ADG with milk (r_p = 0.94, P = 0.005) and protein (r_p = 0.90, P = 0.016) PTA. There was also a strong positive phenotypic correlation between G:F with milk (r_p = 0.93, P = 0.008) and protein (r_p = 0.93, P = 0.007) PTA for R heifers. Results suggested that sires with more favorable predictors for milk and protein production compared with contemporaries produced heifers with increased feed efficiency and growth. Additionally, sires with increased HCR and PL PTA produced heifers with greater feed efficiency. Overall, favorable selection for sire PTA estimates for performance and reproduction may provide an opportunity to increase heifer feed efficiency and growth.

Key Words: feed efficiency, fertility, growth

0745 Dry matter intake, milk yield, and milk composition of dairy cows fed corn silage from corn treated with various application times of foliar fungicide. C. Kalebich*[1], M. Weatherly[1], G. M. Fellows[2], and P. Cardoso[1], *[1]University of Illinois, Urbana, [2]BASF Corporation, Research Triangle Park, NC*.

Little is known about the ideal timing of foliar fungicide application on corn and its effects on corn silage when fed to dairy cattle. The objective of this study was to determine which timing of fungicide application on corn that was further ensiled as corn silage would have the most advantageous impact on DMI and milk yield and composition in dairy cattle. Holstein cows (n = 64) with parity 2.2 ± 0.8, 626 ± 77 kg BW, and 134 ± 37 DIM were blocked and randomly assigned to 1 of 4 treatments (45% of the DM as corn silage). Treatments were as follows: corn silage with no application of foliar fungicide (CON), corn silage from corn that received one application of pyraclostrobin and fluxapyroxad (PYR+FLUX) foliar fungicide (Priaxor; BASF Corp.) at corn stage V5 (V5), corn silage from corn that received one application of PYR+FLUX at corn stage V5 plus another application of PYR+FLUX at corn stage V8 (V5/V8), and corn silage from corn that received one application of PYR+FLUX at corn stage V5 and one application of PYR+FLUX at corn stage V8 plus a third application of pyraclostrobin and metconazole (PYR+MET) foliar fungicide (Headline AMP; BASF Corp) at corn stage R1 (V5/

V8/R1). Corn was harvested at 31.2% DM and three-fourths milk line kernel development, and ensiled for more than 200 d. Treatments were fed to cows for 5 wk with the last week being used for statistical inferences. Data was analyzed using the MIXED procedure in SAS (version 9.4), with cow as the experimental unit. No differences in DMI (19.5, 19.5, 20.8, and 20.4 kg for CON, V5, V5/V8, and V5/V8/R1, respectively; $P = 0.48$) or milk yield (30.55, 31.17, 29.06, and 29.33 kg/d, respectively; $P = 0.55$) were observed. However, corn silage in V5 compared with corn silage in V5/V8 fed to cows tended to increase 3.5% fat-corrected milk (FCM) (32.42 and 28.58 kg/d, respectively; $P = 0.07$) and energy corrected milk (ECM) (31.35 and 27.76 kg/d, respectively; $P = 0.07$). Percentage of milk lactose tended to be greater for cows fed corn silage treated with foliar fungicide when compared with CON ($P = 0.09$). In conclusion, cows receiving corn silage from corn treated with fungicide at V5 tended to have greater FCM and ECM than cows treated with corn silage from corn treated with fungicide at V5/V8.

Key Words: corn silage, foliar fungicide, fat-corrected milk

0746 Identification of loci associated with fertility in United States Holstein heifers. E. Keuter*[1], C. M. Seabury[2], M. Neupane[3], J. N. Kiser[1], J. Moraes[4], G. Burns[4], T. E. Spencer[4], and H. L. Neibergs[3], *[1]Department of Animal Science, Washington State University, Pullman, [2]Texas A&M University, College Station, [3]Department of Animal Sciences, Washington State University, Pullman, [4]Division of Animal Sciences, University of Missouri, Columbia*.

Current conception rates in U.S. Holstein heifers are estimated to be between 55 and 60%. The objective here was to identify genomic loci associated with fertility in Holstein dairy heifers. Breeding and health records of Holstein heifers were analyzed from a commercial dairy heifer raising facility in southern Idaho. All heifers were bred by AI at observed estrus, and pregnancy was determined at Day 35 after AI via palpation. Records analysis identified 497 heifers that could be classified as highly fertile (HF) due to conceiving on first AI service and 429 subfertile (SF) that did not conceive until after fourth AI service or were culled due to failure to conceive. Deoxyribonucleic acid was extracted from blood samples and genotyped using the Illumina Bovine HD BeadChip. Quality control consisted of removing animals with <90% of genotypes and removing markers with <90% of genotypes or a minor allele frequency <1% or if they failed Hardy–Weinberg equilibrium testing. A total of 466 HF and 368 SF heifers and 590,904 SNP remained for the analysis. A genomewide associated analysis (GWAA) was conducted using an additive model of the efficient mixed-model association expedited statistical test with a genomic relationship matrix. Covariates used in the analysis accounted for relatedness (identity by descent ≥ 0.2) of heifers and the AI bull the heifer was bred to as conception rates differed between AI sires ($P < 6.9 \times 10^{-13}$). The GWAA identified 153 SNP representing 147 QTL ($P < 5.5 \times 10^{-5}$) that were moderately associated and 34 SNP representing 26 QTL ($P < 5.5 \times 10^{-7}$, proportion variance explained ranged from 0.032 to 0.115) that were strongly associated with heifer fertility. Pseudo-heritability was estimated to be 0.46 and l = 0.98. These results indicate that there is ample opportunity to make significant gains in fertility in Holstein heifers with genomic selection. This project was supported by Agriculture and Food Research Initiative Competitive Grant number 2013-68004-20365 from the USDA National Institute of Food and Agriculture.

Key Words: dairy, fertility, quantitative trait loci

0747 The effects of increased metabolizable protein and amino acid supplementation in fresh dairy cattle. E. G. Carder*, *The Ohio State University – OARDC, Wooster*.

The first few weeks after parturition in dairy cattle is a time marked by low but increasing feed intake and sharply increasing milk production. Because of low intake, nutrient density of the diet may need to be higher during this period to support increasing milk yields. We hypothesized that feeding higher levels of MP or feeding supplemental rumen protected methionine and lysine would increase milk yield and protein concentration. Fifty-six Holstein cows (21 primiparous and 35 multiparous), starting at 3 DIM, were used in a randomized-block design with three diets. The treatments were control (16.5% CP, 10.9% RDP, and 5.6% RUP, formulated for 25.1 kg/d MP allowable milk based on an NRC model), high protein (HP; 18.5% CP,11.6% RDP, 6.9% RUP, and 29.9 MP allowable milk), and AA treatment (AA; 17.5% CP, 10.5% RDP, 7.0% RUP, and 29.7 MP allowable milk). The AA diet included a proprietary spray-dried blood meal product (Perdue Agribusiness, Salisbury, MD) that provided 174 and 62 g/d of rumen-protected lysine and methionine, respectively, per the NRC model. The HP diet provided an estimated 156 g/d lysine and 45 g/d methionine and the control diet provided 149 g/d lysine and 41 g/d methionine. Milk production and DMI were measured daily and milk was sampled for components on Day 8, 15, and 20 after moving into tie stalls. Statistical model included parity, treatment, and week fixed effects, random effect of block, and cow as the experimental unit. Treatment and treatment by parity interaction did not affect milk yield (33.6, 34.5, and 33.1 kg for control, HP, and AA), DMI (17.8, 17.8, and 18.5 kg/d for control, HP, and AA), or milk protein yield (1.11 kg/d). Milk protein concentration was higher (3.30 vs. 3.16 and 3.17%; $P < 0.05$) for AA treatment compared with the HP and control, respectively. Energy corrected milk (ECM) was higher (35.1 and 35.1 vs. 32.0 kg; $P < 0.05$) for HP and AA than for the control, respectively. MUN

was higher (14.3 vs. 12.7 and 11.5 mg/dL; $P < 0.05$) for HP than for AA or control, respectively. Plasma BHBA and NEFA were unaffected by treatment or treatment × parity interaction but increased from Day 8 to Day 15 in both multiparous and primiparous cows. Overall, supplementing rumen-protected lysine and methionine with extra MP can increase ECM yield and milk protein concentration.

Key Words: rumen-protected lysine, rumen-protected methionine, metabolizable protein, fresh cow, dairy cow

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0748 Effects of supplementing lactating dairy cow ration with sodium sesquicarbonate on reticulorumen pH, rumination, and dry matter intake. M. L. Jones*[1], J. D. Clark[1], N. A. Michael[2], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Arm & Hammer Animal Nutrition, Princeton, NJ*.

The objective of this study was to assess the effects of sodium sesquicarbonate (SQ-810), a reticulorumen buffer, on rumen pH, rumination time, and DMI. Sixteen early lactation multiparous, Holstein cows were housed in a tie-stall barn and milked twice daily at the University of Kentucky Coldstream Dairy from October 31, 2015, to January 1, 2016. Cows were balanced by parity and milk production and then split into 2 treatment groups for a crossover study with a low-buffer (LB; $n = 8$) group and a high-buffer (HB; $n = 8$) group. The base total mixed ration (TMR) contained 0.16 kg/d sodium bicarbonate. The LB group did not receive SQ-810 whereas the HB group received 0.30 kg of SQ-810 as fed. Eight cows proceeded through sequence 1: three 21-d periods receiving the LB diet in period 1, the HB diet in period 2, and the LB diet in period 3. The remaining 8 cows proceeded through sequence 2: three 21-d periods receiving the HB diet in period 1, the LB diet in period 2, and the HB diet in period 3. Each group was fed ad libitum and DMI was collected. All cows were administered an iNovotec Animal Care (iNovotec Animal Care, Austria) reticulorumen pH and temperature bolus. Daily rumination time was recorded using HR tags (SCR Engineers Ltd., Netanya, Israel) and CowManager SensOor (SENRUM) tags (Agis Automatisering, Harmenlen, Netherlands). Low pH was calculated as the total time pH was <5.60. The MIXED procedure of SAS was used to evaluate the effects of cow, sequence, treatment and period on each parameter measured. Rumen pH and low pH time (pH < 5.60) were influenced by treatment ($P < 0.01$). Rumen pH was 5.82 ± 0.07 for LB cows and 5.85 ± 0.07 for HB cows. Low pH time (pH < 5.60) was greater ($P < 0.01$) for LB days (64.17 ± 11.71 min/d) than for HB days (56.31 ± 11.71 min/d). Dry matter intake was 25.68 ± 0.61 kg/d for LB cows and 26.53 ± 0.61 kg/d for HB cows. Treatment affected SCR rumination times ($P < 0.01$) for LB cows (457.84 ± 19.15 min/d) and HB cows (435.02 ± 19.15 min/d). Rumination time measured using SENRUM was not significantly different between treatments. The addition of SQ-810 to the TMR significantly increased reticulorumen pH and DMI ($P < 0.01$). This research demonstrates the positive effects of SQ-810 rumen buffer in a lactating cow diet.

Key Words: rumen pH, sodium sesquicarbonate

0749 Feeding low crude protein diets in lactating dairy cows during summer months: 2. Improvements in energy metabolism. J. Kaufman*, K. Kassube, K. G. Pohler, and A. G. Rius, *The University of Tennessee, Knoxville*.

Lactating dairy cows experience changes in nutrient partitioning and decrease production during summer months. Dietary concentrations of RDP and RUP affect nutrient partitioning and utilization. A study was conducted to evaluate the effect of feeding low RDP and RUP levels on energy metabolism in cows during peak summer months. Forty-eight primiparous and multiparous midlactation Holstein cows were assigned to treatments using a complete randomized block design in a 2 × 2 factorial arrangement of treatments ($n = 12$/treatment). Treatments included two levels of RDP (10 and 8%) and two levels of RUP (8 and 6%). A common diet (10% RDP and 8% RUP) was fed from d 1 to 21 followed by the respective treatment diets from d 22 to 42. Cows were housed in a freestall barn and exposed to the prevailing temperature and humidity of July and August with no supplemental cooling. Blood samples were collected from individual cows at d 42. Plasma was harvested for analysis of glucose, insulin, NEFA, and β-hydroxybutyrate (BHBA). Main effects and their interaction were tested using the Mixed procedure of SAS and reported as least squares means ± SEM. Rectal temperatures and respiration rates were recorded before noon and after noon during the treatment period. Compared with before noon, after noon increased temperature and respiration rates (38.9–39.7 ± 0.07°C [$P < 0.001$] and 64.0–87.1 ± 1.4 breaths/min [$P < 0.001$]). The 10% RDP treatment decreased ($P < 0.04$) glucose concentrations compared with the 8% RDP treatment (3.0 vs. 3.1 ± 0.05 mmol/L). The 10% RDP treatment increased ($P < 0.01$) insulin concentrations compared with the 8% RDP treatment (20.9 vs. 15.8 ± 1.1 μU/mL). The 8% RUP treatment tended to increase ($P < 0.08$) insulin concentrations compared with the 6% RUP treatment (19.8 vs. 16.9 ± 1.12 μU/mL). The 8% RUP treatment decreased ($P < 0.01$) NEFA concentrations compared with the 6% RUP treatment (141 vs. 173 ± 16.5 μEq/L). Compared with 10% RDP, the 8% RDP treatment decreased BHBA concentrations in the 8% RUP treatment (251 vs. 407 ± 26.5 μmol/L) but increased BHBA concentrations in the 6% RUP treatment (190 vs. 173 ± 26.5 μmol/L; interaction, $P < 0.01$). In conclusion, these results indicate that lower RUP diets promoted lower concentrations of insulin and greater concentrations of NEFA. This may allow metabolic adaptations to mobilize lipids and sustain milk production.

Key Words: crude protein, energy utilization, heat stress

ADSA PRODUCTION DIVISION GRADUATE STUDENT POSTER COMPETITION: PHD

0750 Elevation of circulating serotonin prepartum decreases β-hydroxybutyrate concentrations and improves energy status postpartum in multiparous dairy cows. S. R. Weaver*[1], A. P. Prichard[2], E. L. Endres[2], M. S. Akins[3], R. M. Bruckmaier[4], and L. L. Hernandez[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]University of Wisconsin-Madison, Madison, [3]Univeristy of Wisconsin, Platteville, [4]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland*.

Peripheral serotonin is known to mediate energy homeostasis in late-lactation dairy cows. However, the majority of energy-related disorders occur primarily during the transition period. To establish if serotonin mediates energy homeostasis during the transition period, we intravenously infused multiparous Holstein (n = 12) and Jersey (n = 12) cows daily with either 1 L of saline (CON; n = 6 for Holstein and Jersey) or 1 mg/kg BW of 5-hydroxytryptophan in 1 L of saline (5-HTP; n = 6 for Holstein and Jersey). Holsteins were infused for an average of 5.67 ± 0.78 d and Jersey cows for 8.67 ± 1.53 d prepartum, until parturition. On infusion days, blood was collected before, after, and at 2, 4, and 8 h after infusion. Blood was also collected for 14 d postpartum and on Day 30 postpartum and assayed for glucose, β-hydroxybutyrate (BHBA), and NEFA. Milk yield and feed intake were monitored throughout. All data were analyzed using a two-way ANOVA in SAS for treatment, breed, and day effect and the interaction. Holsteins treated with 5-HTP had elevated circulating serotonin for 6 d before parturition and on Day 0 and Day 1 of lactation (P < 0.05). The5-HTP Jerseys treated with 5-HTP had elevated serotonin concentrations 2 d prepartum and on the day of parturition (P < 0.003). Treatment did not affect milk yield (P > 0.05). There was no treatment effect on feed intake for either breed (P > 0.05). The CON Holsteins had higher circulating glucose than CON Jerseys from Day 8 to Day 15 postpartum (P < 0.05) and this effect was mediated by 5-HTP treatment. There was no treatment effect in either breed on circulating glucose levels (P > 0.05). β-Hydroxybutyrate concentrations tended to be lower on Days 7 and 10 in Holstein 5-HTP compared with Holstein CON (P = 0.09) and were significantly lower on Day 7 in Jersey 5-HTP compared with Jersey CON (P = 0.02). The CON Jerseys had the highest BHBA concentrations on Days 6 to 10 postpartum. There was no effect of BHBA prepartum in either breed. Nonesterified fatty acids were not affected either pre- or postpartum (P > 0.05), although they were elevated in both breeds within an infusion day (P < 0.05). Taken together, these data demonstrate that serotonin administration prepartum may have a positive effect on mediating energy status postpartum. Specifically, decreased BHBA concentrations on Days 6 to 10 postpartum demonstrate serotonin's potential to mediate ketosis incidence.

Key Words: energy, serotonin, transition cow

0751 Temporal effects of ruminal propionate infusion on feeding behavior of Holstein cows in the postpartum period. G. Maldini*[1,2], M. S. Allen[1], and K. M. Kennedy[1], *[1]Michigan State University, East Lansing, [2]CAPES Foundation, Brasilia, Brazil*.

Suppression of appetite during the postpartum (PP) period is likely caused by a signal related to hepatic energy status from oxidation of fuels. Propionic acid (PA) is likely the most important fuel stimulating hepatic oxidation within meals in ruminants. However, PA production rate in the rumen varies greatly among starch sources and the temporal pattern of propionate supply to the liver might affect satiety within meals. The objective of this study was to determine the temporal effect of intraruminal propionic acid infusion at initiation of meals on feeding behavior of PP cows. We hypothesized that a faster rate of PA infusion would decrease meal size by stimulating satiety sooner within a meal. Six ruminally cannulated, multiparous Holstein cows in the PP period were used in a duplicated 3 × 3 Latin square design experiment balanced for carryover effects. Cows were blocked by parturition date and randomly assigned to treatment sequence within square. Treatments included a control (no infusion) or infusion of 1.25 mol of propionic acid over 5 (FAST) or 15 min (SLOW) at each meal. Infusions were initiated at the beginning of the conditioned meal (1200 h) and were triggered at each spontaneous meal for 22 h. Feeding behavior was monitored by a computerized data acquisition system. A 24-h recovery period was included between infusion days to reduce potential carryover effects of treatment. In contrast to our hypothesis, FAST increased meal size 55% (1.30 vs. 0.84 kg DM; P < 0.02) compared with SLOW. FAST also increased intermeal interval 67% compared with SLOW (149.7 vs. 89.8 min; P < 0.05) while decreasing meal frequency 29% (8.0 vs. 11.2 meals/d; P = 0.01). Although both PA treatments decreased DMI 48% compared with the control, DMI was not affected by infusion rate. FAST PA supply to the liver at the initiation of meals might have resulted in a saturation of propionate metabolic pathways in the liver, resulting in greater bypass for FAST compared with SLOW. Increased intermeal interval and reduced meal frequency for FAST compared with SLOW might have been caused by extended anapleurosis and hepatic oxidation of acetyl CoA over a longer time after meals, delaying hunger. These results indicate that the depression in feed intake by more fermentable starch sources might be more related to the amount of PA produced rather than its rate of production within meals.

Key Words: feeding behavior, meal size, hepatic oxidation

0752 Forage yield, nutrient composition, and grain yield of corn and soybeans when intercropped at different seeding rates grown under organic conditions. I. P. Acharya*[1], X. Gu[2], S. Acharya[1], P. Poudel[1], and D. P. Casper[1], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Deparment of Plant Science, South Dakota State University, Brookings*.

Previous research has demonstrated that feeding of forage blends produced through intercropping of corn and soybean could be beneficial for livestock. A field plot study was laid out using a randomized complete block design having three replicates to evaluate an organic corn hybrid, MC 5300 (C), with an organic soybean, Viking 2265 (N) or Vining soybean (V), at five different seeding rates to create nine different treatments (100:0:0 [T1], 0:100:0 [T2], 0:0:100 [T3], 50:50:0 [T4], 67:33:0 [T5], 33:67:0 [T6], 50:0:50 [T7], 67:0:33 [T8], and 33:0:67 [T9] of C with N and V) to determine the optimal intercropping seeding rates. Forages were hand harvested 110 d after planting, inoculated, packed into buckets, weighed, and ensiled for 90 d. Buckets were then reweighed and opened, and forage samples were collected and analyzed for nutrient composition. Fresh biomass yield was higher ($P < 0.01$) for T8 compared with remaining treatments (88.37, 31.34, 17.34, 85.07, 101.49, 68.06, 85.78, 107.00, and 74.86 T/ha for T1, T2, T3, T4, T5, T6, T7, T8, and T9, respectively). Dry matter yield was higher ($P < 0.01$) for T8 compared with others (10.60, 5.93, 27.10, 24.44, 29.31, 36.55, and 25.41 T/ha for T2, T3, T4, T6, T7, T8, and T9, respectively). Nitrogen accumulation by treatments forage was lower ($P = 0.01$) in T3 (0.20 T/ha) compared with the others (0.38 T/ha). Corn grain yield was higher ($P < 0.01$) for T5 and T8 compared with T4, T6, T7, and T9 (11.84, 15.44, 8.84, 11.89, 16.66, and 9.68 T/ha for T4, T5, T6, T7, T8, and T9, respectively). Soybean grain yield was higher ($P < 0.01$) in T4 and T6 compared with T5, T7, T8, and T9 (3.06, 1.80, 3.38, 1.90, 0.53, and 2.36 T/ha for T4, T5, T6, T7, T8, and T9, respectively). Land equivalent ratio was higher ($P < 0.01$) for T4 (1.32) and T5 (1.31) compared with T7 (1.15), T8 (1.16), and T9 (1.11). Crude protein content was higher ($P < 0.01$) for T6 (9.64%) compared with T4 (8.96%), T5 (8.22%), T7 (8.20%), and T8 (7.94%). Starch content was higher for T4 (29.18%) compared with T9 (26.03%). Thirty-hour NDF digestibility was higher ($P < 0.01$) for T4 (45.81%), T6 (47.41%), and T9 (46.19%) compared with T5 (43.86%) and T8 (43.38%). The production of forage blends through intercropping of corn and soybeans has the potential to yield greater quantities of digestible nutrients.

Key Words: corn, silage soybean

0753 Refinement of the *DST* locus associated with bovine respiratory disease complex in Holstein calves. M. Neupane*[1], J. L. Hoff[2], J. F. Taylor[2], C. M. Seabury[3], J. E. Womack[3], T. Bovine Respiratory Disease Complex[3], and H. L. Neibergs[1], *[1]Department of Animal Sciences, Washington State University, Pullman, [2]University of Missouri, Columbia, [3]Texas A&M University, College Station*.

Despite best management practices including vaccination and treatment programs, bovine respiratory disease complex (BRDC) continues to be a major cause of morbidity and mortality in cattle. An additional approach to reduce BRDC is to select animals that are less susceptible to respiratory disease. A previous genomewide association analysis identified a 10-kb QTL region on chromosome 23 (BTA23) that included the dystonin (*DST*) gene that plays a major role in herpes virus infections in cattle. The objective of this study was to determine if there were additional variants on BTA23 with a greater association with BRDC that could be used in the selection of cattle with enhanced BRDC resistance. An analysis was conducted using genotypes imputed to whole genome sequence (WGS) for preweaned Holstein calves from California that consisted of 996 controls and 982 cases as defined by the McGuirk health scoring system. Illumina BovineHD genotypes on BTA23 were imputed to WGS using Run 5 data from the 1000 Bull Genomes Project and accuracy was checked by using the WGS of 30 Holstein calves included in the study. Imputation was conducted using Fimpute and errors were corrected by using Beagle 4.1 software. Single nucleotide polymorphisms were filtered for low minor allele frequency (<1%) and low call rate (<90%), resulting in 2,196 biallelic markers being used for analysis in a 1-Mb region surrounding *DST*. Analyses were performed using an allelic model and an additive model with efficient mixed model association expedited (EMMAX) that included age and sex as covariates. A 2.5-kb region including intron 57 (ENSEMBL) of *DST* contained 19 SNP that were associated with BRDC with both allelic ($P = 6.72 \times 10^{-7}$ to $P = 5.07 \times 10^{-5}$) and additive models ($P = 3.82 \times 10^{-6}$ to $P = 6.88 \times 10^{-5}$). Many of the 19 SNP were highly conserved across species, suggesting that they may have a functional or regulatory role in gene expression. These SNP will be used to confirm the BRDC association in independent cattle populations to determine their value for inclusion in a genomic PTA for BRDC. This project was supported by Agriculture and Food Research Initiative Competitive Grant number 2011-68004-30367 from the USDA National Institute of Food and Agriculture.

Key Words: bovine respiratory disease complex, dairy, calves, imputation, loci

0754 Meta-analysis of factors influencing new intramammary infection rate in natural exposure teat dip efficacy trials. B. D. Enger*[1], R. R. White[1], S. C. Nickerson[2], and L. K. Fox[3], *[1]Virginia Tech, Blacksburg, [2]University of Georgia, Athens, [3]Washington State University, Pullman*.

Teat dips are used to reduce the incidence of new intramammary infection (IMI) on dairies. Although it is widely acknowledged that many factors affect teat dip efficacy and that all teat dips should be confirmed efficacious before commercial circulation, the studies evaluating teat dip efficacy differ in experimental design, pathogen profiles at the herd level, and teat dips tested, among other factors. The objective of the present study was to conduct a meta-analysis of data from peer-reviewed teat dip efficacy trials that used a natural exposure study design to identify factors influencing the new IMI rate. A data set of 16 studies (256 observations) was created, and the new IMI rate, based on percentage of new quarter infections per month (PNQI/mo), was calculated for each observation in the data set. The new IMI rate (PNQI/mo) was used as the dependent variable for model derivation. A linear, mixed-effects model with a random study effect, weighted for the SE of the measurement, was derived in a stepwise manner where parameters were sequentially eliminated for nonsignificance. The final mixed model included the terms of study design ($n = 2$, $P = 0.03$), mastitis pathogen group ($n = 6$, $P < 0.01$), postmilking treatment ($n = 6$, $P = 0.06$), and the two-way interaction between mastitis pathogen group and postmilking treatment ($P < 0.01$). Overall, *Corynebacterium* spp. had the highest new IMI rate, 0.0139 ± 0.0018 PNQI/mo, which was greater than that of the environmental streptococci and Gram-negative species, 0.0023 ± 0.0022 PNQI/mo, both having the lowest new IMI rate ($P < 0.05$). The new IMI rates for *Staphylococcus aureus*, *Streptococcus agalactiae*, and the coagulase negative staphylococci were 0.0046 ± 0.0017, 0.0054 ± 0.0043, and 0.0094 ± 0.0017 PNQI/mo, respectively. The new IMI rate of mastitis pathogen groups was influenced by different postmilking treatments ($P < 0.01$). Studies using a split herd study design had a greater new IMI rate, 0.0089 ± 0.0017 PNQI/mo, than studies using a split udder study design, 0.0046 ± 0.0017 PNQI/mo ($P = 0.03$). The results of this study indicate that mastitis pathogens vary in sensitivity to different postmilking teat dips and suggest that changing the postmilking teat dip used at the farm to a teat dip containing a different active ingredient may increase efficacy against specific pathogens.

Key Words: teat disinfectant, study design, mastitis

0755 Diet starch content and fermentability affects feed intake and milk yield of cows in the postpartum period. R. I. Albornoz* and M. S. Allen, *Michigan State University, East Lansing*.

The objective of this study was to evaluate the effects of diet starch content and fermentability fed during the postpartum (PP) period on DMI, yields of milk (MY) and milk components, and body reserves. Fifty-two multiparous Holstein cows were used in a randomized block design with a 2 × 2 factorial arrangement of treatments. Diets were formulated to 22 (LS) or 28% (HS) starch with dry ground corn (DGC) or high-moisture corn (HMC) as the primary starch source. Treatments were fed from 1 to 23 d PP and then switched to a common diet until 72 d PP to measure carryover (CO) effects. Treatment period (TP) diets were formulated for 22% forage NDF and 17% CP, and starch concentration was adjusted by substitution of corn grain for soyhulls. The diet for the CO period was formulated to 20% forage NDF, 17% CP, and 30% starch. Throughout the experiment, both DMI and MY were measured daily, and milk components, BCS, and back fat thickness (BFT) were measured weekly. During TP, DGC increased DMI by 2.2 kg/d compared with HMC ($P < 0.01$) but tended to increase DMI more with HS (3.4 kg/d) than with LS (1 kg/d; interaction, $P = 0.12$). Treatments also interacted over time; DGC increased DMI throughout the TP for HS but only after the first week for LS compared with the HMC treatments ($P < 0.01$). There was no main effect of starch content on DMI. The effect of corn source diminished over time during the CO period ($P = 0.03$) with no main effects of treatment on DMI. Dry ground corn increased yields of milk by 2.6 kg/d ($P = 0.12$), 3.5% fat-corrected milk (FCM) by 4.3 kg/d ($P = 0.02$), fat by 165 g/d ($P = 0.03$), and protein by 165 g/d ($P = 0.01$) compared with HMC with no effect of starch content throughout the TP. Starch source and content interacted ($P < 0.05$) to affect yields of fat and FCM during the CO period, which were greater for DGC-HS and HMC-LS (1.78 and 52.1 kg/d, respectively) than for DGC-LS and HMC-HS (1.62 and 48.6 kg/d, respectively). Dry ground corn tended to decrease BCS loss until the third week of TP ($P < 0.15$) compared with HMC but had no effect overall. No effects of treatment were detected for BFT during TP but HMC increased BFT 0.1 mm ($P = 0.04$) during the CO period. Ruminal fermentability of starch is an important consideration for diets of cows in the PP period.

Key Words: high-moisture corn, dry corn, fresh cows

0756 Meta-analysis of postruminal microbial nitrogen flows in dairy cattle. Y. Roman-Garcia*[1], R. R. White[2], and J. L. Firkins[1], *[1]The Ohio State University, Columbus, [2]Virginia Polytechnic Institute and State University, Blacksburg*.

The objective of this study was to summarize the literature and derive equations that relate the chemical composition of

diet and rumen characteristics to the intestinal supply of microbial nitrogen (MicN; g/d), efficiency of microbial protein synthesis (EMPS; g MicN/kg OM truly degraded in the rumen), and flow of nonammonia nonmicrobial N (NANMN; g/d). In this study, 619 weighted treatment means were screened from 183 studies using dairy cattle that were sampled from the duodenum or omasum (sample location [SMPLoc]). Backward elimination multiple regression was used to derive equations to estimate flow of nitrogenous components over a large range of dietary nutrients (% of DM) or ruminal pH, NH_3–N (mg/dL), or individual branched-chain VFA (BCVFA; mol/100 mol). An intercept shift indicated greater MicN flow for omasal sampling relative to duodenal sampling in all MicN models, but sample location did not interact with any other variables tested. Microbial nitrogen was associated with DMI and dietary starch percentage: MicN = −18.4 g/d + 109 g/d more (if SMPLoc = omasal) + 10.8(DMI) + 5.31(starch) − 0.0839(starch × starch). Ruminal pH and NH_3–N were negatively related to MicN flow, with a positive association with ruminal isovalerate. The EMPS = 4.71(isovalerate) + 0.260(NH_3–N) − 0.257(NH_3–N × isovalerate). A similar equation with a parallel role for isobutyrate confirms the importance of BCVFA to increase growth rate and, therefore, assimilation of NH_3–N into microbial protein. The flow of NANMN = −37.5 (if SMPLoc = omasal) + 8.70(DMI) + 9.98(NDF) −1.42(NDF×NDF) + 6.08(CP). Because NANMN is calculated by subtracting MicN, omasal sampling underestimated NANMN relative to duodenal sampling. This equation is probably associated with neutral detergent isoluble N contamination of NDF in certain rumen-undegradable protein sources. As in the MicN equation, sampling location did not interact with any other variables tested for NANMN. Equations derived from dietary nutrient composition are robust across dietary conditions and could be used for prediction in protein supply-requirement models.

Key Words: nitrogen, microbial, flow

0757 Milk yield genotype affects hepatic expression of innate immune genes when challenged with lipopolysaccharide.

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Objectives were to determine effects of milk yield genotype on hepatic expression of genes related to innate immune response during a lipopolysaccharide (LPS) challenge. Multiparous cows (n = 12/genotype) from unselected (stable milk yield since 1964; UH) and contemporary (CH) Holsteins that differed by more than 4,500 kg milk/305 d were housed together and fed the same diet ad lib for more than 4 mo before being blocked (2/genotype) by DIM and randomly assigned within genotype to receive saline or 0.25 μg/kg BW of LPS (*Escherichia coli* 055:B5). Cows were synchronized to be at Day 8 of their estrous cycle for the first challenge (C1) at 70 to 84 DIM. Liver biopsies were collected at 0, 4, and 24 h relative to treatment. Acute innate immune responses were assessed in C1. A second identical challenge (C2) and sampling was conducted 4 d later to assess the impact of a repeated challenge. Expression of 44 genes associated with immunity was determined by digital multiplexed analysis (nanoString nCounter). Expression was normalized to the positive control and the geometric mean of 4 internal control genes. Data were transformed (square root) and analyzed by repeated measures using PROC MIXED (SAS) with time as the repeated effect. Means differed when $P < 0.05$. There were time × treatment interactions for 37 genes due to changes in expression after LPS. At 4 h, LPS increased expression of 15 genes and reduced expression of FASLG in UH relative to CH. The 15 genes included TLR4, CD14, ICAM-1, IRF-1, MYD88, IL-6, and TNF. During C2, expression of these genes was less than in C1 and was not affected by genotype. There was a genotype × treatment × challenge interaction for CCL20 as its expression at 4 h in C2 was greater in CH than UH. IL-10 increased at 4 h for both genotypes, but expression during C2 was less than during C1. TGFB1 increased more in UH than CH at 4 h in both challenges. During the acute phase (C1), UH cows had a more robust expression of genes related with immune cell activation, cytokine production, and chemoattractant production and activation than CH. Responses during C2 were diminished in both genotypes, which indicates that compensatory mechanisms invoked by C1 were still affecting the response to LPS. Results indicate milk yield genotype impacts the response to LPS and contributes to a less robust response in the contemporary cow.

Key Words: gene expression, immunity, bovine genotype, lipopolysaccharide

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0758 Effects of feeding different forms of polyunsaturated fatty acids on performance, plasma metabolites, and milk fatty acid composition of dairy cows.

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Objectives were to determine the effects of feeding different types of PUFA on performance and yield of fatty acids in Holstein cows. Eight ruminally cannulated primiparous cows were randomly assigned to a replicated 4 × 4 Latin square design

(28 d; 19 d adaptation, 7 d collection, and 2 d rumen evacuation). Diets were identical except for the type of fatty acid supplements that were incorporated at 2.1% of dietary DM. Supplements were Ca salts (CaS) of palm oil (CaSP), oil (O; a blend of 45% palm and 55% soybean oils), CaS of O in a granular form (CaSOG), and CaS of O in a pelleted form (CaSOP). Intake and yield and composition of milk were averaged from d 20 to 26. The fatty acid profile of milk fat was analyzed in samples collected from d 24 to 26. Blood was sampled at 0, 3, 6, 9, and 12 h relative to feeding on d 26 and analyzed for hormones and metabolites. Ruminal pH was measured for 72 h in each period. Data were analyzed by ANOVA with the MIXED procedure of SAS for a replicated 4 × 4 Latin square. Results of cow performance are presented in Table 1. Results in the text are presented in the following sequence: CaSP, O, CaSOG, and CaSOP. Feeding O increased ($P \leq 0.05$) rumen fluid pH compared with CaSP or CaSOG (6.22, 6.31, 6.20, and 6.26 ± 0.07). Plasma concentration of glucose increased ($P \leq 0.05$) in O compared with CaSP and CaSOG and tended ($P = 0.08$) to be greater than CaSOP (64.8, 66.3, 64.7, and 64.9 ± 0.55 mg/dL). Glucagon concentration in plasma tended ($P = 0.06$) to be greater in CaSP compared with CaSOP (156.4, 152.6, 149.4, and 144.8 ± 8.0 pg/mL). There were no treatment effects on plasma insulin, NEFA, and urea N concentrations. Milk linoleic (3.29, 3.22, 4.88, and 4.71 ± 0.16 g/100 g of fatty acid) and linolenic acids (0.43, 0.46, 0.61, and 0.53 ± 0.02) and total *n*-3 (0.46, 0.48, 0.64, and 0.56 ± 0.02) and *n*-6 fatty acid yields (3.78, 3.64, 5.37, and 5.19 ± 0.17) increased ($P < 0.01$) in cows fed CaSOG and CaSOP compared with cows fed CaSP or O. Conjugated linoleic acids *trans*-10 *cis*-12 and *trans*-9 *cis*-11 were reduced ($P < 0.01$) in cows fed CaSP compared with cows fed other treatments (0.004, 0.013, 0.019, and 0.019 ± 0.003). Source of fatty acids did not affect DMI or milk yield, but feeding O as CaS in a pelleted form improved milk fat content. Feeding CaS of O either as granular or pelleted increased content of PUFA in milk fat.

Key Words: fatty acid, rumen biohydrogenation, performance

Table 0758.

Table 1. Performance of dairy cows fed different forms of FA

	Treatment[1]					
Item	CaSP	O	CaSOG	CaSOP	SEM	P
DM intake, kg/d	20.5	20.6	20.5	20.0	0.68	0.46
Milk yield, kg/d	28.7	28.6	28.7	28.2	0.91	0.96
Milk fat, %	3.47^{a}	3.28^{b}	3.25^{b}	3.44^{a}	0.14	0.05
Milk fat yield, kg/d	$0.99^{a,A}$	0.93^{B}	0.92^{b}	0.96	0.04	0.13
Milk NE_L, Mcal/kg	0.67^{a}	$0.65^{b,B}$	0.65^{c}	$0.67^{a,b,A}$	0.01	0.03
Water intake, L/d	103.4^{b}	109.5^{a}	102.1^{b}	100.0^{b}	4.59	0.03

[a,b,c] Different superscripts differ ($P < 0.05$). [A,B] Different superscripts tend to differ ($P < 0.10$).
[1] CaSP = CaS of palm oil; O = blend of 45% of palm and 55% soybean oils; CaSOG = CaS of O in granular form; CaSOP = CaS of O in pelleted form.

0759 Rumen-protected methyl donors during the transition period: Circulating plasma amino acids in response to supplemental rumen-protected methionine or choline. Z. Zhou*[1], M. Vailati Riboni[1], D. N. Luchini[2], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Adisseo S.A.S., Alpharetta, GA*.

The objective of this study was to profile plasma AA and downstream products of their metabolism during the peripartal period in response to supplemental rumen-protected methionine (MET) and choline (CHO). Forty multiparous Holstein cows were used in a randomized complete block design with 2 × 2 factorial arrangement of MET and CHO level (with or without). Treatments were control (CON), no MET or CHO; CON+MET (SMA); CON+CHO (REA); and CON+MET+CHO (MIX). From −21 (close-up) to 30 d after calving, cows received the same diet (1.52 Mcal NE_L/kg DM) from close-up to calving. From calving to 30 d, cows were on the same diet (1.71 Mcal NE_L/kg DM) and continued to receive the same treatments through 30 d. MET supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow per day. Blood samples were taken at −30, −10, 4, 14, and 28 d relative to calving. Data were analyzed as a factorial design with repeated measures using PROC MIXED in SAS. Previous results from this experiment revealed that both pre- and postpartum DMI was greater with MET ($P = 0.01$) but did not change with CHO ($P > 0.05$). As expected, MET supplementation led to greater ($P < 0.01$) plasma methionine concentration compared with other treatments. Similarly, sulfur-containing AA derivatives (homocystine, cystathionine, and cystine) and taurine (an antioxidant) also were greater in MET-supplemented cows, suggesting an enriched sulfur pool. In addition to plasma methionine concentration, lysine ($P = 0.01$), arginine ($P = 0.02$), tryptophan ($P < 0.01$), and threonine ($P = 0.07$) also were greater in MET-supplemented cows, all of which contributed to the strong tendency ($P = 0.06$) for greater essential AA (EAA) in response to MET. An overall greater ($P = 0.02$) total plasma AA concentration was observed in MET cows due to greater ($P < 0.05$) proline, asparagine, alanine, and citrulline compared with other treatments. In contrast, CHO supplementation had no effect ($P > 0.05$) on overall EAA

and total AA, as only tryptophan ($P = 0.02$) and cystine ($P < 0.01$) were greater with this treatment. Plasma concentration of 3-methyl-histidine was lower ($P < 0.05$) in response to CHO, suggesting less protein mobilization in these cows. Overall, data from the present study indicate that peripartal supplementation of rumen protected methionine has positive effects on plasma AA status.

Key Words: amino acid, choline, methionine, transition cow

ADSA–SOUTHERN SECTION GRADUATE STUDENT ORAL COMPETITION

0760 The nutritional quality of winter crops for silage in monoculture or with legumes. A. N. Brown*[1], G. Ferreira[1], C. L. Teets[1], W. E. Thomason[2], and C. D. Teutsch[3], *[1]Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Department of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg, [3]Dep. of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg*.

The objectives of this study were to determine the nutritional quality of different winter crops for silage within various regions of Virginia and to determine the impact of the various winter crops on the succeeding productivity of corn and sorghum. Experimental plots were planted with 15 different winter crop treatments at 3 locations in Virginia. At each site, 4 plots of each treatment were planted in a randomized complete block design. The 15 treatments included 5 winter annual grasses (barley, wheat, rye, ryegrass, and triticale) in monoculture [NO] or with one of two winter annual legumes (crimson clover [CC] and hairy vetch [VE]). The nutritional composition (DM, ash, CP, NDF, ADF, ADL, starch, and sugars) was determined for the fresh samples. Additionally, 200

Table 0760.

Table 1. Effect of winter crops in monoculture or with legumes on nutritional quality of feed.

	Grass					Legume				P-Value		
	Barley	Ryegrass	Rye	Triticale	Wheat	NO	CC	VE	SEM	Grass	Legume	Interaction
Fresh												
DMY, kg/ha	2767	2189	2223	1983	2283	2141	2538	2188	367.7	0.04	0.08	
DP,%	19.5	18.9	17.5	17.0	18.7	19.9	17.7	17.3	0.9	< 0.01	< 0.01	
Ash,%	8.8	9.2	8.8	8.7	8.8	8.8	8.8	9.1	0.6			
CP,%	14.2	14.2	16.1	16.1	15.7	13.0	15.5	17.3	1.3	< 0.01	< 0.01	
NDF,%	54.0	43.3	49.9	46.0	44.5	49.7	46.4	46.5	1.6	< 0.01	< 0.01	
ADF,%	31.8	26.9	30.5	27.8	26.8	28.5	28.7	29.1	1.5	< 0.01		0.03
ADL,%	2.7	2.6	2.5	2.5	3.0	2.3	2.7	2.9	0.3	0.02	< 0.01	
Starch, %	3.0	2.7	3.5	3.5	4.0	3.2	3.6	3.2	0.2	< 0.01	0.02	
Sugar, %	10.8	9.9	13.2	13.4	15.9	14.2	13.2	10.5	2.2	< 0.01	< 0.01	
Silage												
DP,%	29.3	27.4	24.1	23.5	25.3	28.4	24.6	24.8	2.5	0.04	0.04	
Ash,%	9.3	10.6	9.6	10.3	9.5	9.0	10.2	10.4	1.0	< 0.01	< 0.01	
CP,%	15.1	15.8	16.5	17.3	17.0	14.2	16.6	18.3	0.9	< 0.01	< 0.01	
NDF,%	59.1	45.4	54.7	49.7	46.7	53.3	49.3	50.7	1.9	< 0.01	< 0.01	0.04
ADF,%	32.6	28.7	31.8	29.2	28.9	29.9	29.3	31.5	1.4	< 0.01	0.04	
Sugar, %	2.2	3.5	2.3	2.5	3.0	3.1	3.0	2.0	0.7	< 0.01	< 0.01	
ADL,%	3.3	3.5	3.3	3.1	4.0	3.0	3.5	3.9	0.6		0.02	
pH	4.39	4.17	4.28	4.30	4.11	4.14	4.20	4.42	0.13	0.01	< 0.01	

to 400 g of chopped material were placed into mini-silos and analyzed after 60 d of ensiling. The statistical model included the effects of grass, legume, the 2-way interaction, and the random effect of site. Sorghum and corn were planted after harvesting the winter crops in split plots. For the split-plot design, the statistical model included the effects of treatment, the random effect of site, treatment × site, summer crop, summer crop × site, and summer crop × treatment. There were no grass × legume interactions except for fresh ADF and silage NDF. Crimson clover tended to increase forage DM yield. Adding legumes increased CP and decreased NDF of both fresh and silage samples. However, addition of legumes increased ADL in contrast to NO. Legumes did not affect ADF concentrations of fresh samples, but for silage, VE increased ADF compared with CC and NO. In contrast to VE, inclusion of CC increased sugar content for both fresh and silage samples. Corn yields were greatest succeeding barley compared with the other grasses (15,800 vs. 14,700 kg/ha). Addition of legumes did not affect DM yield of corn (14,900 kg/ha) or sorghum (15,300 kg/ha). We conclude that although inclusion of legumes did not have a residual effect on summer annual yields, including CC could increase yield of winter crops. Addition of legumes increases CP, decreases NDF, and, for VE, decreases the sugar content of the silage.

Key Words: winter crops, cover crops, nutritional quality

0761 Housing and demographic effects on somatic cell score in southeast United States dairies. A. Stone*[1], C. Blakely[2], K. Bochantin[1], P. D. Krawczel[2], M. Myers[1], D. T. Nolan[1], C. S. Petersson-Wolfe[3], G. M. Pighetti[2], S. Ward[4], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]University of Tennessee, Knoxville, [3]Virginia Tech University, Blacksburg, [4]Mississippi State University, Mississippi State*.

The objective of this study, as part of the Southeast Quality Milk Initiative, was to evaluate the effects of housing systems and farm demographics on SCS. From June 22, 2014, to June 21, 2015, dairy producers in Kentucky (n = 96), Tennessee (n = 83), Virginia (n = 96), and Mississippi (n = 7) participated in an on-farm survey. Each survey variable's effect on SCS was evaluated using the GLM procedure in SAS with no covariates. Significant farm demographic variables were then included as covariates in a GLM alongside herd size, state, and all two-way interactions. The same process occurred for significant housing variables with confinement type also included (total confinement, <4 h outside access, ≥4 h outside access, or exclusively pasture). Backward stepwise elimination was used to eliminate nonsignificant interactions ($P > 0.05$). In the housing model, state ($P < 0.01$) and confinement type ($P < 0.04$) were significantly associated with SCS. Herds in Kentucky (4.33) and Virginia (4.43) had a lower SCS than Mississippi (4.84) and Tennessee (4.70; $P < 0.02$) herds. Total confinement herds had a lower SCS than herds with outside access (4.23, 4.67, 4.51, and 4.71 for total confinement, <4 h outside, ≥4 h outside, and exclusively pastured herds, respectively; $P < 0.03$). Nonsignificant variables included herd size, alley scraping frequency, fan availability, sprinkler availability, year of last housing renovation, and all interactions. In the farm demographic model, state ($P < 0.01$), age ($P < 0.01$), and plans to be in business in 5 yr ($P = 0.02$) were significantly associated with SCS. Producers ≥66 yr old managed herds with higher SCS compared with all other age groups (4.43, 4.38, 4.56, 4.45, 4.58, and 5.06 for <26, 26 to 35, 36 to 45, 46 to 55, 56 to 65, and ≥66 yr old, respectively; $P < 0.01$). Producers responding that they were "almost certainly" going to be in business in 5 yr had lower SCS than producers responding they were "very likely" to be in business in the same time frame (4.38 and 4.72, respectively; $P < 0.01$). Nonsignificant variables included herd size, regularly scheduled veterinarian visits, producer education level, plans to be in business in 10 yr, and all interactions. These results suggest both housing and demographics are associated with SCS in the southeastern United States.

Key Words: management, mastitis, Southeast Quality Milk Initiative

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0762 Feeding low crude protein diets in lactating dairy cows during summer months: 1. Improvements in milk production and nitrogen utilization. J. Kaufman*, K. Kassube, and A. G. Rius, *The University of Tennessee, Knoxville*.

Heat stress increases protein catabolism and urinary nitrogen excretion resulting in reduced nitrogen-use efficiency (NUE) in livestock. Feeding low CP diets may improve performance of lactating dairy cows during summer. A study was conducted to evaluate the effect of feeding low RDP and RUP levels in cows during summer. Forty-eight midlactation Holstein cows were assigned to treatments using a complete randomized block design in a 2 × 2 factorial arrangement of treatments (n = 12/treatment). Treatments included two levels of RDP (10 and 8%) and two levels of RUP (8 and 6%). A common diet (10% RDP and 8% RUP) was fed from d 1 to 21 followed by the respective treatment diets from d 22 to 42. Milk samples were collected from d 36 to 42. Cows were housed in a freestall barn and exposed to the prevailing temperature and humidity of July and August with no supplemental cooling. Main effects and their interaction were tested using the Mixed procedure of SAS and reported as least squares means ± SEM. Rectal temperatures and respiration rates were recorded before noon and after noon during the treatments. Compare with before noon, after noon increased temperature and respiration rates (38.9–39.7 ± 0.07°C [$P < 0.001$] and 64.0–87.1 ± 1.4 breaths/min [$P < 0.001$]). Compared with the 10% RDP, the 8% RDP treatment increased DMI and milk protein yield in the 6% RUP treatment (19.0 vs. 18.4 ± 0.32 kg/d and 1.02 vs.

0.96 ± 0.02 kg/d) but decreased DMI and milk protein yield in the 8% RUP treatment (19.4 vs. 20.1 ± 0.32 kg/d [interaction, $P < 0.01$] and 1.02 vs. 1.08 ± 0.02 kg/d [interaction, $P < 0.01$]). There was a trend ($P < 0.07$) for an interaction such that the 8% RDP treatment increased energy-corrected milk (ECM) yield compared with 10% RDP in the 6% RUP treatment (31.7 vs. 29.4 ± 0.76 kg/d) but reduced ECM yield in the 8% RUP treatment (32.5 vs. 33.0 ± 0.76 kg/d). The 10% RDP treatment increased ($P < 0.001$) milk-urea nitrogen compared with the 8% RDP treatment (10.2 vs. 6.9 ± 0.28 mg/dL). The 8% RUP treatment increased ($P < 0.001$) milk-urea nitrogen compared with the 6% RUP treatment (9.8 vs. 7.2 ± 0.28 mg/dL). The 8% RDP treatment increased ($P < 0.001$) NUE compared with 10% RDP (35.1 vs. 31.6 ± 0.76%). The 6% RUP treatment increased ($P < 0.001$) NUE compared with 8% RUP (35.1 vs. 31.6 ± 0.76%). Therefore, lower RDP diets can be fed with 6% RUP diets without compromising milk production, whereas the combination of low RDP with 8% RUP depressed productivity. Lower RDP and RUP diets increase NUE in heat-stressed cows.

Key Words: crude protein, nitrogen-use efficiency, heat stress

0763 Influence of a bovine respiratory disease complex vaccine with a modified live virus or KV infectious bovine rhinotracheitis component on estrous cycle parameters and anti-Müllerian hormone concentration in nulliparous heifers.

C. L. Widener*, D. J. Hurley, W. M. Graves, A. H. Nelson, D. A. L. Lourenco, and J. F. Bohlen, *University of Georgia, Athens*.

The objective of this study was to examine the impact of a bovine respiratory disease complex (BRDC) vaccine with a modified live virus (MLV) infectious bovine rhinotracheitis (IBR) component on estrous cycle parameters and the follicular pool. Twenty-four Holstein heifers (mean 12.4 mo [SD 0.5]) in two replicates (spring, $n = 10$, and fall, $n = 14$) were synchronized for estrus using a 7-d CIDR protocol with 2 injections of PGF_{2a}, one at CIDR removal and a follow-up injection 16 h later. Heifers were calf-hood vaccinated with an IBR MLV. Heifers were observed for one complete estrous cycle to establish normal cyclicity. At Heat 2, heifers were vaccinated with either the calf-hood MLV (MLV; $n = 12$) or a BRDC vaccine with a killed (K; $n = 12$) IBR component. Heifers were blocked into treatment groups according to prevaccination bovine viral diarrhea virus (BVDV) serum neutralizing titers. Heifers were then tracked for two complete estrous cycles. Serum samples for estradiol (E2) and progesterone (P4) and ultrasound of ovarian structures were collected to track cyclicity every other day. Serum samples for anti-Müllerian hormone (AMH) were collected at estrus and mid cycle to evaluate the follicular pool. Data was normalized with ovulation as Day 0. Data were analyzed with the PROC MIXED procedure of SAS with cycle number, season, and vaccine as fixed effects. The model for P4 analysis added day of cycle as a fixed effect. There was no difference ($P > 0.05$) in postvaccination titers. Vaccination had no impact on P4 concentrations, luteal tissue area, peak E2 production, or estrous cycle lengths ($P > 0.05$). Overall variables that affected AMH concentrations were season (spring = 138.92 ± 43.1 pg/mL; $P = 0.0043$), vaccine type (MLV = −92.4 ± 42.9 pg/mL; $P = 0.0435$), and cycle number ($P < 0.0001$). Anti-Müllerian hormone concentration decreased between cycles 1 and 2 and cycles 1 and 3 for MLV vaccinated heifers ($P < 0.0003$). Anti-Müllerian hormone concentrations of cycle 2 were numerically lower between vaccine types (K = 308.22 ± 33.3 pg/mL and MLV = 181.13 ± 32.9 pg/mL; $P = 0.0953$), although not statistically different. This may be due to low animal numbers, the variability between animals, or the differences observed in the Fall killed vaccine (−70.93 ± 21.1 pg/mL; $P = 0.0145$) from cycle 1 to 2 but not in the Spring killed vaccine (3.40 ± 45.1 pg/mL; $P = 0.9969$). Anti-Müllerian hormone was weakly correlated with small follicle count ($r^2 = 0.15$, $P < 0.0001$). Although no differences were seen in overall cycle parameters, these differences in AMH concentrations may indicate a reduction of the follicular pool as a result of vaccination with an IBR MLV.

Key Words: infectious bovine rhinotracheitis modified live virus, cyclicity, anti-Müllerian hormone

GROWTH AND DEVELOPMENT

0764 Functional characterization of porcine SCD1 in stably transduced porcine SK6 cells.

J. Hwang*, N. Singh, C. Long, and S. B. Smith, *Texas A&M University, College Station*.

Fatty acid composition is an important component of foods derived from livestock species, as it contributes to both the healthfulness and the functionality of beef, lamb, pork, and dairy products. The most highly regulated and most abundant fatty acid in animal tissues and dairy products is oleic acid (18:1*n*-9). Oleic acid is synthesized by the Δ9 desaturase, stearoyl CoA desaturase (SCD1), which also is responsible for the synthesis of the putative cytokine palmitoleic acid (16:1*n*-7) and *cis*-9, *trans*-11 CLA. Owing to the importance of SCD1 in lipid metabolism, we generated a porcine SK6 transgenic cell lines for sustained overexpression or knockdown of pSCD1 in an inducible manner by using a novel All-in-One Tet-On Lentiviral expression system. We combined the inducible transcriptional activator (tetracycline-controlled transactivator protein) vector and the vector encoding the pSCD1 gene under the influence of a tetracycline-responsive promoter element into one to generate an inducible all-in-one lentiviral vector system. The cell culture models were validated for expression and functionality of pSCD1 by documenting that

the pSCD1 transformed cells overexpressed pSCD1 protein and mRNA over 1,000-fold ($P < 0.0001$). Similarly, an SCD1 shRNA designed to inhibit SCD1 gene expression decreased pSCD1 mRNA and pSCD1 protein expression levels by over 75% ($P < 0.001$). The pSCD1-transformed cells increased the synthesis of palmitoleic acid nearly 4-fold ($P < 0.05$), which was almost completely abolished when SK6 cells were transfected with the SCD1 shRNA. These results indicate that the lentiviral constructs used in this study can be further used to document the regulation of lipid metabolism by SCD1 in pigs.

Key Words: stearoyl-CoA desaturase-1, SK6 kidney cells, transfection, palmitoleic acid

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0765 Gene expression profiling and fatty acid composition in muscle during growth of Yanbian Yellow Cattle. X. Li*[1], C. Yan[1], S. Choi[2], J. Shin[3], and S. B. Smith[4], *[1]Yanbian University, Yanji, P. R. China, [2]Chungbuk National University, Chengju, the Republic of Korea, [3]Kongwon National University, Chuncheon, the Republic of Korea, [4]Texas A&M University, College Station*.

We hypothesized that gene expression and fatty acid composition would differ among different muscle depots and over time on a finishing diet. The present study was conducted with 16 Yanbian Yellow cattle steers (approximately 8 mo of age). Yanbian Yellow cattle are genetically similar to Korean Hanwoo and Japanese Wagyu cattle. Steers were fed a corn-based diet and were randomly assigned to 4 sampling groups. Five consecutive biopsy samples were taken from the chuck, loin, and round muscle at age 12, 16, 20, and 24 mo. Fat content in each muscle increased from 12 to 24 mo of age and the order of fat content in muscles was loin > round > chuck at 12, 16, 20, and 24 mo of age. There were significant differences in the concentrations of stearic acid (18:0), oleic acid (18:1*n*-9), linoleic acid (18:2*n*-6), SFA, MUFA, and the MUFA:SFA ratios with age. At the earliest sampling period, muscle lipids had low MUFA:SFA ratios (0.9 to 1.1), and the muscle lipid MUFA:SFA ratios were highest at 24 mo of age (1.29 to 1.41). There were significant depot effects for stearic acid, linoleic acid, SFA, MUFA, PUFA, and the MUFA:SFA ratio across muscles. Expression of *SREBP1*, *A-FABP*, *SCD1*, *ACC*, and *LPL* in the muscle biopsy samples increased with age, whereas the expression of *PPARγ* and *FAS* decreased with age ($P < 0.05$). The presence of adipogenic gene expression indicated that the muscle biopsy samples also contained intramuscular adipose tissue. Between 12 and 24 mo of age, stearic acid decreased from approximately 16 to 10%, whereas oleic acid increased from approximately 34 to 45% of total muscle fatty acids. Correspondingly, *SCD1* gene expression increased approximately 4-fold between 12 and 24 mo of age. There also were significant muscle main effects for gene expression. Gene expression in biopsies from the loin exhibited the highest expression of all adipogenic genes included in this study; conversely, samples from the chuck had the lowest adipogenic gene expression ($P < 0.05$ for all genes). These results were consistent with loin biopsy samples having the highest fat content. The findings of this study support our hypothesis that adipogenic gene expression varies across muscles and across time on feed and provide novel information about the development and composition of marbling in Yanbian Yellow cattle.

Key Words: Yanbian Yellow cattle, fatty acids, gene expression

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0766 α-Chaconine induces myogenesis of bovine satellite cells isolated from semimembranosus and longissimus muscle tissue. K. Y. Chung*, S. C. Jang, E. M. Lee, S. H. Yang, and E. G. Kwon, *Hanwoo Research Institute, NIAS, RDA, Pyeongchang, the Republic of Korea*.

α-Chaconine is a steroidal glycoalkaloid that found in leaves, fruit, and tubers of the solanaceae family such as potato, tomato, and eggplant. Alkaloid poisoning of potato plant was reported in various animal models such as mice, rabbit, and chicken. However, it is also used as a treatment for human asthma. Some medicine used for treating human asthma has been used to induce myogenesis of bovine skeletal muscle. We hypothesized that α-chaconine may affect myogenesis of bovine satellite cells isolated from different muscle depots. Bovine satellite cells were pronase-liberated from semimembranosus (SM) and longissimus dorsi (LD) muscle tissues of three newborn Hanwoo calves. Bovine SM and LD satellite cells were incubated with Dulbecco's modified Eagle medium (DMEM) with 10% fetal bovine serum for proliferation and induced differentiation with DMEM with 3% horse serum. Bovine satellite cells were treated with various levels of α-chaconine (control and 0.001, 0.01, 0.1, 1, and 10 μ*M*). Messenger RNA abundance for myosin heavy chain 1 (MHC1), MHC2X, glucose transporter 4 (GLUT4), myogenin, G-coupled protein receptor 43 (GPR43), and β2-adrenergic receptor (β2-AR) were measured by real-time quantitative PCR. Data were analyzed as a completely randomized design using the MIXED model, with each treatment performed in triplicated. Means were considered different at $P < 0.05$. Relative MHC2X mRNA abundance was increased at dose-dependent levels in both SM and LD satellite cells with α-chaconine treatments compared with the control ($P < 0.05$). However, MHC2X and GLUT4 levels were decreased in 10 μ*M* treatments ($P < 0.05$). Relative level of MHC2X and β2-AR were greater in LD satellite cell compared with SM satellite cells ($P < 0.05$). There was no tissue × dose interaction among MHC1 mRNA concentration ($P > 0.05$). These results indicated that α-chaconine has a dose-dependent effect on MHC2X mRNA but did not affect to MHC1 mRNA in bovine satellite cells.

Key Words: α-chaconine, Hanwoo, semimembranosus, longissmus dorsi, satellite cells

0767 Vitamin C supplement increased intramuscular adipose tissues but not affect myogenic development of Hanwoo steers. S. C. Jang, K. Y. Chung*, E. M. Lee, S. H. Yang, and E. G. Kwon, *Hanwoo Research Institute, NIAS, RDA, Pyeongchang, the Republic of Korea*.

Vitamin C (VC) supplements have been used for enhancing marbling fat in high-quality beef cattle. However, mode of action of vitamin C was not clearly studied for long time. The aim of this experiment was to determine the effect of additional saturated parm-oil coated VC supplement compare to a control diet (saturated parm-oil only) on the level of adipogenic and myogenic gene expressions at liver (LV), subcutaneous adipose tissue (SC), perirenal adipose tissue (PR), and longissimus dorsi muscle (LD). A 2 × 4 factorial arrangement (control, VC, and LV, SC, PR, and LD tissues) was used to feed 10 Hanwoo steers. Two steers were fed in same pen and 5 pens were used for treatment. Tissues were collected within 10 min of harvest for analysis of PPARγ, SCD, GLUT4, MHC1, MHC2X, and GPR43 mRNA abundance. Real-time RT-PCR was used to measure the quantity of respective mRNA relative to a ribosomal protein subunit 9 (RPS9) mRNA. Data were analyzed as a completely randomized design using the MIXED model. Difference between the control and treatments were determined using the LSD procedure. Overall ADG did not differ between VC supplement and the control ($P > 0.05$). Marbling score was greater in the VC treatment than in the control ($P < 0.05$). Lipid percentage tended to greater ($P = 0.084$) in the VC treatment but share force tended to be lower in the VC treatment ($P = 0.068$). Real-time quantitative PCR revealed that the mRNA content of SCD in PR from VC supplement cattle increased ($P < 0.05$) compared with the control. There was no mRNA effect at MUS in cattle. However, mRNA level of GLUT4 and GPR43 were increased at LV tissues in VC-treated cattle ($P > 0.05$). These data indicated that VC supplement increased relative mRNA level of GLUT4 and SCD in SC and LV tissue but not affect myogenic gene expression on final fattening periods of Hanwoo steers.

Key Words: Hanwoo, adipogenic, myogenic, |gene expression

0768 Chromium propionate supplementation alters feedlot performance and GLUT4 activity in feedlot steers. J. O. Baggerman*[1], Z. K. F. Smith[1], A. J. Thompson[1], J. Kim[1], P. W. Rounds[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Kemin Industries, Inc., Des Moines, IA*.

The objective was to evaluate the effects of increasing concentrations of chromium propionate (CrP) on feedlot performance, blood parameters, carcass characteristics, and skeletal muscle changes over time in feedlot steers. Crossbred steers ($n = 32$, 16 pens, 2 hd/pen) were blocked by BW, and each pen was randomly assigned to one of four treatments: control, 150 ppb supplemental CrP (KemTRACE Chromium, 0.04%; Kemin Industries, Des Moines, IA), 300 ppb supplemental CrP, and 450 ppb supplemental CrP. Steers were fed 1x daily ad libitum a steam-flaked corn–based diet, and the treatment was top-dressed at the time of feeding. Body weights, blood samples, and skeletal muscle biopsies were collected before time of feeding on d 0, 28, 56, 91, 119, and 147. Blood sera were harvested for analysis of glucose, insulin, serum urea nitrogen, and NEFA concentrations. Skeletal muscle biopsy samples were used for immunohistochemical analysis. Data was analyzed using the GLIMMIX procedure of SAS 9.4, with pen as the experimental unit for live and carcass data and steer as the experimental unit with day as a repeated measure for laboratory analysis. Starting on d 56 through the end of the trial, cattle fed the 450-ppb treatment were the heaviest ($P < 0.05$). A linear effect ($P < 0.05$) of treatment on BW and ADG was observed starting on d 56 until the end of the trial. For HCW, there was also a linear effect of treatment, with the greatest HCW in the cattle fed the 450-ppb treatment ($P < 0.05$). There was no effect of treatment on any blood parameter measured ($P > 0.05$). For skeletal muscle fiber cross-sectional area, there was a treatment × day interaction ($P < 0.05$), with the greatest increase in the 450-ppb treatment group. Density of total GLUT4 decreased over time for all treatments ($P < 0.05$), with the treatments receiving CrP having less of a decrease than the control group ($P < 0.05$). Internalization of GLUT4 was increased in the 300-ppb and 450-ppb treatments ($P < 0.05$). For total nuclei density and myonuclei density, there were treatment × day interactions ($P < 0.05$), where the 450-ppb treatment exhibited a greater density of total nuclei and myonuclei on d 147. These results indicated supplementation of 450 ppb CrP increases HCW, possibly due to changes in GLUT4 activity in skeletal muscle.

Key Words: beef cattle, growth, muscle

0769 Feeding five percent grass hay or wheat straw with high-starch, textured diets to weaned dairy calves between eight and sixteen weeks of age. F. X. Suarez-Mena*, T. S. Dennis, T. M. Hill, J. D. Quigley, and R. L. Schlotterbeck, *Provimi, Brookville, OH*.

This research had the objective to determine if changing diet forage fiber concentration by feeding different forages affected BW gain and structural growth of dairy calves from 8 to 16 wk of age. Male Holstein calves (24 per treatment in 6 pens with 4 calves/pen) initially 76 ± 1.6 kg BW were fed a common, textured grain-based concentrate (95% of the total mixed ration; 37% whole corn, 25% whole oats, 35% protein supplement pellet, and 3% molasses; 22% CP, 40% starch, 9% ADF, and 16% NDF) with either 5% chopped grass hay (13% CP, 40% ADF, and 67% NDF) or 5% chopped wheat straw

(2% CP, 48% ADF, and 80% NDF). During the previous nursery phase, calves were fed 0.66 kg DM from milk replacer (25% CP and 17% fat) and weaned at 42 d. Calves were also fed a similar textured, grain-based concentrate and water ad libitum. Calves remained in the nursery after weaning for 14 d. Calves were weighed and scored for body condition, and hip widths were measured initially (8 wk) and at 12 and 16 wk (periods 1 and 2; 56-d trial). Body condition score was a 5-point system (1 being thin and 5 being obese). Treatments were analyzed as a completely randomized design with repeated measurements. Initial BW, hip width, and BCS did not differ ($P > 0.10$) among treatments. The hay diet contained 3.3% NDF from forage whereas the straw diet contained 4.0% NDF from forage. There tended ($P < 0.09$) to be an interaction of treatment with 4-wk period for DMI as a percent of BW (2.87 vs. 2.76% BW in period 1 and 2.87 vs. 2.93% BW in period 2 for hay vs. straw, respectively), but there were no interactions ($P > 0.10$) for other measurements. Overall BW gain tended ($P < 0.07$) to be greater for calves fed hay vs. straw (1.04 vs. 0.97 kg/d). Change in hip width (5.0 vs. 4.6 cm) and feed efficiency (0.350 vs. 0.334 BW gain/feed) were greater ($P < 0.05$) for calves fed hay vs. straw. Change in BCS was 0.5 points for each treatment. These results further suggest that BW and structural growth in Holstein calves less than 16 wk of age is very sensitive to forage fiber concentration.

Key Words: forage, calves, growth

0770 Effects of a milk balancer protein supplement on growth and performance of dairy calves.

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In Argentina, dairy calves are commonly fed 4 L/d of milk plus starter pelleted feed containing 20% of CP during the first 8 wk of life. The objective of the study was to evaluate the effect of a milk balancer protein supplement on growth and performance of dairy calves during the first 30 d of this period. Fourteen newborn calves were randomly assigned to one of two treatments: 1) control (fed 4 L/d of raw milk) and 2) supplement (SUP; fed 4 L/d of raw milk and 0.2 kg/d of supplement). All calves had access to water and were individually offered starter feed. Body weight and body measurements (withers and hip height, thoracic diameter, and body length) were taken weekly and every 2 wk, respectively. Intake of starter feed was calculated daily based on offered and remaining feed, and total DMI was calculated taking into account milk, supplement, and starter feed intake. Milk, starter feed, and milk balancer were sampled weekly and chemically characterized. The data was analyzed as a randomized complete block design and the statistical model included treatment, time (repeated), sex, and interactions. Body measurements and weight at calving were used as a covariate. Compared with the control, calves fed SUP had greater total DMI (0.83 vs. 0.65 kg/d; SEM = 0.04) and thoracic diameter (0.83 vs. 0.85 cm; SEM = 0.01). No effect of supplement was observed on starter intake (0.14 vs. 0.15 kg/d; SEM = 0.05), daily gain (0.51 vs. 0.44 kg/d; SEM = 0.04), feed efficiency (0.61 vs. 0.67; SEM = 0.04), withers (0.80 vs. 0.81; SEM = 0.006) and hip heights (0.83 vs. 0.84; SEM = 0.007), or body length (0.73 vs. 0.73; SEM = 0.007). In conclusion, the use of the milk balancer supplement increased intake but did not significantly improve growth during the first month of age. Considering that under normal conditions, calves lose weight during the first 2 wk, it would be important to carry out a new trial considering the total 8 wk that calves are kept in the calf unit.

Key Words: calves, growth, milk supplement

0771 Effects of *trans*-10, *cis*-12 conjugated linoleic acid on gene expression and lipid content of adipocytes derived from lactating dairy cows.

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The antilipogenic effects of *trans*-10, *cis*-12 CLA are widely reported across monogastric species. However, abomasal infusions of this CLA isomer have been shown to increase expression of lipogenic genes in the adipose of lactating dairy cows. It is not clear if this is a result of energy repartitioning due to a decrease in milk fat synthesis or a direct effect of *trans*-10, *cis*-12 CLA on adipocytes. Our objective was to examine the effects of *trans*-10, *cis*-12 CLA on cultured adipocytes derived from subcutaneous adipose of lactating dairy cows ($n = 4$). Adipose samples were digested with collagenase type II and cells from the stromal vascular fraction were cultured in DMEM/F12 supplemented with 10% fetal bovine serum. Preadipocytes were obtained from outgrowth of plastic adherent cells and seeded in assay plates. After reaching confluence, cells were induced to differentiate and maintained in the plates for 10 d. From d 2 to 10, the medium was supplemented with one of two treatments: 50 μ*M trans*-10, *cis*-12 CLA (T10C12) or 50 μ*M cis*-9, *trans*-11 CLA (C9T11). On d 10, intracellular triglyceride was quantified using an AdipoRed assay and RNA was extracted to analyze gene expression using RT-qPCR. Statistical analysis was performed using linear mixed models. Fold changes (FC) in gene expression are presented relative to the C9T11 treatment. Conjugated linoleic acid supplementation did not affect triglyceride content of the adipocytes ($P = 0.47$), but the ratio of triglyceride content of adipocytes to preadipocytes indicated differentiation occurred in both treatment groups (T10C12 = 60.0 and C9T11 = 55.0). T10C12 decreased expression of the lipogenic genes ACACA (FC = 0.75; $P = 0.01$), ELOVL6 (FC = 0.73; $P = 0.03$), and SCD1 (FC = 0.52; $P = 0.03$). Expression of C/EBPβ, FAS, GAPDH, LPL, and PPARγ were not affected by treatment ($P \geq 0.43$). In contrast to what has been observed in murine-derived 3T3-L1 cells, T10C12 increased the expression of the

fatty acid transport gene FABP4 (FC = 2.06; $P = 0.01$) and tended to increase the expression of DGAT1 (FC = 1.07; $P = 0.06$), which is associated with triglyceride synthesis. Although *trans*-10, *cis*-12 CLA decreased the expression of several lipogenic genes, it did not inhibit lipid accumulation. This suggests that cultured adipocytes derived from dairy cows respond differently to *trans*-10, *cis*-12 CLA than those derived from monogastric species.

Key Words: adipocyte, conjugated linoleic acid, lipogenesis

0772 Effects of maternal exercise on postnatal growth and carcass characteristics of swine.

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Our laboratory has previously reported that pregnant swine allowed to exercise during mid to late gestation have increased umbilical blood flow to the piglets. Our objective was to determine how maternal exercise would impact postnatal growth and carcass parameters of their offspring at 6 mo of age. Yorkshire gilts were paired to either remain in their individual stall from d 40 to term (CON; $n = 4$) or exercise for 30 min 3 times per week from mid to late gestation (EX; $n = 4$). Within 12 h postpartum, litter size was normalized within a pair of gilts. Pigs were weighed monthly. Upon reaching an average BW of 58.1 kg, loin muscle area (LMA) and backfat were obtained every 28 d via ultrasonography. Pigs were harvested at 118 kg with organ masses recorded and carcass composition and meat quality determined. Data were analyzed with sow as the experimental unit. Maternal treatment did not impact ADG or LMA, but there was greater ($P = 0.03$) backfat in female piglets from EX dams compared with CON and male piglets from CON dams compared with EX. Backfat in female-EX and male-CON was similar. Although there were limited organ and muscle mass differences due to maternal treatment, pigs from EX dams had an increased ($P \leq 0.05$) longissimus muscle pH at 24 h (5.36 vs. 5.27 ± 0.03), decreased drip loss (6.31 vs. 4.54 ± 0.48%), and increased L* (55.73 vs. 52.40 ± 0.74) compared with CON. Maternal activity during gestation appears to have limited impacts on gross body measurements but may be advantageous to carcass quality of their offspring. Future studies are needed to confirm that the increased meat quality relates to better pork for consumers.

Key Words: carcass, maternal activity, pigs

0773 The effect of phase feeding on feed cost, growth, and performance of calves fed milk replacer.

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Ninety-six 3- to 10-d-old Holstein bull calves with an average initial BW of 44.1 kg (SD 1.67) were shipped from Wisconsin to the Land O'Lakes Research Facility in northwest Iowa. The objective of this study was to evaluate the use of phase feeding with a milk replacer (MR) containing only milk protein in the first phase and a MR using hydrolyzed soy protein modified (HSPM) in the second phase of calf rearing. Calves were randomly assigned according to BW and blood γ globulin to one of four MR diets offered in a 15% solution: 1) 27% CP containing only milk protein, 10% fat (control); 2) phase feeding, 28% CP, 20% fat in Phase 1 and 22% CP, 15% fat with HSPM in Phase 2; 3) phase feeding, 28% CP, 20% fat in Phase 1 and 25% CP, 15% fat with HSPM in Phase 2; and 4) phase feeding, 28% CP, 20% fat in Phase 1 and 28% CP, 15% fat with HSPM in Phase 2. Calves were fed to provide 816 g DM/d during Days 1 to 6 and 1,135 g DM/d during Days 7 to 41, in 2 feedings at 0600 and 1515 h. Calves were offered 567.5 g in one feeding at 0600 h during the last week. Calf starter (22% CP, as-fed basis) was offered ad libitum throughout this 48-d trial. Data were analyzed by Mixed procedures of SAS. Total weight gain, MR consumption, feed:gain ratio, and starter intake did not differ ($P > 0.05$) among treatments. Total feed costs over the 7-wk trial were significantly lower ($P < 0.05$) for the three phase-feeding treatments. Calves on the three phase-fed diets performed equally to calves on the control-fed diets and the feed costs were significantly reduced, making this a viable option where applicable.

Key Words: calf, milk replacer, phase feeding

0774 The effect of weaning over a fourteen-day versus a twenty-one-day period on the performance of calves fed milk replacer on a controlled ad libitum curve through an automatic feeder.

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Thirty-eight 3- to 10-d-old Holstein bull calves with an average initial BW of 39.2 kg (SD 1.12) were shipped from Wisconsin to the Land O'Lakes Research Facility in northwest Iowa. The objective of this study was to better understand

the impact of weaning period on the performance of calves fed a 26% CP, 20% fat milk replacer (MR) on a controlled ad libitum curve (40FIT Technology, Foerster-Technik, Engen, Germany) through an automatic feeder. Calves were randomly assigned according to BW and blood γ globulin to either a 14-d or a 21-d weaning period. Calves were limited to meal size, but not number of meals, before the start of weaning. Weaning began at either Day 29 (21-d weaning) or Day 36 (14-d weaning), offering 1.65 kg of MR DM on Day 1 of weaning and gradually decreasing MR offering daily to 0.299 kg of MR DM on the day of weaning. Milk replacer was offered in a 13.0% solids solution throughout the 49-d milk feeding phase. All calves were followed for 5 wk after weaning to monitor starter intake and growth. Calf starter (22% CP, as-fed basis) was fed ad libitum throughout this 84-d trial. Data were analyzed by Mixed procedures of SAS. There were no statistical differences ($P > 0.05$) in total BW gain or MR consumption between treatments. Calves fed according to the 21-d weaning period schedule appeared to consume more starter over the 12 wk trial compared with the calves fed according to the 14-d weaning period schedule (140.9 vs. 129.9 kg, respectively); however, due to group feeding of starter and no individual starter intake values, no statistical analysis could be performed. Either a 14-d or 21-d weaning period could be successfully used for calves fed on a controlled ad libitum curve through an automatic feeder.

Key Words: automatic milk replacer feeder, calf, weaning

0775 Effects of maternal dietary restriction during the second trimester on offspring growth and feedlot performance. S. M. Quarnberg*, J. F. Legako, J. M. Gardner, D. R. ZoBell, C. E. Carpenter, K. A. Rood, and K. J. Thornton, *Utah State University, Logan*.

This study determined the impacts of maternal dietary insult during the second trimester on offspring growth and early feedlot performance. Angus-influenced commercial cows ($n = 34$) were naturally bred to a purebred Angus sire. During preparturition, individual cow served as the experimental unit for one-way ANOVA. During 84 d of mid gestation, cows were stratified into two groups, maintenance ($n = 16$) and restricted ($n = 18$), by initial weights ($P = 0.804$) and BCS ($P = 0.723$). Restricted cows were provided with lower forage biomass (1,662 kg/ha, DM) in comparison with maintenance (2,309 kg/ha, DM). Following the insult period, restricted cows had a mean BCS 1.55 lower ($P = 0.001$) than maintenance cows and a BW difference of 85.3 kg ($P = 0.024$). Dams were commingled and uniformly managed following mid gestation. Calves were weaned approximately 215 d of age and placed on a background diet for 7 wks before entering the feedlot phase where calves were kept in individual pens and fed a grower ration ad libitum. Calves BW were measured at birth, weaning, and every 28 d of the feedlot phase. Ultrasound was used for measurement of BF and REA during the feedlot phase. Calf temperament was evaluated at weaning and during the feedlot phase. Serum glucose, insulin, IGF-1, and cortisol were determined for calves at weaning, 1 wk before the feedlot phase, and the last day of the feeding trial. One-way ANOVA was used to determine impacts of fetal programming on calves. Individual calf served as the experimental unit. Calf BW at birth, weaning, and during feeding showed no differences ($P \geq 0.245$). No differences were determined for ADFI ($P \geq 0.428$), ADG ($P \geq 0.338$), G:F ($P \geq 0.273$), REA ($P \geq 0.285$), or BF ($P \geq 0.416$) during the feedlot stage. Concentrations of glucose ($P \geq 0.504$), insulin ($P \geq 0.224$), IGF-1 ($P \geq 0.107$), and cortisol ($P \geq 0.709$) were found to be similar at all time points. Restricted calves were found to be more excitable, with greater temperament scores at weaning ($P = 0.026$). Recent work has indicated that fetal programming alters progeny carcass characteristics. However, concerns for negative impacts on performance of progeny exist. This study determined little impact on calf performance during early feedlot stages.

Key Words: feedlot performance, fetal programming, temperament

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0776 Neonate immunity, growth, and puberty in dairy calves: Influence of dietary conjugated linoleic acid supplementation of the dam. C. L. Cardoso*[1], D. Somwe[2], and G. Esposito[3,4], *[1]Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Pretoria, South Africa, [2]Department of Animal and Wildlife Science, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa, [3]Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Pretoria, South Africa, [4]Institute of Food, Nutrition and Well-Being, University of Pretoria, Pretoria, South Africa*.

Colostrum provides the calf with maturational, immune-modulatory, and antimicrobial factors. Feeding isomers of CLA reportedly increase immunoglobulin production in rats and circulating IGF-I levels in cows. The objective of the study was to evaluate the effect of CLA dietary supplementation of the dam on colostrum quality, calves immune system, growth, and attainment of puberty. Forty Holstein cows blocked by parity, BW, and BCS were randomly assigned to two groups: control (CTL; 100 g/cow per day of Ca salts) and CLA (100 g/cow per day of CLA). Individual top-dressed supplementation started 20 ± 7 d before calving until 35 d in milk. From Day 0 to 4, each calf was fed its mother's colostrum. The latter was sampled for IgG quantification. Calves were bled every other day from 0 to 15 d for IgG and total protein (TP) levels. Weekly, from Day 0 to 35, body measurements and weight were recorded for growth rate; furthermore, calves were bled

for GH and IGF-I quantification. Attainment of puberty was monitored from the age of 180 d. Monthly, body measurements and weight were recorded. Semen collection by electroejaculation was performed in males with scrotal circumference ≥23 cm for semen parameters evaluation (volume, color, mass/individual motility, and concentration). Puberty was declared with concentration of 50 million spermatozoa/ejaculate with at least 10% progressive motility. Females were bled fortnightly for progesterone levels, whereas ovarian activity was monitored by ultrasonography. Puberty was attained with progesterone levels ≥1 ng/mL and the presence of a corpus luteum. Growth rate, blood, and colostrum parameters were analyzed by ANOVA for repeated measures using the GLM procedure. Age at puberty was compared by one-way ANOVA. No differences between groups were observed for blood and colostrum IgG levels, blood GH levels, and attainment of puberty. Treatment showed decreased levels of IGF-I ($P < 0.05$) compared with the control. A trend for higher TP levels (treatment × age, $P = 0.079$) and overall ADG ($P = 0.1$), calculated from Day 0 to 300, was observed in CLA calves. However, from Day 0 to 35, growth rate was significantly higher in CLA females (treatment × age, $P < 0.05$) and lower in CLA males (treatment, $P < 0.05$) compared with the CTL. These differences were not observed from 180 to 300 d. Colostrum from CLA supplemented dams showed a gender and time-dependant effect on calf's growth; however, it did not alter immune response and attainment of puberty. Further investigation is needed to unveil CLA's possible mechanism of action.

Key Words: conjugated linoleic acid, growth, immunoglobulin G

0777 Repeatability of residual feed intake and indices of body composition in growing Columbia ewes fed the same diet. K. A. Perz*, J. G. Berardinelli, L. N. Park, R. K. Pollard, C. M. Page, W. C. Stewart, and J. M. Thomson, *Montana State University, Bozeman*.

Residual feed intake (RFI), an efficiency measurement based on the difference in expected feed intake for a given weight and growth rate and actual feed intake, is used to improve production efficiency of domestic ruminants. The purpose of this study was to evaluate the repeatability of RFI of sheep measured for two consecutive years and to investigate the relationship between indices of body composition and RFI in yearling ewes. Two trials, using the same Columbia ewe lambs ($n = 17$ per trial), were conducted in consecutive years. Ewes were individually fed for 47 and 45 d, respectively, beginning in September of each year. The diet, an alfalfa–barley pellet, was the same composition and batch for both years. Residual feed intake was calculated for each ewe in each year. Ewe was the experimental unit. Residual feed intake and performance data were analyzed using ANOVA. Residual feed intake did not differ ($P > 0.05$) between years, indicating that on the same diet and environmental conditions, RFI does not appear to change with age. Ewes were categorized into 3 RFI classes (efficient, average, and inefficient) based on RFI values 1 SD below and above the yearly average. In 2014, initial and final liveweights, ADG, and DMI did not differ due to RFI classification ($P > 0.05$). In 2015, DMI was greater for inefficient ewes ($P < 0.05$), but there was no difference in initial and final liveweights or ADG ($P > 0.05$). Ultrasound data were analyzed using ANOVA with repeated measures. Rib eye area (REA; cm^2) and backfat thickness (BF; cm) were measured by ultrasound on Day 0, 17, and 45 in 2015. These variables were used to calculate estimates of final body composition: whole-body muscle mass, intramuscular fat, empty BW, empty BW DM, empty BW fat, empty BW protein, carcass weight, carcass weight DM, carcass weight fat, and carcass weight protein. Residual feed intake classification did not affect REA or BF ($P > 0.05$). Regression analysis indicated that both REA and BF increased ($P < 0.05$) from Day 0 to 17 and BF increased ($P < 0.05$) again from Day 17 to 45. No body composition estimates were affected by RFI classification ($P < 0.05$). Results suggest that RFI is repeatable; however, indices of body composition seem to be independent of RFI in Columbia ewes fed the same diet under similar conditions.

Key Words: residual feed intake, repeatability, body composition

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0778 A new view on the growth of pigs in relation to frequent body weight monitoring. A. H. Stygar*[1], K. A. Dolecheck[2], and A. R. Kristensen[1], [1]*University of Copenhagen, Department of Large Animal Sciences, Frederiksberg, Denmark,* [2]*University of Kentucky, Lexington*.

Frequent BW monitoring of growing pigs can be useful for identifying production (e.g., feeding), health, and welfare problems. However, to construct a tool that will properly recognize abnormalities in pigs' growth, a precise description of the growth process should be used. In this study, we proposed a new model of pig growth accounting for daily fluctuations in BW. Data on BW measurements of 1,710 pigs (865 gilts and 843 barrows) originating from 5 consecutive batches from one Danish commercial farm was collected. Pigs were inserted into a large pen (maximum capacity = 400) between November 2014 and September 2015. On average, each pig was observed for 42 d and weighed 3.6 times a day when passing from the resting to the feeding area. Altogether, 243,160 BW measurements were recorded. To properly account for the diurnal pattern, the time of BW measurements was corrected for daylight saving time. A multilevel model of pig growth was constructed and fitted to available data. The BW of pigs was modeled as a quadratic function of time. A diurnal pattern was incorporated into the model by a cosine wave with known length (24 h). The model included pig effect, which was defined as a random autoregressive process

with exponential correlation. Variance of within-pigs error was assumed to increase with time. The intercept, time, square value for time, and cosine wave were significant fixed effects ($P < 0.0001$). Additionally, the interaction between these fixed effect elements and each batch was determined to be significant ($P < 0.0001$). The gender effect was not significant and was removed from the final model ($P = 0.52$). According to results, pigs were lighter in the morning and heavier in the evening (the minimum BW was obtained around 1000 h and the maximum was obtained around 2200 h). However, the exact time of obtaining maximum and minimum BW during the day differed between batches. Pigs had access to natural light, and therefore, existing differences could be explained by varying daylight level during observation periods. Because the diurnal amplitude for pig growth ranged between batches from 0.9 to 1.4 kg, BW monitoring tools based on frequent measurements should account for diurnal variation in BW of pigs. This proposed description of growth was built into a monitoring tool (a dynamic linear model) consisting of an updating, forecasting, and filtering procedure. The constructed monitoring tool will be applied to farm data in future studies.

Key Words: body weight, pigs, diurnal pattern

0779 Effect of prior fiber consumption on diet-induced obesity susceptibility and metabolic health indicators in Ossabaw pigs. V. V. Almeida[1] and K. M. Ajuwon*[2], [1]*Purdue University, West Lafayette, IN,* [2]*Department of Animal Sciences, Purdue University, West Lafayette, IN*.

Sixty-three mixed-sex pigs (28 d of age and 5.63 ± 0.20 kg BW) were used to evaluate the effects of dietary fiber source and fat level on growth performance, backfat thickness (BF), and metabolic status. Pigs were blocked by BW and allotted by sex and litter to 1 of 4 treatments with 8 pens per treatment and 2 pigs per pen. Treatments were arranged in 2 × 2 factorial with 2 fiber sources (inulin and cellulose) and 2 fat levels (5 and 15%, as-fed basis, for the low-fat diet [LF] and high-fat diet [HF], respectively). Pigs received diets containing 4% of either inulin or cellulose on an as-fed basis for the first 56 d (nursery phase) and thereafter were fed LF and HF containing no added fiber source from d 56 to 140 (growing phase). On d 140, BF was measured by ultrasound and jugular blood samples were taken for insulin, glucose, and triglyceride (TAG) analyses. Data were analyzed using the MIXED procedure of SAS. There were fiber × fat interactions for final BW ($P = 0.02$) and G:F ($P = 0.01$), as pigs receiving cellulose had greater ($P < 0.05$) final BW (63.96 and 70.31 ± 1.15 kg for LF and HF, respectively) and G:F (0.136 and 0.157 ± 0.003 for LF and HF, respectively) when fed HF diet than pigs fed LF. Feeding HF, regardless of fiber source, tended to increase ADG (0.432 and 0.464 ± 0.01 kg for LF and HF, respectively; $P = 0.07$) and reduce ADFI (3.184 and 3.013 ± 0.05 kg for LF and HF, respectively; $P = 0.07$). Moreover, HF, regardless of fiber source, resulted in higher BF (13.41 and 18.18 ± 0.12 mm for LF and HF, respectively; $P < 0.01$). There was a tendency for a fiber × fat interaction ($P = 0.07$) for serum TAG concentration, as pigs receiving cellulose had greater serum TAG (0.264 and 0.392 ± 0.02 mg/mL for LF and HF, respectively; $P < 0.05$) when fed HF than pigs fed LF. Pigs fed HF, regardless of fiber source, had greater ($P < 0.01$) insulin (0.014 and 0.016 ± 0.001 mg/L for LF and HF, respectively) and glucose (100.89 and 125.03 ± 4.39 mg/dL for LF and HF, respectively) concentrations in the serum. In summary, dietary cellulose inclusion during the early life of pigs increased susceptibility to obesity and metabolic syndrome in the future, whereas dietary inulin inclusion prevented future metabolic disorders.

Key Words: early nutrition, fiber metabolic disorders, pig model

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0780 Body composition at first heat of gilts exposed to three different feeding regimens. S. Van Vliet[1], T. S. Bruun[2], J. Hales[3], C. F. Hansen[3], and P. K. Theil*[1], [1]*Aarhus University, DK-8830 Tjele, Denmark,* [2]*SEGES Pig Research Centre, 1609 Copenhagen V, Denmark,* [3]*University of Copenhagen, DK-1870 Fredriksberg C, Denmark*.

This study was conducted to evaluate the possibility of increasing body fatness of gilts by nutritional means during rearing. Forty-eight gilts (Danish Landrace × Yorkshire [LY]) with an initial BM of 62 ± 2 kg were selected from 16 litters (3 littermates from each).Gilts were fed individually with one of three diets from 62 to 105 kg LW and then transferred to diets lower in CP and Lys. Littermates stratified for BM were randomly allocated to one of three dietary regimens: low protein ad libitum (LPAD) (4.3/3.5 g SID Lys/kg feed), moderate protein restriction (MPRE) (5.4/4.3 g SID Lys/kg feed), or high protein ad libitum (HPAD) (7.0/5.4 g SID Lys/kg feed). The experiment was designed to limit growth by lysine (LPAD), energy (MPRE), or the growth potential of gilts (HPAD). Body water content was measured using the deuterium oxide dilution technique before the dietary intervention were initiated ($n = 9$) and at first heat ($n = 47$). Body contents of fat, protein, and ash were calculated using prediction equations developed for LY gilts by Rozeboom and coworkers and back fat depth was measured at the P2 site. Statistical analysis of fixed effect of treatment was performed using a mixed model to account for repeated measurements. Initially, no differences were observed in body water content or derived contents of fat, protein, or ash ($P > 0.20$). On average, gilts initially contained 61.2% water, 11.2% fat, 17.9% protein, and 3.4% ash. At first heat, the measured water content was lowest in LPAD, highest in MPRE, and intermediate in HPAD gilts ($P < 0.001$), whereas the body fat content was changed inversely, as LPAD (26.6%), MPRE (23.1%), and HPAD gilts (25.3%) had highest, lowest, and intermediate body fat contents ($P < 0.001$), respectively. The

protein and ash contents were lowest ($P < 0.001$) in LPAD fed gilts (15.5 and 2.8%, respectively), highest in MPRE fed gilts (16.1 and 3.0%, respectively), and intermediate in HPAD fed gilts (15.8 and 2.9%, respectively). The change in body fatness was supported by measurements of back fat depth, which at first heat was highest ($P < 0.001$) in LPAD gilts (15.1 mm), lowest in MPRE gilts (11.8 mm), and intermediate in HPAD sows (14.3 mm). In conclusion, body fatness of gilts can be considerably increased through dietary means even in breeds that thoroughly have been genetically selected for leanness.

Key Words: body condition, body fatness, dietary composition, gilt rearing, growth performance

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0781 Preweaning diet and exogenous estrogen alter mammary epithelial cell proliferation and progesterone and estrogen receptor expression.

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Preweaning diet and estrogen treatment alters mammary development. Our objectives were to study the effects of diet and estrogen on mammary histology, proliferation, and expression of estrogen (ESR1) and progesterone (PR) receptors. Thirty-six Holstein heifer calves were reared on 1) a control milk replacer (MR) fed at 454 g powder/d (R; 20% CP and 20% fat) or 2) an enhanced MR fed at 1,135 g powder/d (E; 28% CP and 25% fat). Milk replacer was fed for 8 wk. At weaning, a subset of calves were sacrificed ($n = 6$/diet). Remaining calves received E_2 implants and were sacrificed at wk 10. Treatments were 1) R, 2) R + E_2 (R-E2), 3) E, and 4) E + E_2 (E-E2). One day before harvest, calves were given bromodeoxyuridine (BrdU; 5 mg/kg). At sacrifice, parenchyma (PAR) was removed and fixed. Sections from lower, middle, and distal zones were stained with H and E and antibodies to measure expression of ESR1, PR, and BrdU. Comparisons with PROC GLIMMIX in SAS on a per-area and per-cell basis were similar. At wk 8, R-fed calves had more ($P < 0.01$) PR-expressing cells in distal PAR. But PR expression intensity was greater ($P < 0.01$) in E-fed calves. The proportion of cells expressing ESR1 was not affected by diet, but expression intensity was increased for E-fed calves across all zones (62 to 81%; $P < 0.01$). Percent BrdU-positive cells was 2- and 0.5-fold greater ($P < 0.01$) for E-fed calves in zone 2 and 3, respectively. At wk 10, calves treated with estrogen had 3.9-fold greater PR expression intensity. The intensity and percent of cells expressing ESR1 was lowest in estrogen-treated calves. Overall, estrogen-treated calves had the most proliferating cells ($P < 0.01$). However, in zone 3, E-E2 calves had a higher percentage of proliferating cells than calves on all other treatments ($P < 0.01$). Results indicate both diet and estrogen administration alter proliferation rates of the mammary epithelium and that changes in expression of ESR1 and PR are at least partially responsible for changes in mammary PAR development associated with enhanced preweaning feeding of dairy calves. However, furthermore, more detailed analyses are needed to fully understand mechanisms at play.

Key Words: estrogen receptor, progesterone receptor, mammary gland

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0782 In vivo knockdown of FGFR2 and MET mRNA in trophectoderm of ovine conceptuses retards their development via abrogation of MAPK and MTOR pathways.

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The paradigm of downregulation of progesterone receptor in uterine epithelia before implantation is common to sheep, cow, pigs, rhesus monkey, women, and mice. Therefore, progestamedins, which derive from PGR-positive uterine stromal cells and include hepatocyte growth factor (HGF), fibroblast growth factor 7 (FGF7) and FGF10, regulate uterine luminal (LE), superficial glandular (sGE), and glandular (GE) epithelia during the estrous cycle/early pregnancy. Previous studies with sheep demonstrated the existence of receptors for HGF (HGFR; encoded by MET) as well as FGF7 and FGF10 (FGFR2) in conceptus trophectoderm (Tr). However, the biological roles of progestamedins in conceptus development are unknown. In this study, we conducted an in vivo morpholino antisense oligonucleotide (MAO)–mediated knockdown of translation of *FGFR2* and *MET* mRNA in ovine conceptus Tr. Normality of data and homogeneity of variance were tested using the Shapiro–Wilk test and the Brown–Forsythe test, respectively, in SAS. Data were analyzed by least squares one-way ANOVA and post hoc analysis (the Fisher LSD), with each ewe/conceptus as an experimental unit. $P < 0.05$ was considered significant. Translational knockdown of MET mRNA severely retarded conceptus development whereas translational knockdown of FGFR2 mRNA resulted in small, thin, and less elongated conceptuses compared with MAO control conceptuses. Both MAO-MET and MAO-FGFR2 conceptuses were functionally abnormal based on lower ($P < 0.05$) production of interferon tau, the pregnancy recognition signal in sheep. Quantitative immunofluorescence (IF) analysis demonstrated that MAO were evenly delivered ($P > 0.05$) into Tr but not uterine LE, sGE, and GE and that the abundance of both MET and FGFR2 proteins in Tr was decreased ($P < 0.01$) by 83.3 and 93.3%, respectively. Western blot analysis using ovine Tr cells treated with respective MAO also validated knockdown efficiencies of both MAO-MET and MAO-FGFR2. Further quantitative IF revealed that compared with MAO control, active caspase-3 in Tr of MAO-MET and MAO-FGFR2 conceptuses was increased ($P < 0.01$) by 4.5- and 6.5-fold, respectively. Moreover, phosphorylation of P38 was decreased ($P < 0.01$) by 68.7 and 84.4% in MAO-MET and MAO-FGFR2, respectively, compared with MAO control, whereas phosphorylation of MTOR was decreased ($P < 0.01$) by 75.0

and 83.3% in MAO-MET and MAO-FGFR2 conceptuses, respectively. Interestingly, phosphorylation of TSC2 was decreased ($P < 0.01$) by 79.2% in Tr of MAO-MET compared with MAO control but was no different ($P > 0.05$) between MAO-FGFR2 and MAO control conceptuses. Collectively, these results demonstrate critical roles for progestamedins (i.e., HGF, FGF7, and FGF10) in ovine conceptuses that are mediated via their receptors (MET and FGFR2) and activation of MAPK and MTOR pathways and that translational knockdown of *MET* and *FGFR2* mRNA increased apoptosis and retarded conceptus development during early pregnancy.

Key Words: progestamedin, trophectoderm, MTOR, MAPK, sheep

GROWTH AND DEVELOPMENT SYMPOSIUM: NEW -OMICS TECHNOLOGIES TO UNDERSTANDING THE BIOLOGICAL PROCESSES AND NETWORK PATHWAYS ASSOCIATED WITH CATTLE GROWTH AND HEALTH

0783 Objective-oriented genomic relationship matrices.

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The advent of affordable high-density SNP genotyping platforms has boosted the implementation of genomic selection program in many livestock species. However, large reference populations are required to accurately compute genomic predictions of breeding value (GEBV). Combining information from (seemingly independent) separate populations has been highlighted as a beneficial strategy and methods to adjust the realized genomic relationship matrix (GRM) to accommodate the heterogeneity in allele frequencies have been proposed. Simulation studies based on real sequence data have shown the importance of using only variants as close as possible or identical to the causative mutations. Recently, we showed that data from reference populations from two distinct breeds can be merged to generate GEBV, provided the SNP used to build the GRM are carefully selected based on their significance and direction of the effect associated to the phenotype. We show that this approach can optimize the genomic correlation for the phenotype of interest in the two populations. We further show how a "hybrid" GRM permits the linking of genotypic data of pooled DNA samples of commercial cattle pooled according to phenotype with individual DNA samples from animals available for selection. Our examples are concerned with beef cattle raised extensively in tropical and subtropical regions of Australia. We anticipate that the use of traditional "one size fits all" relationship matrices, based on pedigree information only, is coming to an end and predict the time has come for "objective-oriented" GRM purpose built for a specific breeding objective.

Key Words: genomic selection, genomic predictions, genomic relationship matrix

0784 Multi-omics data resources and use in genetic improvement of cattle growth and health.

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Interactions of growth and health influence the progression of cattle to maturity. Growth and carcass traits typically have moderate to high heritability ($h^2 = 0.2–0.5$), whereas pathogen-disease related health traits tend to have low heritability ($h^2 \leq 0.2$). Genetic improvement in beef cattle involves selection with EPD predicted from multitrait, and often multibreed, models that incorporate genomic data derived from SNP chips. Available genotyping platforms have genomewide distance gaps of 49.4 (BovineSNP50) and 3 kb (BovineSNPHD). Genetic prediction accuracy can be improved with use of genomic data; however, process varies greatly depending on trait heritability and quality–quantity of data. Because most economically relevant traits are polygenic and single SNP within a positional-candidate gene explain limited variation, there is great interest in discovery and use large numbers of causal-mutation SNP in genetic prediction. These SNP will likely be located within nodes and hubs of gene networks and can be added to the current chips to improve their effect. Various "omics" tools evaluating transcriptome, proteome, and metabolome assist with discovery of coding and tag SNP. Differentially expressed targets from the latter two tools reveal gene products closely associated with an animal's physiologic phenotype, which can correlate with gene expression levels observed in RNA. Concordant results and enrichment analyses from these tools yield confidence to analyze target sequence, either DNA or RNA, to discover functional SNP. However, transcript splicing, peptide processing, and post-translational modifications complicate comparing results from the various approaches. The animal's epigenome and microbiome also influence phenotype. To identify functional SNP, RNA must be harvested from tissues of animal models designed to be informative for a trait collected from large breeding populations. Case versus control or comparisons of cattle from the tails of the quantitative trait distribution curves have proven useful strategies in several multi-omics growth and health studies of which pulmonary arterial pressure (PAP; $h^2 = 0.2–0.4$), an indicator of hypoxia-induced pulmonary hypertension, is an example. Here, cardiopulmonary tissues were collected from high- and low-PAP Angus steers ($n = 10$/group) with sire-pedigree diversity to growing seed stock bulls. Transcript abundance was assessed and differential expression results were obtained and are being merged with QTL and whole-genome sequence information to discover SNP genotypes for incorporation into a PAP EPD, a tool for selecting cattle for high elevation tolerance. Therefore,

strategic application of multi-omic resources to discover functional SNP and obtain population-level genotype data provides opportunity to enhance EPD accuracy.

Key Words: cattle, growth, health, omics

TRIENNIAL GROWTH AND DEVELOPMENT SYMPOSIUM

0785 Muscle gene expression patterns associated with differential intramuscular fat in cattle and markers for skeletal muscle growth rate and major cell types. B. P. Dalrymple*, *CSIRO Agriculture, Brisbane, Australia*.

Growth rate, intramuscular fat content (IMF%), and IMF composition influence the value of individual animals. However, for IMF, there are many different pathways to the final common process of triacylglyceride (TAG) synthesis and storage in intramuscular adipocytes. Gene expression data from a number of cattle and sheep experiments was used to identify the pathways involved in the synthesis of IMF and the genes correlated with growth rate and as markers of cell populations. The data sets were from a time course of longissimus muscle (LM) development in Piedmontese (PxH) and Wagyu cross Hereford (WxH) cattle, from the LM of a group of 48 Brahman cattle of similar age and from the LM of a group of 20 sheep of similar age. The differential expression of genes between WxH (high marbling) and PxH (high muscling) cattle and the correlation of gene expression with measured IMF in the Brahman and sheep data sets was integrated with known biochemical pathways. Expression of genes encoding proteins involved in the synthesis and deposition of TAG was most correlated with IMF%. In well-fed immature animals, TAG deposition rate (estimated by TAG gene expression) was proportional to current IMF%. By comparing TAG gene expression and IMF%, we identified a small number of animals with unexpectedly low or high rates of IMF deposition for their IMF%. The genes in the fatty acid synthesis pathway were less correlated with IMF%, presumably as IMF TAG can contain preformed fatty acids from circulation as well as those synthesized de novo by intramuscular adipocytes. By comparing changes in expression of the TAG and fatty acid genes, we estimated the relative contributions of synthesized and preformed fatty acids to IMF deposition on different diets. The expression of two groups of genes in the LM of the Brahman steers, significantly enriched for "cell cycle" and "ECM (extracellular matrix) organization" GO terms, was correlated with ADG per kilogram liveweight. However, expression of the same genes was only partly related to growth rate across the development time course in (PxH and WxH). *K*-means clustering of genes with similar expression profiles to the ECM genes was undertaken. Analysis of the clusters and published markers of different cell types in muscle suggested that the "cell cycle" and "ECM" signals were from the fibro/adipogenic lineage. The increase in ECM remodeling required for increased IMF deposition probably altered the relationship between the expression of these genes and animal growth rate.

Key Words: cattle, lipid

0786 Factors influencing bovine intramuscular adipose tissue development and cellularity. E. Albrecht*[1], L. Schering[1], Y. Liu[1], K. Komolka[1], C. Kühn[2], K. Wimmers[3], and S. Maak[1], *[1]Muscle Biology and Growth, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [3]Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany*.

Appearance, distribution and amount of intramuscular fat (IMF) or marbling are highly variable depending on nutrition, gender, and environmental and genetic factors. On the molecular level, the concerted action of several factors, including hormones, receptors, transcription factors, etc., determines where clusters of adipocytes arise. Therefore, the aim remains to identify biological markers of IMF to increase the ability to identify animals that deposit IMF early in age to ensure the competitiveness of meat products and increase efficiency of high-quality meat production. In an attempt to unravel the cellular development of marbling, we investigated on the one hand the abundance of markers for adipogenic differentiation during fattening of cattle and on the other hand the transcriptome of muscle and dissected IMF from different breeds. Markers of different stages of adipogenic differentiation are well known from cell culture experiments. However, early markers are transiently expressed and late markers may reflect the number of mature adipocytes in the sample rather than gene activity in a tissue. On the cellular level, the development of marbling requires recruitment, proliferation, and differentiation of adipogenic cells. Hypertrophy of adipocytes is limited and hyperplasia occurs to store excess energy in the form of lipids in new cells. Within muscles, hyperplasia and hypertrophy of adipocytes can be observed throughout life. In a recent study, we investigated the localization and abundance of delta-like homolog 1 (DLK1) and CCAAT/enhancer-binding protein β (CEBPB), early markers of adipogenic differentiation, in bovine muscle tissue. Cell culture models demonstrated high expression of DLK1 in preadipocytes and complete disappearance during differentiation to adipocytes. Accordingly, we could demonstrate an inverse relationship between IMF content and number of DLK1 positive cells in bovine muscle. Considering the cellular environment of differentiating adipocytes in muscle and accepting mature adipocytes and myocytes as secretory cells, it becomes obvious that cross talk between cells via adipokines and myokines may be important

for IMF development. Secreted proteins can act on other cells, inhibiting or stimulating their development via autocrine and paracrine actions. Among them, agouti signaling protein and thrombospondin 4 were further investigated. Thromospondin 4 is a potential myokine with supposed impact on IMF development, which has been identified in a cross species comparison of muscle transcriptomes and secretomes. Furthermore, results from transcriptome analysis suggest involvement of genes that are not directly related to adipogenesis and lipid metabolism providing new candidates for future research.

Key Words: intramuscular adipogenesis, adipokines, myokines

0787 Growth and growth rate influences bovine intramuscular adipose tissue gene expression in a differential manner. C. R. Krehbiel*[1], P. A. Lancaster[2], G. W. Horn[3], J. D. Starkey[4], E. D. Sharman[5], and S. L. Roberts[6], *[1]Oklahoma State University, Stillwater, [2]Missouri State University, Springfield, [3]Oklahoma Agricultural Experiment Station, Stillwater, OK, [4]Starkey Consulting Services, Gainsville, GA, [5]Johnson Research, LLC, Parma, ID, [6]Department of Agricultural Sciences, West Texas A&M University, Canyon*.

Intramuscular (IM) adipose tissue is the last adipose depot to mature in the growing bovine, and nutrition and management practices that influence growth and growth rate can influence IM adipose tissue deposition. Diet leading to changes in rumen VFA profile can influence substrates utilized for fatty acid synthesis, but diet has a greater effect on subcutaneous (SC) than IM adipose tissue. Subcutaneous adipose tissue has a greater ability to utilize glucose and lactate to produce reducing equivalents and to use lactate and acetate for lipid synthesis than IM adipose tissue regardless of diet. The greater ability of SC adipose tissue to utilize glucose to produce reducing equivalents and acetate and lactate for fatty acid synthesis indicates limited ability to manipulate site of fat deposition through changes in rumen fermentation. Our data suggest that differentiation and lipid synthesis in IM adipose tissue are primarily related to BW whereas differentiation and lipid synthesis in SC and perirenal (PR) adipose tissue are influenced by energy intake and rate of gain. It is perplexing as to why differentiation and lipid synthesis of IM adipose tissue is not affected by rate of gain as in SC and PR adipose tissue. The close proximity of IM adipose tissue to muscle tissue during development suggests that intercellular signaling between these 2 tissues might be crucial for development of IM adipose tissue. Early in the development of IM adipose tissue, changes in gene expression in muscle that effect remodeling of the extracellular matrix along with angiogenesis appear to be critical for development of IM adipose tissue. The strong correlation of angiogenic growth factors in LM with angiogenic growth factors and markers of adipocyte differentiation in immature IM adipose tissue suggest that there is a highly coordinated change that occurs between skeletal muscle and IM during the early stage of adipose development. However, the mechanisms of IM adipose tissue development are still not fully clear and more in vitro and in vivo studies are needed to further elucidate the pathways and mechanisms involved in IM adipose tissue development. Further understanding the interactions between skeletal muscle and adipose tissue during IM development could allow for development of management strategies that optimize carcass quality in bovine.

Key Words: bovine, growth, intramuscular adipose tissue

0788 Molecular mechanisms of bovine intramuscular fat deposition. M. Baik*, H. J. Kang, S. J. Park, and M. Y. Piao, *Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul, the Republic of Korea*.

Intramuscular fat (IMF) content in the longissimus dorsi muscle (LM), also known as marbling fat, is one of most important factors that determine beef quality in Korea and Japan as well as in the United States. Intramuscular fat deposition is influenced by both genetic (e.g., breed, genotype) and nongenetic factors (e.g., gender, castration, nutrition, stresses, age). Castration markedly increases IMF deposition, resulting in improved beef quality in Korean cattle. We present a comparative approach in gene expression between bulls and steers in bovine tissues. The marling trait has relatively higher heritability compared with other phenotypes such as feed efficiency and BW and is quantitative, being influenced by variety of genes involved in nutrient metabolism. The identification of genes associated with IMF deposition is an important area for elucidating mechanisms of IMF deposition. Intramuscular fat deposition is determined by a balance between fat deposition and fat removal in the LM. Fat deposition is determined by lipogenesis, fatty acid uptake and transport, and fatty acid esterification and fat removal is regulated by lipolysis and fatty acid oxidation. Studies on these lipid metabolic gene expression patterns provide understanding of role and relative significance of lipid metabolic genes in IMF deposition. Several peripheral tissues, including LM and adipose as well as the liver, are involved in lipid metabolism. Therefore, understanding of significance of the tissue network on lipid metabolism is important. Our studies with several peripheral tissues provide involvement of many lipid metabolic genes in the IMF deposition as well as body fat deposition in beef cattle. Application of newly developed functional genomic tools is very efficient for elucidation of molecular aspect of metabolism. We present detailed molecular events associated with IMF deposition through the application of functional genomics tools, including microarray, RNA sequencing analyses, and bioinformatics. Expression of

gene is also influenced by epigenetic factors such DNA methylation and histone modification. Possible involvement of DNA methylation levels in regulating bovine gene expression will be discussed. New information on molecular mechanisms of bovine IMF deposition could be applicable to design nutritional or genetic methods to increase IMF deposition and to modify fatty acid composition in the LM of beef cattle.

Key Words: beef quality, intramuscular fat, functional genomics

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0789 Dedifferentiated fat cells: Potential involvement in intramuscular adipogenesis. M. S. Duarte*[1], R. Bueno[1], M. V. Dodson[2], and G. J. Hausman[3], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Washington State University, Pullman, [3]University of Georgia, Athens*.

Intramuscular adipogenesis and the dynamics of lipid metabolism by mature adipocytes have been investigated primarily due to the importance of altering marbling to enhance meat quality. Knowledge regarding intramuscular fat development has relied on the conversion of a variety of preadipocyte-like cells (such as stromal vascular cells) and their differentiation into lipid-assimilating adipocytes, which was thought to be the end of their cell cycle. However, a great number of studies have demonstrated the ability of the mature adipocyte to dedifferentiate into a population of a proliferative-competent cells known as the dedifferentiated fat (DFAT) cells. As early as the 1970s, in vitro studies have shown that DFAT cells may be obtained by ceiling culture, which takes advantage of the buoyancy property of lipid-filled cells. It is documented that DFAT cells may acquire a phenotype similar to mesenchymal stem cells and may redifferentiate into multiple cell lineages. From an animal science/meat science perspective, the main question that arises from the current knowledge of DFAT cells is how do DFAT cells contribute to intramuscular fat accumulation? What regulation causes the intramuscular mature adipocytes to dedifferentiate or resume their capability to proliferate? Moreover, are DFAT cells controllable so that they differentiate into lipid-assimilation cells (and perhaps other cells) and thus contribute to overall increase of intramuscular fat in vivo? Considering the fact that marbling fat accumulation is the last step in meat production, a (muscle and fat cell) intercellular regulation might trigger the differentiation of intramuscular adipocytes (regardless of origin). For example, feed restriction followed by realimentation may lead to dedifferentiation of mature adipocytes followed by its redifferentiation of proliferative competent (DFAT) progeny cells (as well as other preadipocytes/adipofibroblasts) into lipid-assimilating cells on realimentation, which may be one of the causes of changing the body composition and increase of fatness. Dedifferentiated fat cells originating from different adipose depots possess different rates of redifferentiation, whereas those originated from intramuscular fat depot are more active in adipogenesis than other fat depots. In summary, although the mechanisms of dedifferentiation of mature adipocytes have not been well defined, DFAT cells may contribute to intramuscular adipogenesis. Dedifferentiated fat cells may lead to the adoption of strategies in livestock production to enhance fat deposition in specific (desired) depots.

Key Words: adipose tissue, ceiling culture, marbling

0790 Metabolic programming and intramuscular adipogenesis. G. Takafumi*, *Kyushu University, Taketa-city, Japan*.

The study was conducted to clarify how early nutrition as metabolic programming events affected intramuscular adipogenesis of Japanese Black cattle fattened with only roughage. As a control group, the roughage group (R; n = 11) was fattened on only roughage ad libitum from 4 to 31 mo of age (mo) after nursing at standard level (replacer milk intake of 0.6 kg/d) until 3 mo. As a treatment group, the high-energy group of metabolic programming events (MP; n = 12) was also fattened on only roughage ad libitum from 11 to 31 mo after intensively nursing and feeding a high-energy diet until 10 mo. The intramuscular fat content in longissimus muscle was significantly larger in MP (13.2%) than in R (9.4%) at slaughter (Soxhlet analysis). Expression of the adipogenic genes, C/EBPb, PPARγ, C/EBPa, FASN, SCD, LEP, FABP4, ADIPOQ, IGFBP4, PPARγ2, and PRMT5, was investigated at each stage by quantitative real-time PCR analysis by using longissimus muscle biopsy samples. At 3 mo, the expression levels of PPARγ, C/EBPa, PPARγ2, ADIPOQ, IGFBP4, and PRMT5 were significantly higher in the MP than in the R. At 10 mo, the expression levels of PPARγ, C/EBPa, FASN, SCD, and LEP were significantly higher in the MP. At 14 mo, only PPARγ and LEP in the MP showed significantly higher expression. PPARγ, PPARγ2, and C/EBPa and other adipogenesis markers such as LEP, ADIPOQ, FABP4, IGFBP4, and PRMT5 were expressed at higher levels in the MP compared with the R at 30 mo. This effect may involve several factors including metabolic additivity and response to nutritional stimulus and the unstable nature of expression of these genes. Conversely, at 20 and 30 mo, FASN and SCD were expressed at significantly lower levels in the MP. Nevertheless, according to investigation of fatty acid composition of intramuscular adipose tissue, early metabolic programming events positively affected the relatively higher amounts of C18:1, MUFA, and the US:S ratio in MP at slaughter compared with R. It may be concluded that metabolic programming through high nutrition at neonatal ages can positively change adipogenic gene expression at the molecular level. These effects stimulate the early development of adipocytes at an early age and these changes were maintained over the study period. These suggest that early nutrition affects final meat quality and that early metabolic programming has potential to advance the field of

meat sciences and support the meat industry.

Key Words: cattle, metabolic programming, intramuscular adipogenesis, grass-fed beef cattle

0791 Genetics and breeding for intramuscular fat and oleic acid content in pigs. J. Estany*[1], R. Ros-Freixedes[2], M. Tor[1], and R. N. Pena[1], [1]*University of Lleida – Agrotenio Center, Lleida, Spain,* [2]*Universitat de Lleida, Lleida, Spain*.

Total fat and fatty acid content affect both food quality and human health, and therefore, they are becoming increasingly important to industry and consumers. The intramuscular fat (IMF) and oleic acid (C18:1) content have been favorably related to pork quality, particularly in dry-cured products. This has triggered the interest of including them in the breeding goal of pig lines producing for high-valued markets. It is known that IMF responds to selection, but there is little evidence on the opportunities for genetic change in fatty acid composition. Based on research conducted on a Duroc line, we showed that C18:1, like IMF, has a moderate heritability and is genetically associated with increased IMF, BW, and backfat thickness. Despite this correlation structure, we proved that there exist selection schemes leading to response scenarios where C18:1, IMF, and lean content can be simultaneously improved. A limitation for implementing direct selection for C18:1 is that phenotypes are costly to obtain and cannot be measured on selection candidates themselves. Furthermore, results may depend on the reference tissue used for genetic evaluations. Deoxyribonucleic acid markers and genomic selection provide a complementary approach to overcome this problem. A genomewide association study was performed on Duroc pigs genotyped with a 60,000-SNP chip to detect genomic variants exhibiting influence on fat content and composition. We detected strong associations with IMF and C18:1 for two chromosomal regions colocalizing with the *SCD* (SSC14) and *LEPR* (SSC6) genes, which were then validated using a set of data from around 1,000 pigs. The DNA variant at the *SCD* gene affected the oleic to stearic desaturation index (C18:1/C18:0), C18:1, and SFA and MUFA and was consistently detected in several muscles and subcutaneous fat and both in raw and dry-cured pork. The association of *LEPR* with fatty acid composition was detected in muscle and was, at least in part, a consequence of its effect on overall fatness, with increased IMF resulting in more SFA, less PUFA, and greater SFA:PUFA ratio. With the benefits of genomic selection needing further assessment, selection combining pedigree-connected phenotypic data on IMF and C18:1 and some singled-out genetic markers is presented as a suitable alternative. However, if adopted, the response on lean growth is expected to be reduced. The extent to which it is affordable relies on how much consumers are prepared to pay for high-IMF and C18:1 pork products.

Key Words: fatty acid, intramuscular fat, meat

0792 The genetic landscape of intramuscular fat content and composition in pigs. M. Amills*, *Center for Research in Agricultural Genomics, Bellaterra, Spain*.

Intramuscular fat content and composition are relevant selection goals in pig breeding schemes because of their significant influence on meat tenderness, juiciness, and flavor. Muscle lipid phenotypes are determined by both nutritional and genetic factors, displaying moderate heritabilities and a polygenic architecture. In this way, genome scans with microsatellites have revealed the existence of more than 200 intramuscular fat content QTL scattered throughout the pig genome. Unfortunately, experimental limitations related with population size and marker density have prevented the identification of mutations with causal effects. The comparison of QTL maps among muscles and fat depots has evidenced a modest positional concordance, suggesting that the penetrance of polymorphisms with causal effects on lipid metabolism is modulated by tissue-specific factors. This is an important consideration that should be kept in mind when implementing gene-assisted or genomic selection schemes aimed to improve intramuscular fat content and composition in swine. Gene expression studies based on microarrays have also provided valuable clues about the biology of muscle fat deposition in pigs, showing that it is modulated by a complex network of pathways related with lipid (lipogenesis, lipolysis, and PPAR signaling) and carbohydrate (insulin signaling) metabolism. However, microarrays have a limited power because they do not allow exploring transcript structure or the expression patterns of noncoding RNA. The recent advent of high-throughput genotyping and sequencing technologies has made it possible to circumvent many of these limitations. Now, genomewide association studies take advantage of the information provided by tens of thousands of SNP markers to fine map genomic regions associated with intramuscular fat content and composition in pigs. In parallel, the RNA-seq technology is expanding the analysis of differential expression to mRNA splicing variants as well as to many noncoding RNA with functions yet to be discovered. Particularly powerful are those approaches integrating genomewide polymorphism and expression data, because they can offer an unprecedented view about the molecular mechanisms that regulate lipid deposition in the porcine skeletal muscle.

Key Words: intramuscular fat, pig, genomics

0793 Statistical models and tools for integration of omics data to uncover the genetic control of pork quality and growth traits. J. P. Steibel*[1], D. Velez-Irizarry[1], S. Casiro[1], and C. W. Ernst[2], *[1]Department of Animal Science, Michigan State University, East Lansing, [2], Michigan State University, East Lansing*.

Next-generation sequencing is drastically changing the way we study the interactions between genomes, transcriptomes, and phenomes. The next generation of animal genomics data sets should be matched by the next generation of analysis models. Those models should be flexible and adaptable to complex designs pervasive in animal genomics, statistically sound to test hypotheses and estimate parameters that are important for animal genomic research, and computationally efficient and able to accommodate massive multilayer data sets that are typical of animal genome research. The goals of this presentation are to 1) propose models for genomewide association (GWA) that can be used for expression QTL (eQTL) and phenotypic QTL (pQTL) mapping and to show their properties using simulations and real data analyses. As part of the analysis, we specify significance thresholds to control type I error rate, we compute confidence intervals of QTL positions using cross-validation, and we demonstrate under simulation that intervals have the intended coverage. Finally, we derive a meta-analysis procedure to integrate results of several independent GWA. We use plasmode simulations to show that our proposed method has a series of desirable properties for implementation of high-throughput association analyses: 1) computational cost linearly scales with the number of markers allowing rapid GWA with massive data sets, 2) genetic substructure and relationships among animals are fully accounted for, and 3) type I error rates are controlled at nominal levels. Finally, we present graphical and descriptive summary tools to represent results of massively parallel GWA analyses. To illustrate the usefulness and computational efficiency of proposed models, we present results from several projects: 1) GWA analysis of over 50 pork quality, carcass composition, and growth traits for almost 1,000 Duroc × Pietrain F_2 pigs; 2) GWA of over 40,000 gene expression phenotypes from backfat and longissimus muscle tissues of 176 individuals of the same population; and 3) meta-analysis of five meat quality traits across three divergent pig populations. We show that using our proposed methods, we can map eQTL overlapping pQTL and confirm their joint association. More importantly, we demonstrate that such mapping can be performed and represented in an unsupervised way (with minimal human input) by integrating genomewide expression and genotyping as well as high-throughput phenotyping data through proper data analysis models and tools.

Key Words: expression quantitative trait loci, genetical genomics, genomewide association

0794 Marbling: Management of cattle to maximize the deposition of intramuscular adipose tissue. S. B. Smith*[1] and B. J. Johnson[2], *[1]Texas A&M University, College Station, [2]Texas Tech University, Lubbock*.

Consumers in the United States, Japan, and Korea have valued highly marbled beef for nearly a century. In the United States, most consumers prefer beef that is reasonably marbled and juicy. Early studies demonstrated that the more oleic acid in beef, the greater the overall palatability of the beef. Scientists have taken a two-prong approach to understand the biology of marbling development. Biochemists, molecular biologists, and geneticists have worked to gain a better understanding of the intracellular and extracellular factors that regulate the development of marbling adipose tissue (also known as intramuscular tissue), whereas beef cattle nutritionists have worked to optimize diets and time on feed to provide high-quality beef carcasses without exacerbating carcass adiposity. Marbling adipose tissue preferentially uses glucose as the carbon source for fat synthesis, whereas subcutaneous adipose tissue preferentially uses acetate. Early weaning of beef steers promotes greater marbling development at slaughter than normal weaning of steers, and this may be caused by increased glucose availability (from the grain-based rations) at the early stages of marbling development. In addition to providing carbon for marbling adipose tissue development, grain-based diets also increase MUFA such as oleic acid in marbling by stimulating the expression of stearoyl CoA desaturase (SCD). There is a significant correlation between the concentration of MUFA and amount of intramuscular lipid in longissimus muscle in cattle with the genetic propensity to marble that are fed grain-based diets for extended periods of time. Marbling adipose tissue can be distinguished from other fat depots by its location within perimysial connective tissues alongside muscle fibers. However, in longissimus muscle from Japanese Black A5 cattle, marbling adipocytes have been observed within muscle bundles, suggesting that muscle satellite cells can be induced to differentiate into marbling adipocytes. To date, the mechanisms responsible for this *trans*-differentiation of satellite cells to adipocytes in beef cattle have not been identified, as this process is quite difficult to measure in situ. Marbling adipose tissue from Japanese Black cattle are exceptionally high in oleic acid, and recent cell culture studies have demonstrated that oleic acid promotes *trans*-differentiation of muscle cells to marbling adipocytes. The results of these studies indicate that grain-based diets are necessary to promote the development of marbling. Furthermore, grain-based diets increase the healthfulness and juiciness of beef by promoting the production of oleic acid in marbling and other fat depots.

Key Words: beef, marbling, oleic acid

0795 Linking from the farm to the table.
M. R. McMorris*, *Beef Improvement Opportunities, Guelph, ON, Canada*.

Genomics promises tremendous opportunity to the beef industry; however, that opportunity is currently stymied by the structure of the industry and the limited use of long-standing traditional genetic evaluations. Industry segmentation and poor, or in some cases lack of, market signals can be seen in the industry response of the past decade to a demand for more highly marbled beef. From 2005 to 2015, the feeding sector simply overfed animals to achieve higher marbling at the very great expense of excess fat, poor carcass yield, and poor feed efficiency. Although a logical decision in itself at the finishing level, this approach ignored the potential of "supply-chain" genetics to meet an end goal. A further persistent need that the beef supply must address is inconsistency of tenderness of beef at the consumer level. Beef is a premium protein product and, as such, must meet a higher standard for consumer satisfaction. Considering the heritability of tenderness, it would seem obvious as a supply-chain breeding goal. And yet no selection has been attempted, due in part to the nature of the trait: difficult to measure on breeding animals. This is an area of particular interest to make use of genomics. A simple DNA test can give an estimate for tenderness, which, applied to three generations of sire selection, could have a dramatic impact on consumer satisfaction. A third trait that should be of interest to every beef producer is feed efficiency. Although a great deal of focus has been placed on residual feed intake and affordable panels have been developed, little selection pressure has been brought to bear. Again, this is due, in large part, to the segmentation of the beef industry. Genetic improvement in the beef industry will only reach its potential following a fundamental shift in outlook. Current segmentation by sector and "ranch-level" genetics must be replaced with a more holistic approach in which information and market signals flow up and down the supply chain. Only then will producers and, more importantly, consumers benefit from the promise of genomics.

Key Words: beef genomics, breeding goals, industry structure

HORSE SPECIES: MANAGEMENT

0796 Stress responses in horses tied with overchecks.
K. Bennett-Wimbush*, J. K. Suagee-Bedore, and M. Amstutz, *The Ohio State University, Wooster*.

Little information is available on the welfare of horses used for transportation. It is common to observe horses wearing a complete harness, hooked to horse-drawn vehicles, tied up for extended periods of time where horse-drawn transportation is popular. An observational survey of 305 horses at 7 locations in northeast Ohio found 29.5, 51.5, and 13.8% of the horses were tied wearing harnesses with high, low, or no overchecks. Six Standardbred mares were used in a Latin square (treatment × period) designed experiment to evaluate the effects of tying horses wearing overchecks. All horses were acclimated to harness and tying before testing. Three 90-min test periods (May and June 2015) were used, and horses were randomly assigned to treatment groups: high overcheck (HC), low overcheck (LC), or no overcheck (NC). Each test period was followed by a 2-wk recovery period. Heart rate was measured before the test; during the test at 15 (T15), 45 (T45) and 90 (T90) min; and after the test at 45 (P45) and 90 (P90) min. Plasma cortisol (ELISA) was measured before the test and at T45, T90, P45, and P90. Muscle soreness and tightness at 20 sites—(right and left) rhomboideus, trapezius, deltoideus, latissimus dorsi, triceps, biceps femoris, longissimus, gluteus, hamstrings, and tensor fascia lata—were scored by a trained professional (Powel et al. 2008. J. Equine Vet. Sci., 28(1):28–33) before testing and 24 h after testing. Heart rate tended to be higher (45 ± 2.5 bpm; $P = 0.098$) at T15 in all horses compared with pretesting values (40 ± 2.5 bpm), regardless of treatment. Plasma cortisol was higher ($P < 0.001$) in HC at T45 and T90 (159.7 and 166.3 ng/mL, respectively) compared with both LC (106.4 and 105.2 ng/mL) and NC (116.1 and 93.5 ng/mL) at T45 and T90, respectively. There was no treatment effect on muscle soreness and tightness. Overall, muscles were more sore ($P < 0.05$) and more tight ($P < 0.001$) following the test compared with pretest values in all horses. The rhomboideus ($P < 0.001$), latissiumus dorsi ($P < 0.05$), and longissimus ($P < 0.05$) showed significant changes in both muscle soreness and tightness whereas the trapezius, deltoideus, and biceps femoris were only tighter ($P < 0.05$). We recommend loosening or removing overchecks while horses are tied and advocate additional studies on the common practice of tying up horses.

Key Words: horse, welfare, cortisol

0797 Effect of prerace behavior on performance in racing quarter horses.
C. E. Ferguson*, *McNeese State University, Lake Charles, LA*.

It is purported that prerace behavior of a race horse can diminish their performance, known as "washing out." This study observed prerace behaviors of 1,040 Quarter Horse (QH) race horses that competed in 137 races over a 14-night duration at Delta Downs Racetrack (Vinton, LA). A total of 46 variables were recorded by experienced horsemen. The prerace period was divided into four different subsections: before saddling (BSAD), which was the time when the horse walked across the track's infield to right before they entered the stall to be saddled; during saddling (SAD), which was the time while the horse was being saddled; after saddling (ASAD), which was the time from when the horse was finished being saddled to when the jockey mounted the horse; and after the parade (POSTP), which was the time from when the jockey mounted

to when they were finished with the postparade. During subsections, each horse assessed a behavior type of calm, ready, or nervous. Upon completion of each race the finish type (tired, pulled-up, or running) was recorded as well as finish position, which was checked the next day on the Equibase website. Categorical variables were statistically compared using a χ^2 test and quantitative variables were compared using general linear models in SAS. The average number of previous races at Delta Downs was statistically greater ($P < 0.05$) for calm horses (3.3 ± 0.2) than ready (2.2 ± 0.1) and nervous (0.9 ± 0.1) horses during all periods. The average finish position was not different for calm (5.1 ± 0.1) and ready (5.0 ± 0.1) horses but both were significantly better than nervous (5.9 ± 0.3) horses for all periods. However, horses (during POSTP period) that were ready (4%) were less likely ($P < 0.05$) to finish tired compared with calm (10%), which was also less likely ($P < 0.05$) to finish tired compared with nervous (19%). The results show that horses that appear nervous are more likely to finish behind horses that appear calm or ready to race and are three times more likely to finish the race tired compared with ready and twice as likely compared with calm. These data support that a nervous behavior can negatively impact their performance in races, even at short distances.

Key Words: quarter horse, horse racing, stress, behavior, performance

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0798 Evaluating the effectiveness of varying doses of supplemental tryptophan as a calmative in horses. B. Davis*[1], T. Grandin[1], T. E. Engle[1], and J. Ransom[1,2], *[1]Colorado State University, Fort Collins, [2]National Park Service, Sedro-Woolley, WA*.

The objective of this study was to examine how various doses of tryptophan supplementation impacted reactive behavior and physiological stress measurements in the horse. Eleven horses (9 geldings and 2 mares) were given four treatments—a control dose, consisting of 0 mg Trp/kg BW (CON); 20 mg Trp/kg BW (LOW); 40 mg Trp/kg BW (MED); and 60 mg Trp/kg BW (HIGH)—in a randomized crossover design. Each treatment lasted 3 d. On Days 1 and 3 of each treatment, horses underwent a behavior test to measure startle response. Heart rate measurements and the speed at which the horses fled from startling stimuli were recorded. In addition, serum glucose, lactate, and cortisol levels were analyzed both immediately before the startle test and again 15 min after the test. Significant sedative effects were seen at LOW Day 1 on heart rate increase during the startle test ($P = 0.05$) and on change in serum lactate levels ($P = 0.03$). At MED Day 1, sedative effects were seen on change in serum cortisol levels ($P = 0.01$). Some excitatory effects were seen at MED Day 3 on the time for heart rate to return to baseline after the startle test ($P = 0.03$). A subset of blood samples was analyzed for serum free Trp and the ratio of Trp to other large neutral AA, which verified treatment effect.

Key Words: behavior, horse, tryptophan

0799 Effects of barefoot trimming and shoeing on the lower forelimb: Hoof morphology. D. K. Proske[1], J. L. Leatherwood*[1], M. J. Anderson[1], K. J. Stutts[1], C. J. Hammer[2], and J. Coverdale[3], *[1]Sam Houston State University, Huntsville, TX, [2]North Dakota State University, Fargo, [3]Texas A&M University, College Station*.

Limited information is available pertaining to potential benefits of barefoot trimming techniques under standard management conditions. Therefore, 12 mature Quarter horses (8–14 yr and 450–572 kg) were used in a switch back design for a 140-d trial to determine effects of barefoot trimming and shoeing on joints of the forelimb and digital cushion thickness. Before the start of the trial, all horses were adapted to a standardized exercise protocol and lameness examinations were performed by a veterinarian; hooves were allowed to grow naturally with minimal farrier interventions. This study was divided into 3 phases: d 0 to 42, horses were barefoot trimmed (BF1); d 49 to 91, horses were shod (SD) on the forehand with standard St. Croix plain lite shoes; and d 98 to 140, horses received another barefoot trim (BF2). Between phases, a 7-d transition period was given to allow for farrier practices. Horses were group exercised 3 times/wk on a 132 by 3.7 m linear dirt track to a mean HR of 80.00 ± 1.90 bpm. Measurements were obtained every 21 d immediately following exercise. Digital cushion thickness was ultrasonically measured through the superficial frog using a 5.0-MHz convex probe and stand-off pad following previously described methods. Stride lengths were also recorded following exercise at a walk and trot (EquineTec, Monroe, GA). Data were analyzed using the PROC MIXED procedure of SAS. There was no influence of day ($P = 0.25$) on mean HR; however, there was an influence of treatment. Mean HR was lower ($P < 0.01$) during the BF1 phase (75.50 ± 1.90 bpm) compared with the SD (82.08 ± 1.90 bpm) and BF2 (82.42 ± 1.90 bpm) phases. Mean stride lengths at the walk ($P < 0.05$) and trot ($P < 0.01$) were greater in SD horses compared with BF1 and BF2 horses. There was no main effect ($P \geq 0.47$) of day or treatment on digital cushion thickness. However, on d 42 of each of the 3 phases, mean digital cushion thickness was greater ($P \leq 0.01$) during the BF1 (1.41 ± 0.03 cm) and BF2 (1.43 ± 0.03 cm) phases compared with the SD phase (1.26 ± 0.03 cm). These data indicate that a shod fore digit may cause changes in hoof morphology due to alterations in lower limb movement and hoof load dispersion and, therefore, may cause an increase in the incidence of lameness over time.

Key Words: shoeing, digital cushion, stride length

0800 Effects of barefoot trimming and shoeing on the lower forelimb: Joint inflammation. D. K. Proske[1], J. L. Leatherwood*[1], K. J. Stutts[1], M. J. Anderson[1], C. J. Hammer[2], and J. Coverdale[3], *[1]Sam Houston State University, Huntsville, TX, [2]North Dakota State University, Fargo, [3]Texas A&M University, College Station*.

Limited information is available pertaining to potential benefits of barefoot trimming techniques under standard management conditions. Therefore, 12 mature Quarter horses (8–14 yr and 450–572 kg) were used in a switch back design for a 140-d trial to determine effects of barefoot trimming and shoeing on the hoof and joints of the forelimb. Before the start of the trial, horses were adapted to a standardized exercise protocol and lameness examinations were performed by a veterinarian. This study was divided into 3 phases: d 0 to 42, horses were barefoot trimmed (BF1); d 49 to 91, horses were shod (SD) on the forehand with standard St. Croix plain lite shoes; and d 98 to 140, horses received a second barefoot trim (BF2). Between phases, a 7-d transition period was given to allow for farrier practices. Horses were group exercised 3 times/wk on a 132 by 3.7 m linear dirt track to a mean HR of 80.00 ± 1.90 bpm. Measurements were obtained every 21 d immediately following exercise protocol and included thermography images (FLIR Systems, Boston, MA) of carpal and metacarpal joints, superficial horn of the frog, and medial and lateral sole of the front digits. Joint circumferences were obtained using a soft tape measure at the accessory carpal and proximal sesamoid bones, respectively. Additionally, blood samples were collected to evaluate PGE_2 concentrations after exercise. Data were analyzed using the PROC MIXED procedure of SAS. An influence of treatment ($P < 0.01$) was detected in all areas measured, with mean surface temperatures being greatest during the BF1 phase. Although no difference was detected ($P = 0.38$) in the joint circumference of the metacarpal joint, there was an influence of treatment ($P < 0.01$) at the carpal joint with the BF1 phase having the lowest mean joint circumference compared with all other phases. PGE_2 concentration decreased throughout each phase of the trial ($P < 0.01$) independent of the treatment applied. This is likely due to an increased cardiovascular stamina of the horses from repetitive exercise as the study progressed. In the BF1 phase, the lower joint circumferences and the increased surface temperatures illustrate the presence of greater blood flow and lack of joint inflammation and swelling. These data indicate that a shod fore digit may cause inflammation on the joints of the lower forelimb accompanied by a reduction in blood flow and, therefore, may cause an increase in the incidence of lameness over time.

Key Words: shoeing, thermography, joint

0801 Characterizing the physiological response of a novel vaccine in mature horses. J. L. Leatherwood*, D. L. Parker, M. J. Anderson, K. J. Stutts, M. M. Beverly, and S. F. Kelley, *Sam Houston State University, Huntsville, TX*.

The vaccination of animals has been implemented to prevent the spread of infectious diseases through the use of inactivated or modified live organisms. Vaccination serves to induce an immune response that is effective at limiting the exposure to a natural born pathogen. Criteria for successful vaccination programs is to ensure that the vaccine does not cause the disease or produce negative side effects that may overwhelm the ability of the immune system to provide a means of protection. Therefore, the objective of this study was to characterize the physiological response of mature horses to a novel vaccine through the use of thermography and assessment of vital parameters as well as to determine differences in surface temperatures at the injection sites of the vaccine and saline to better understand the localized inflammatory response to injection. Thirty horses (5–10 yr and 413–551 kg) were vaccinated against bovine respiratory syncytial virus, bovine viral diarrhea virus, and infectious bovine rhinotracheitis as a one-time vaccination with a saline contralateral injection that was completed on the opposite side of the neck. Horses were assumed to be naïve to bovine diseases. Vitals including heart rate (HR), respiration rate (RR), and rectal temperature along with thermal images (FLIR Systems, Boston, MA) of the ocular globe (OG), rectum (RM), and injection sites were recorded at 0 and 6, 12, 24, and 48 h following vaccine administration. Data were analyzed using the GLM procedure to evaluate differences over time and a paired *t* test to evaluate differences between injection sites. Vitals including HR and RR decreased ($P < 0.01$) following initial handling at 0 h and remained consistent up to 48 h following vaccine administration. Rectal temperature increased ($P < 0.01$) and peaked at 12 h ($P < 0.01$) compared with other time points measured. Similarly, thermography data of OG and RM followed a similar pattern and peaked at 12 h ($P < 0.01$). Comparison between the vaccine and saline injection sites revealed that the vaccine site had an elevated temperature ($P < 0.01$) compared with the injection site of the saline control. This illustrates the localized inflammation detected is a result of a response to the vaccine rather than the injection alone. Similarly, changes in rectal temperature along with thermography of the OG and RM are valid indicators of a response to vaccination whereas HR and RR were not altered and may not be reliable predictors.

Key Words: equine, thermography, vaccine

0802 Application of either a single or multiple doses of an intravaginal gonadotropin-releasing hormone agonist to induce ovulation in mares.

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Triptorelin acetate (TA) is a GnRH agonist that is used in the swine industry to induce ovulation. In a previous study, we investigated the efficacy of an intravaginal TA gel to induce ovulation in mares. Treatment with TA gel tended ($P = 0.08$) to elicit an increase in LH concentrations by 12 h after treatment but failed to shorten the interval from treatment to ovulation or cause a greater percentage of mares to ovulate within 48 h of treatment compared with placebo-treated controls. Because peak LH concentrations were observed at 12 h after treatment and declined to nearly baseline concentrations by 24 h, we postulated that LH concentrations may not have remained elevated sufficiently to induce ovulation. Therefore, the objective of this study was to investigate whether 2 doses of TA gel would result in elevated LH concentrations sustained for a sufficient period to reduce the interval from treatment to ovulation and cause ovulation to occur within 48 h of treatment. Twenty-three cyclic mares were stratified by parity and age and randomly assigned to 3 treatments: 500 μg TA (TA5); two 500-μg doses of TA, given 24 h apart (TA5x2); or 5 mL vehicle gel only (control). Ultrasonography occurred once daily until detection of a follicle ≥25 mm in diameter was detected, at which point ultrasonography and blood collection occurred every 12 h. Once a follicle ≥35 mm was detected, treatment was administered intravaginally and ultrasonography and blood collection then occurred every 6 h until 48 h after ovulation. At 6 and 12 h after treatment, LH was increased ($P < 0.05$) in both TA5 and TA5x2. In TA5x2, the second dose of TA failed ($P > 0.05$) to elicit more LH release compared with both TA5 and control. With regard to LH concentrations, the overall treatment effect was not significant ($P > 0.05$); however, a treatment × time interaction was identified ($P < 0.05$). A greater ($P < 0.05$) percentage of mares ovulated by 48 h after treatment in TA5 but not TA5x2 compared with control. Interval from treatment to ovulation was shorter ($P < 0.01$) in both TA5 and TA5x2 compared with control. We concluded that both 1 and 2 doses of 500 μg TA hastened ovulation in cyclic mares; however, 2 doses failed to cause sustained release of LH or cause a greater percentage of mares to ovulate within 48 h of treatment.

Key Words: mare, ovulation, gonadotropin-releasing hormone

Table 0802.

Table 1 – Effects of TA gel on the interval from treatment to ovulation and the percentage of mares ovulating by 48 h post-treatment

	n	Hours from TRT to ovulation Mean ± SEM	% ovulating by 48 h
Control	7	123.1 ± 21.7[a]	0.0%[a]
TA5	8	61.5 ± 8.8[b]	75.0%[b]
TA5x2	8	61.5 ± 9.6[b]	50.0%[a]

[a,b] $P < 0.05$; TRT = Treatment.

0803 Incidence of exercise induced pulmonary hemorrhage in race horses in Puerto Rico.

V. Morales[1], S. Glass[1], J. De Angel[2], B. Vallejo[2], and A. A. Rodriguez*[1], [1]*University of Puerto Rico, Mayaguez,* [2]*Equus PR, Caguas, PR*.

Exercise-induced pulmonary hemorrhage (EIPH) is a very common disease in race horses characterized by an alteration of the respiratory system. Depending on the magnitude, the EIPH causes bleeding in lung passages making breathing difficult. Exercise-induced pulmonary hemorrhage is evaluated by endoscopies on a scale from 0 to 5, with 0 corresponding to no hemorrhage and 5 to a severe condition. In Puerto Rico, the only preventive measure used is the administration of a diuretic 4 h before the race. A data set was analyzed to determine factors associated with the incidence of EIPH and the preventive effect of the diuretic. The data were supplied by Equus PR and the factors considered were month of the year, sex (male or mare), distance of the race in meters (C1, 400 to 1,200; C2, 1,300–1,400; and C3, >1,600), and the use or not of the diuretic. The randomly selected data of 2,632 endoscopies of race horses running or not represented 20% of the total endoscopies recorded in 2014. Of this number, 1,377 were from horses within 1 h after the race, representing 52% of the total. A χ^2 test analysis was performed to determine the frequency of EIPH regarding the factors, month, sex, distance of the race, and use of the diuretic. Of the 1,377 animals, 488 presented some degree of EIPH, equivalent to 35% of the total sample. The percentage of horses suffering EIPH condition from 1 to 5 was 52.8, 23.6, 13.5, 7.3, and 2.8, respectively. The frequency and severity of EIPH was similar ($P = 0.435$) during the 12 mo of the year. Males and mares also had similar ($P = 0.587$) incidence. Horses running shorter races (C1 and C2) had a higher ($P < 0.02$) incidence of EIPH than those running longer races (C3). The number of healthy horses or those suffering the condition was similar ($P = 0.375$) regardless of diuretic use. In summary, 35% of the race horses competing presented some level of EIPH; month of the year and sex did not alter the incidence. Horses running shorter distance showed more incidence of the condition and the use of the diuretic was not effective as a preventive method for EIPH.

Key Words: diuretic, race horses, exercise induced pulmonary hemorrhage

0804 Application of gait analysis to determine if the Galiceno horse breed is a gaited horse breed.
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The Galiceno horse breed is classified as critically endangered by The Livestock Conservancy (LC) with less than 200 pure Galicenos in the United States. The Galiceno is one of several breeds classified as a Spanish Colonial horse breed. The breed has been noted for its ground-covering movement and its capacity for performing a running walk. Although other Spanish Colonial horse breeds have been classified using gait analysis as gaited, research documenting the gait mechanics of the Galiceno breed is unavailable. The objective of the study was to evaluate symmetrical gaits at various velocities performed by the Galiceno documenting gait mechanics that would be classified as gaited. Horses (n = 12) were selected by the LC and Galiceno Horse Registry (121.9–137.2 cm height) to represent the breed. Horses were asked to move freely along an arena railing while being filmed. Frame-by-frame analysis was performed documenting hoof contact and lift-off. A full stride cycle was determined from the time the right hind hoof made ground contact to the time it returned back to the ground. Only gaits demonstrating gait symmetry were used for this study. Student's paired t tests were performed to determine gait symmetry ($P < 0.05$). Stance durations between left and right variables that were not significantly different indicated gait symmetry. A total of 30 symmetrical strides were selected for each horse. From the strides evaluated, 32% demonstrated a 4-beat rhythm with a lateral footfall sequence and no period of suspension similar to the walk. The velocity for these strides (1.36 + 0.19 m/s) fell within the range of a typical walk for the height of the horse, thus falling under the velocity of that of a running walk performed by a gaited breed. Stride duration (1,220 + 89 ms) was comparable to a slow walk. The remaining strides demonstrated a diagonal footfall sequence with 8 to 23% of the stride duration spent in a period of suspension. Only 4% of those strides had a 4-beat rhythm demonstrating diagonal couplets as the rest demonstrated a true 2-beat rhythm. The velocity for the diagonal leaping gait was 3.78 + 0.63 m/s with disassociation of diagonal pairs occurring at the upper range of the velocity. Stride duration was 690 + 72 ms. Both stride duration and velocity were comparable to the trot seen in other nongaited Spanish Colonial horse breeds. In conclusion, those strides evaluated did not suggest the Galiceno should be classified as a gaited horse breed.

Key Words: Galiceno, kinematics, gaited

0805 Effect of body condition score on fatty acid composition of equine subcutaneous adipose tissue.
R. M. Humphrey*, A. T. Sukumaran, R. L. Lemire, E. N. Ferjak, C. Cavinder, D. D. Burnett, and T. T. N. Dinh, *Mississippi State University Department of Animal and Dairy Sciences, Mississippi State*.

Body condition score serves as a proxy indicator of the health and metabolic disposition of horses; however, this subjective assessment does not take into account the fatty acid composition of adipose tissue (AT) depots. The objective of this study was to investigate the relationship between BCS and fatty acid composition of subcutaneous AT. Fourteen horses with BCS of 4 (n = 4), 5 (n = 6), and 6 (n = 4) were euthanized, and the subcutaneous fat was collected at the junction of the last rib and the vertebral column. Samples were frozen in liquid nitrogen, pulverized, and stored at −80°C. Fat samples were directly derivatized for fatty acid identification and quantification on a gas chromatography system (Agilent Technologies, Santa Clara, CA) using an internal standard for calibration. Fatty acid methyl ester concentrations were used to calculate fatty acid percentages. Statistical analysis was performed by the GLIMMIX procedure of SAS 9.4 (SAS Inst. Inc., Cary, NC), and statistical significance was determined at $P \leq 0.05$. Overall, there was no effect of BCS on fatty acid percentages composition ($P \geq 0.129$), except that capric acid was greater in horses with BCS of 4 than in those with BCS of 6 (P = 0.008). In terms of overall composition, equine subcutaneous AT was composed of approximately 35.36 to 37.77% SFA, 35.80 to 36.90% MUFA, and 25.33 to 28.84% PUFA, which were markedly distinguishable from the relative percentages reported in ruminants and other monogastric species. Palmitic, oleic, and linolenic acids were the predominant SFA, MUFA, and PUFA with respective relative percentages of approximately 24.68, 28.96, and 16.41%, respectively. Linoleic acid, the predominant PUFA found in most ruminant and monogastric species, was the second most predominant PUFA in equine, at 6.78%. Vaccenic acid, a typical *trans* fatty acid found in ruminants, was not detected in horse subcutaneous adipose tissues. These data indicate that BCS did not have a marked impact on the fatty acid composition of the subcutaneous AT depot in the equine animal for the range of BCS investigated in the current study.

Key Words: equine, adipose, body condition

0806 Feeding a small amount of hay before concentrate neutralizes the effects of high starch diets on inflammation in horses. J. K. Suagee-Bedore*[1], K. Wimbush[1], D. R. Linden[1], and R. K. Splan[2], [1]*The Ohio State University, Wooster,* [2]*Virginia Tech, Middleburg*.

When fed to horses, high starch diets elevate plasma concentrations of IL-1β as soon as 1 h post eating. This increase in IL-β is possibly due to changes in intestinal pH that result from rapid bacterial fermentation of starches and sugars in the digestive tract. This altered pH may disrupt the gut microbial environment and ultimately lead to inflammation. The purpose of this research was to investigate the effect of feeding 0.9 kg of grass hay 30 min before feeding a concentrate meal (HF) on the postprandial rise in IL-1β, as compared to control horses receiving the same concentrate without hay first (HS). Six mature light-breed geldings of moderate body condition (5–6 on a scale of 1–9) were used in a switchback design. Horses were fasted overnight before being offered a concentrate feed at 0800 h that provided 1.2 g/kg bodyweight of nonstructural carbohydrates. Plasma from blood was harvested at −30 min (sample obtained before hay feeding), 1, 2, 4, 6, and 8 h post feeding. Horses were offered ad libitum grass hay following completion of their concentrate meal. Concentrations of IL-1β, D-lactate, glucose, and insulin were analyzed by repeated measures ANOVA (SAS v. 9.3). Where necessary, values were log transformed and are presented as geometric means. The HF treatment reduced ($P < 0.01$) postprandial geometric mean concentrations of IL-1β compared to the HS treated horses at post-feeding hours 2 (296 [263–330] vs. 449 [402–500] pg/mL), 4 (272 [244–303] vs. 474 [425–530] pg/mL), and 6 (257 [230–287] vs. 439 [394–490] pg/mL). The HF treatment also decreased ($P < 0.05$) mean D-lactate concentrations at post-feeding hours 2 (1188 ± 110 vs. 1509 ± 110 μmol/L) and 4 (1186 ± 110 vs. 1581 ± 110 μmol/L), as compared to HS treated horses. Plasma glucose and insulin increased postprandially for both treatments ($P < 0.001$) with no effect of HF treatment ($P > 0.5$). Given these findings, we believe that feeding a small amount of hay before feeding a meal of moderate starch and sugar content reduced the negative effects of rapid starch and sugar fermentation in the equine digestive tract, as seen through reduced postprandial D-lactate and IL-1β concentrations.

Key Words: high-starch diet, IL-1β, inflammation

0807 Feeding DigestaWell Buffer to horses neutralizes the effects of high starch diets on blood pH and inflammation. J. K. Suagee-Bedore*[1], A. L. Wagner[2], and I. D. Girard[2], [1]*The Ohio State University, Wooster,* [2]*Probiotech International Inc., St-Hyacinthe, QC, Canada*.

When fed to horses, high starch diets elevate plasma concentrations of lipopolysaccharide (LPS) at 2 h post eating and IL-1β at 1 h post eating. These changes are possibly due to rapid bacterial fermentation of starches and sugars in the digestive tract, which may alter the pH in the digestive tract and lead to inflammation. The purpose of this research was to investigate the efficacy of a dietary supplement containing bicarbonate, DigestaWell Buffer (DB), to mitigate these postprandial changes, as compared to control horses receiving the same concentrate but without the supplement (HS). Six mature light-breed geldings were used in a switchback design. Horses were fasted overnight before being offered a concentrate feed at 0800 h that provided 1.2 g/kg bodyweight of nonstructural carbohydrates. The DB treatment supplied 150 g of top dressed DB supplement. Plasma from blood was harvested at −30 min, 1, 2, 4, 6, and 8 h post feeding. Whole blood was analyzed for pH and TCO2. Horses were offered ad libitum grass hay following completion of their concentrate meal. Concentrations of IL-1β, LPS, D-lactate, glucose, and insulin, and pH and TCO2 values were analyzed by repeated measures ANOVA (SAS v. 9.3). Where necessary, values were log transformed and are presented as geometric means. Supplementation with DB reduced ($P < 0.01$) postprandial geometric mean concentrations of IL-1β at post-feeding hours 4 (284 [253–321] vs. 474 [421–534] pg/mL), and 6 (261 [232–294] vs. 439 [390–494] pg/mL), tended to decrease geometric mean D-lactate ($P = 0.060$) concentrations at 8 h post feeding (1215 [1120–1318] vs. 1457 [1344–1581] μmol/L), and decreased mean LPS concentrations across all time points ($P < 0.001$). Meal consumption reduced blood pH in both treatments; however, pH was higher in DB than HS (7.414 ± 0.003 vs. 7.398 ± 0.003) treated horses ($P < 0.05$). Plasma glucose and insulin increased postprandially for both treatments ($P < 0.001$) with no effect of DB treatment ($P > 0.1$). Blood TCO2 levels were below the upper limit of 37mmol/L but tended to be higher in DB treated horses (31.4 ± 0.3 vs. 30.6 ± 0.3 mmol/L, $P = 0.068$). Given these findings, we believe that DB mitigates the negative effects of rapid starch and sugar fermentation in the equine digestive tract, as seen through reduced postprandial inflammation.

Key Words: DigestaWell, IL-1β, lipopolysaccharide

0808 Efficacy of a brewer's yeast supplement with or without fat added to an energy restricted diet for performance horses. L. B. Hodge[*1], A. Boyer[2], and B. J. Rude[1], *[1]Mississippi State University, Mississippi State, [2]FL Emmert, Cincinnati, OH.*

Objectives of the current trial were to evaluate effects of additional fat to a brewer's yeast supplement on hoof, coat, mane, and body condition of performance horses fed an energy deficient diet. Twelve performance geldings were randomly allotted to one of 3 dietary treatments: 1) a commercially available horse feed (10% CP, 4.5% fat) at 0.35% BW/d; 2) diet 1 plus a brewer's yeast supplement at 226 g/d; 3) diet 2 plus corn oil at 10% of the diet. Diet 1 was fed to be deficient in energy to evaluate additional energy supplied by fat. Geldings were fed half of their diet treatment twice per d for 84 d. Geldings had ad libitum access to bermudagrass pasture, hay, and water. Body weight (BW) measurements and body evaluations were collected at initiation of the trial and every 28 d until 84 d. Body evaluations included coat and mane condition, body condition score (BCS), and hoof condition. Coat, mane and hoof condition were evaluated on a scale from 1 to 5 (1 reflecting poor or damaged and 5 reflecting glossy and smooth) accounting for condition, texture and appearance. Body condition was based on the standard BCS scale of 1 to 9 (Henneke et al., 1983). Data were analyzed through ANOVA using the GLM procedures of SAS. No effect of diet was found for hoof (3.5, 3.3, and 3.6; $P = 0.7973$), coat (3.2, 3.6, and 3.7; $P = 0.2724$), mane (3.5, 3.5, 3.4; $P = 0.9885$) or BCS (5.1, 5.5, and 5.2; $P = 0.9982$) for diets 1, 2, and 3, respectively. Body weights were not different (505.6, 516.7, and 505.5 kg; $P = 1.000$) among diets 1, 2, and 3, respectively. Addition of fat to brewer's yeast supplement did not enhance body scores or body weight. In a previous trial (Seidle et al., 2014), concentrate was fed at 0.9% BW/d and fat was supplemented at 5% of diet. It was concluded that feeding concentrate at this amount may have masked the effects of increased energy from fat. In the current trial, diet 1 (basal diet fed to all treatments) was fed to be energy deficient in an attempt to evaluate if additional fat (10% of diet) added to brewer's yeast supplement had an effect on body weights and condition. Results may have been influenced by forage quality, which was not measured. Research should be conducted to evaluate brewer's yeast supplement and fat while feeding a larger amount of Brewer's yeast.

Key Words: equine, brewer's yeast, fat supplementation

0809 Modeling ammonia emission rate from horses fed different concentrations of dietary crude protein. J. Weir[*1], H. Li[2], L. K. Warren[1], E. Macon[3], and C. Wickens[1], *[1]University of Florida, Gainesville, [2]University of Delaware, Newark, [3]Middle Tennessee State University, Murfreesboro.*

Evaluating the impact of animal agriculture on air quality has been the focus of recent research. Ammonia (NH_3) volatilization occurs when excess crude protein is fed and excreted as urinary nitrogen. Information regarding NH_3 emission from equine facilities is limited, and the effects of dietary CP intake on NH_3 emission have not been investigated. Nine mature (mean ± SE, 562 ± 13.1 kg) geldings were used in a 3 × 3 replicated Latin square design study to determine the effects of dietary CP concentration on potential NH_3 losses from urine of horses fed an all forage diet. We hypothesized that increasing dietary CP concentration would increase NH_3 emission rate. Three diets were formulated using bahiagrass and bermudagrass hays fed at 3 different crude protein concentrations: LOW-CP, MED-CP, and HIGH-CP (10.6, 11.5, and 12%, respectively). Horses consumed a commercial ration balancer to meet micronutrient requirements. Each study period consisted of an 11-d diet adaptation phase, followed by a 3-d total collection of urine. Samples were pooled within a period by diet ($n = 3$) and mixed with either wheat straw or wood shavings. Ammonia emission of these samples were measured using a 12-vessel emission system with a constant airflow rate (2.5 L/min) at 20°C over a 7-d period. Concentration of NH_3 in each vessel was measured using a photoacoustic multi-gas analyzer. Temperature, airflow rate and NH_3 concentration in each vessel were used to calculate NH_3 emission rate (ER). Data were analyzed as a Latin square using the Mixed Model procedure with repeated measures (JMP Pro v. 11). Concentration and ER data were log transformed. Crude protein intake differed ($P < 0.05$) from LOW-CP to MED-CP and HIGH-CP, as designed. Vessel NH_3 concentrations were different across diets ($P < 0.05$), ranging from 51.8 ppm (LOW-CP) to 87 ppm (HIGH-CP), and bedding types ($P < 0.01$) with straw being higher than shavings (97 vs. 73.5 ppm, respectively). Cumulative urinary NH_3 ER also differed across diets ($P < 0.01$) ranging from 4.9 g/m^2 to 8.2 g/m^2 and bedding types ($P < 0.01$), with straw being higher than shavings (11.1 vs. 6.9 g/m^2, respectively). This study confirms that high crude protein intake and wheat straw bedding increases NH_3 ER from equine urine.

Key Words: ammonia emission, equine, dietary protein

0810 Dietary supplementation of DigestaWell NRG to unconditioned Warmblood mares may reduce lactate rise following exercise. A. L. Wagner*[1], R. K. Splan[2], J. K. Suagee-Bedore[3], and I. D. Girard[1], *[1]Probiotech International Inc., St-Hyacinthe, QC, Canada, [2]Virginia Tech, Middleburg, [3]The Ohio State University, Wooster*.

Lactate rise during strenuous exercise and prolonged recovery to pre-exercise levels may partially contribute to elevated muscle soreness in humans and horses. Many equine disciplines require consecutive days of competition, and thus, horses may be challenged with soreness during successive days of work or competition. Additionally, during training, muscle soreness may affect or impair progress while trying to increase fitness in horses. There are a number of commercially available dietary supplements containing spices that are marketed to improve performance or exercise recovery; however, research on their efficacy is limited. Therefore, the objective of this research was a preliminary evaluation of a novel proprietary blend of spices in the supplement, DigestaWell NRG (NRG) on lactate rise and post-exercise lactate recovery in unconditioned horses. Nine mature warmblood mares were used in a crossover design with a 7-d washout period. Mares were fed twice daily with 1 kg concentrate supplemented with or without 100 g of NRG for 7 d. On Day 7 horses performed a standardized exercise test during which venipuncture blood samples were collected pre- and 10 and 30 min post-exercise. Plasma lactate was determined using a YSI 2300 STAT Plus glucose and lactate analyzer, and changes in lactate concentration were determined using repeated measures analysis of variance in the PROC MIXED procedure of SAS 9.3. The rise in lactate concentration (change from pre-exercise to 10 min post-exercise) as a result of exercise tended to be lower ($P = 0.10$) in NRG (52 ± 15%) compared to control horses (101 ± 15%). Additionally, the return post-exercise determined by the change in lactate concentration from 10 to 30 min post-exercise tended to be higher ($P = 0.10$) in NRG (28 ± 3%) compared to control horses (20 ± 3%). The results of this preliminary trial show the promise of NRG to reduce lactate rise and improve lactate recovery in unconditioned horses in response to exercise after consuming NRG after 7 d. This may indicate the potential for NRG to reduce muscle soreness following exercise; however, additional research is warranted with a longer supplementation period to determine the effects of NRG on lactate, inflammation, and muscle soreness following exercise.

Key Words: horse, exercise, lactate

0811 Maturity of bermudagrass hay affects digestibility by horses. T. L. Hansen*, E. C. Lee, O. K. Zugay, and L. K. Warren, *University of Florida, Gainesville*.

Bermudagrass (*Cynodon dactylon*) hay is one of the most common preserved forages fed to horses in the southeastern United States. Bermudagrass, a C4 plant, typically has greater fiber concentrations than C3 plants. The objective of this study was to evaluate equine digestibility of Coastal bermudagrass hays differing in maturity. We hypothesized DM digestibility (DMD) would be reduced in bermudagrass diets, but NDF and ADF digestibility (NDFD and ADFD) would be greater in the bermudagrass diets compared to C3 legume and grass hays due to greater fiber intake. Five dietary treatments (alfalfa hay, *Medicago sativa*, ALF; orchardgrass hay, *Dactylis glomerata* L., ORCH; early maturity bermudagrass hay 4 wk regrowth, EARLY-BG; mid-maturity bermudagrass hay 5–6 wk regrowth, MID-BG; late maturity bermudagrass hay 8 wk regrowth, LATE-BG) were evaluated in this 5 × 5 Latin square design experiment with 5 mature geldings ($n = 5$, BW = 552 ± 14 kg, mean ± SEM). Hay was fed at 1.62 ± 0.02% BW (DM basis), and horses were fed a commercial ration balancer to meet micronutrient requirements. A 7-d dietary adaptation was imposed followed by a 3-d total fecal collection. A 2% subsample of daily fecal excretion was saved for DM, NDF, and ADF analyses. Fiber concentrations were determined using an ANKOM 200 Fiber Analyzer. Digestibility was calculated by difference between intake and excretion. Data were analyzed as Latin square design using a generalized linear model (SAS, v. 9.3). Statistically different means were separated by Sheffe's method. Diets differed in DMD (Table 1, $P < 0.001$). Dry matter digestibility was greatest for ALF and least for MID-BG and LATE-BG diets ($P < 0.05$). Fiber digestibility differed by diet ($P < 0.001$) with NDFD and ADFD greater ($P < 0.05$) for ALF, ORCH, and EARLY-BG diets compared to MID-BG and LATE-BG diets. Despite similar fiber concentrations among the bermudagrass hays, digestibility of EARLY-BG was comparable to other forage types with lower fiber concentrations. These findings indicate fiber structure in bermudagrass changes with maturity, reducing forage digestibility.

Key Words: equine, fiber, warm-season grass

Table 0811.

Table 1.

	ALF	ORCH	EARLY-BG	MID-BG	LATE-BG	SEM	$P <$
DMD, %	61.2[a]	50.6[b]	46.3[b]	35.0[c]	33.6[c]	1.3	0.001
NDFD, %	48.0[a]	48.9[a]	51.9[a]	38.9[b]	38.8[b]	1.4	0.001
ADFD, %	44.4[a]	49.6[a]	45.1[a]	30.7[b]	31.1[b]	2.6	0.001

[abc]$P < 0.05$

0812 Investigation of equine hindgut microbiota development in young horses. B. St-Pierre*, M. E. Graf, B. M. Schlaikjer, and R. C. Bott, *South Dakota State University, Brooking*.

The gastrointestinal microbiota is an important contributor to the health and nutrition of mammals. Since the gut of young mammals is devoid of microorganisms at birth, its colonization by symbiotic microbes and their arrangement into complex communities is a critical aspect of a young host's post-natal development. Compared to most other experimental animal models or livestock, the gut microbiome of the horse remains largely unexplored, particularly in young foals. To gain further insight on development of the equine hindgut bacterial microbiota, fresh fecal samples were collected from 2 foals over their first 4 mo of life. Fecal samples from their respective dams were also collected as representative of mature hindgut microbial communities. Microbial DNA was extracted from the samples and used as template to generate PCR amplicons of the bacterial 16S rRNA gene (V1-V3 region), which were sequenced using the Illumina MiSeq 2×300 platform. A combined total of 333,300 high quality sequence reads corresponding to the expected full length PCR amplicons were used to determine the hindgut bacterial composition of the sampled animals. The number of sequence reads per sample ranged between 17,613 and 59,964. At the youngest age sampled (3.7 wks), the bacterial profile consisted predominantly of Verrucomicrobia (50.9%) and Bacteroidetes (22.9%) related sequences, with the most abundant species-level OTU (operational taxonomic unit) for each phylum found at 44.9% (OTU SDEc-1) and 10.7% (OTU SDEc-2), respectively. At later time points (5.86–18.57 wks), Verrucomicrobia representation was reduced dramatically (0.7– 2.1%), while Bacteroidetes appeared to be maintained within a similar range (20.3– 37.7%). However, population shifts were detected within Bacteroidetes. For instance, OTU SDEc-2 abundance was greatly reduced during this period (< 0.05%), and OTU SDEc-3 was transitionally higher (range of 5.1–7.2%) between 5.6 wks to 9.57 wks. We also observed an overall increase from 13.1% to 65.0% in Firmicutes representation among foal samples during the sample period. In comparison with the fecal bacterial composition of their dams (2.2–15.5% Bacteroidetes; 71.6–83.3% Firmicutes), our results suggest that hindgut bacterial populations in horses younger than 4 mo have not yet developed a mature microbiota.

Key Words: gut microbiota, microbial ecology, 16S rRNA, bacteria

0813 Evaluation of chromic oxide and titanium dioxide as external markers for estimating digestibility in horses. A. Fowler*[1], M. B. Pyles[1], B. Harlow[1,2], S. H. Hayes[1], A. Crum[1], and L. M. Lawrence[1], *[1]University of Kentucky, Lexington, [2]USDA-ARS Forage Animal Production Research Unit, Lexington, KY*.

Total fecal collections are frequently used when performing digestibility studies in horses, however collection of all fecal output (FO) is labor intensive. The use of indigestible markers to determine digestibility indirectly will simplify digestibility studies. The objective of this study was to evaluate the accuracy of chromic oxide (Cr_2O_3) and titanium dioxide (TiO_2) in predicting daily FO. Eight Thoroughbred mares were used in this study: four mares were fed Cr_2O_3 and four mares were fed TiO_2. The daily ration was split into two equal feedings per day and consisted of timothy hay cubes, a pelleted concentrate, and soybean oil. External markers were top-dressed on the timothy cubes and complete consumption was ensured. Diets and markers were fed for 10 d before and during the 4-d total fecal collections. Fecal samples (250 g) were obtained every 4 h for external marker analysis; the remaining feces were composited by horse per day. Actual total FO was measured using daily composites and compared to FO calculated from marker concentrations in the 4-h fecal samples using a paired *t* test. For horses fed Cr_2O_3, mean actual FO was 2.62 ± 0.16 kg DM/d and mean calculated FO was 2.64 ± 0.07 kg DM/d ($P > 0.1$). For horses fed TiO_2, mean actual FO was 2.57 ± 0.12 kg DM/d and mean calculated FO was 2.79 ± 0.12 kg DM/d ($P > 0.1$). The absolute difference between actual FO and calculated FO was determined for each horse. The absolute difference was different from 0 for all horses consuming either TiO_2 or Cr_2O_3 ($P < 0.001$) probably because some horses did not achieve constant marker excretion during the collection period. Constant marker excretion is necessary if fecal grab samples are to be used to calculate digestibility. Increasing the frequency of marker dosing may result in a more stable marker excretion. With more validation, Cr_2O_3 and TiO_2 as external markers may be useful for estimating mean daily FO.

Key Words: digestibility, equine, external marker

0814 Effect of starch source in pelleted concentrates on fecal bacterial communities in thoroughbred mares. M. B. Pyles*[1], A. L. Fowler[1], V. Bill[1], B. E. Harlow[1,2], A. Crum[1], S. H. Hayes[1], M. D. Flythe[1,2], and L. M. Lawrence[1], *[1]University of Kentucky, Lexington, KY, [2]United States Department of Agriculture, Agricultural Research Service, Forage-Animal Production Research Unit, Lexington*.

Dietary starch source has been shown to affect fecal bacterial communities of horses fed cereal grains with little to no processing. Others suggest that grain processing, such as

pelleting, increases foregut starch digestibility, possibly mitigating effects of starch source on bacterial communities. The aims were to (i) determine the effect of starch source in pelleted concentrates on *Lactobacillus* spp., total starch utilizing bacteria (TSU), and cellulolytic bacteria in mares, and (ii) evaluate pre- and postpartum changes in fecal bacterial communities from 324 d of gestation to 28 d postpartum. Nineteen Thoroughbred mares were paired by last breeding date then randomly assigned to either an oat-based (OB) or a corn and wheat middlings–based (CWB) pelleted concentrate in addition to forage. Beginning at 310 d of gestation, mares were fed 3.2 kg/d (DM) of assigned concentrate (OB or CWB). After parturition, concentrate intake gradually increased to 4.8 kg/d (DM). The concentrates contained 38.0%, 36.2% starch, 6.6%, 8.8% WSC, and 5.4%, 7.5% ESC for OB and CWB, respectively. Fecal samples were collected at 324 d of gestation, before parturition, 24 h, 14 d, and 28 d postpartum. Fecal samples were collected immediately after defecation by catch or from the center of the pile into single use plastic bags and transported to the lab in an insulated cooler (37°C) under CO_2. Samples were serially diluted 10-fold with phosphate buffered saline and the dilutions were used to inoculate selective media. Selective media were used for enumeration of *Lactobacillus* spp., TSU, and cellulolytic bacteria. Data were log transformed then analyzed with PROC MIXED (SAS 9.3) to test the main effects of treatment (OB or CWB), time of sample, and treatment by time interaction. Results were considered significant when $P < 0.05$. There was no effect of starch source on enumerated bacterial communities ($P > 0.05$), in contrast to previous work. These results suggest that pelleting concentrates may alter some of the effects of starch sources. There was no effect of time on TSU ($P > 0.05$), however *Lactobacillus* spp. and cellulolytic bacteria decreased 24 h postpartum ($P < 0.05$). Therefore, major physiological events, such as parturition, appear to alter the hindgut microbiota.

Key Words: bacteria, concentrate, horse

HORSE SPECIES SYMPOSIUM: NUTRITION AND IMMUNOLOGY

0815 Nutritional immunology for the geriatric horse.

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Over the past century, improvements in health care and advancements in science and medicine have extended the average lifespan of humans and companion animals, including horses. We are now facing new challenges with the paradox of an older horse population with increased longevity and the potential of increased age-associated diseases. One of the most recognized consequences of aging is a decline in function of the immune system. Two main terms that characterize a declining immune system of the old horse are immunosenescence and inflamm-aging. Immunosenescence in the aged individual is characterized by changes in various aspects of cellular and humoral immunity, in particular a decline in lymphoid cell numbers and function. It has been well documented that the aged, including horses, have increased susceptibility to and prolonged recovery from infectious disease, poor vaccine responses, and increased incidence of cancers. Somewhat paradoxically, advanced age is also associated with increased production of pro-inflammatory cytokines and other inflammatory mediators, a phenomenon termed inflamm-aging. Inflamm-aging predicts both increased morbidity and mortality for a variety of chronic diseases. Together, immunosenescence and inflamm-aging may increase susceptibility to infection and contribute to aged-related health conditions such as arthritis, equine Cushing's disease, and laminitis. Nutritional immunology is a new field of study, in which nutrition is used as a modifiable factor in impacting immune function in particular to delay/reverse immunosenescence and to improve the aged resistance to infection. Further, nutritional interventions are practical, cost-effective approaches to mitigating this age-related breakdown in immune function. Natural dietary compounds found in a variety of plants, roots, fruits, vegetables, nuts, and seeds are promising candidates in helping to combat the effects of an aging immune system. Several natural dietary compounds (carotenoids, flavonoids, isothiocyanates, terpenoids, proanthocyanidins, omega fatty acids, and polyphenolic compounds) have been shown to possess broad biological activities of anti-oxidation, anti-inflammation, detoxification, regulation of signaling pathways, modulation of enzyme activities, and improvement of immune responses to vaccination. Unfortunately, few studies have been conducted to better understand what effect nutrition may have on modulating or improving immune responses of the aged horse. Previous and current nutritional studies to improve immune function in old horses by supplementation with vitamin E, n-3 polyunsaturated fatty acids (DHA), prebiotics, and polyphenols will be reviewed here. More research is needed to identify effective and optimal conditions for various nutritional intervention regimens to improve the function of the aged immune system of the horse.

Key Words: horse, aging, immune

0816 Nutrition and immunity: General principles.

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The development, maintenance, and response of the immune system are influenced by nutrition. For most nutrients the most important nutritional strategy for optimizing immunity is meeting the established requirements for maximizing growth, reproduction, and feed efficiency and avoidance of traditional signs of deficiency. Severe deficiencies of required nutrients typically impair host immunity and resistance to disease, but such deficiencies should be rare in modern animal production.

More relevant are marginally deficient and surfeit levels of nutrients. In the case of several essential nutrients, leukocytes, especially T lymphocytes, are very sensitive to marginal deficiencies, while for many other nutrients the immune system is largely unaffected by marginal deficiencies. This difference in sensitivity is due the types and amounts of nutrient transporters expressed on each cell type. Nutrients also support the anabolic processes of pathogens and increase their pathogenicity, though this troublesome effect is likely limited to a small subset of nutrients. Iron in particularly can increase the pathogenicity of some pathogens when provided in excess. Several essential and nonessential nutrients have regulatory effects on leukocytes. Required nutrients with indisputable immunoregulatory actions in rodents and livestock include the long-chain polyunsaturated fatty acids (PUFA) and vitamins A, D, and E. Many nutrients that are not normally considered as being dietary essential also modulate immunity, including carotenoids, vitamin C, and phytonutrients (e.g., capsicum, genistein, curcumin, essential oils, conjugated linoleic acids). In general those nutrients that are not structural components or cofactors for enzymes are most likely to be immunomodulatory. Unlike increases in nutrients from deficient to sufficient levels, where many indices of immunocompetence go from impairment to normal function, supplementation of immunomodulatory nutrients causes some components of immunity to be elevated and others to be diminished; in other words, the type and intensities of responses have been changed (i.e., immunomodulated). In situations where a single infectious disease dominates the production losses and where it is clearly known what type of immune response optimally protects against that disease, supplementation of a nutrient that modulates the immune system toward that optimal response is indicated. Thus, the value of an immunomodulatory nutrient to "improved" immunity is context dependent and depends on the types of disease challenges in a herd. In summary, nutritional impacts on immunity are complex and their understanding and applications requires a "first principles" approach.

Key Words: disease, immunity, deficiency

0817 Optimizing nutrition to improve immune function in horses. L. K. Warren*, *University of Florida, Gainesville*.

Nutrition plays a supportive role in immunity; thus, a balanced diet is critical to mount an appropriate immune response to infection or trauma. Many nutrients have widely recognized roles in host defense; however, nutrient requirements for horses who are stressed or immunocompromised are not fully known. Owners and farm managers are increasingly interested in holistic approaches to maintaining the health of horses in their care, which has encouraged research on the impact of various nutrients and dietary supplements on immune function. Investigations have typically targeted three populations: performance horses, foals, and horses with compromised or inappropriate immune responses (e.g., senior horses, horses with recurrent airway obstruction). Sport horses face many immunosuppressive stressors, including strenuous exercise training, frequent competition, and transport over long distances, including international shipping. This group also has increased exposure to pathogens via contact with outside horses at competition venues. Foals present a different set of challenges, which center on delayed onset of adaptive immune responses. Protection against pathogens are provided to the foal through the ingestion of immunoglobulins in colostrum soon after birth; thus, investigations often focus on the diet of the mare as a means to improve colostrum quality. Immuno-nutrition research in horses has typically been inspired by positive outcomes observed in other species. Although a comparatively small body of research has been conducted in horses, several nutrients have been explored, including vitamins (E, C), trace minerals (Zn, Se), amino acids (arginine), and fatty acids (omega-3, omega-6, conjugated linoleic acid). Additionally, prebiotic fibers (mannan-oligosaccharides, β-glucans), probiotics (lactic acid bacteria, live yeast cultures), and nonnutritive dietary supplements (resveratrol, superoxide dismutase) have received some attention in equine research. Collectively, the impact of these nutrients and supplements on the status and functional capacity of the immune system have been variable. Differences in study outcomes may be due to high variability in responses among horses, health status, dosage, length and timing of supplementation, basal diet composition, type of immune system challenge evaluated, and immunological variables measured. The latter is often more limited in scope in equine compared to other livestock research, where tissues can be harvested postmortem for more detailed evaluation of response to diet. Ultimately, the study of nutrition's impact on immunity in horses is in its infancy, with many other nutrients to explore and much to learn. Pairing equine nutritionists with immunologists could hasten research progress and improve study effectiveness.

Key Words: equine, immuno-nutrition, diet

0818 Effect of selenium and vitamin E supplementation on blood glutathione peroxidase activity and selenium in moderately exercised horses. E. Velázquez Cantón*, A. H. Ramírez Pérez, L. A. Zarco Quintero, R. Rosiles Martínez, and J. C. Ángeles Hernández, *FMVZ-UNAM, Mexico*.

The objective was to evaluate the effect of selenium (Se, Se-yeast) and vitamin E (E, α-tocopheryl acetate) supplementation on red cell glutathione peroxidase activity (GPx) and Se blood concentrations in moderately exercised horses. The Institutional Animal Care and Use Committee of the School of Veterinary Medicine, National University of Mexico, approved the experimental procedures. Twenty-four clinically healthy horses (5–15 yr, 450 kg BW) from the Mexico City Police, without physical activity the month before this trial,

Table 0818.

Blood glutathione peroxidase activity (GPx, U/L) and selenium (Se, ng/mL) in supplemented moderately exercised horses

	Adaptation period					Exercise				Re-adaptation period		
										Unsupplemented		
Day	0	7	14	21	28	35	42	49	56	63	70	77
GPx[1] (effect of interaction day×Se×E)												
LSeLE[2]	1179	1071	1009	1069	1343	1513	1734	1516	1318	1114	1031	851
LSeHE	1082	971	899	935	1117	1559*	1564*	1484*	1631	1050	1002	876
HSeLE	1235	1112	1126	1015	1397	1638	1757	1598	1660	1201	1054	951
HSeHE	1422	1331	1261	1132	1502	1869*	1955*	1862*	1705	1285	1163	994
Se[3] (effect of day)												
	41.9^{d}	61.6^{c,d}	74.0^{c,d}	117.0^{b,c}	210.8^{a}	118.4^{b}	76.9^{c,d}	80.7^{b,c,d}	105.1^{b,c}	60.4^{c,d}	76.1^{c,d}	54.6^{c,d}

[1]SEM: GPx, 98.9; Se, 7.0.
d0, baseline concentrations
[2]LSe, 0.1; HSe, 0.3 mg Se/kg DM; LE, 1.6; HE, 2.0 IU/kg BW
*Groups LSeHE and HSeHE are different (P<0.05) within the same column
[3]Mean values within a line with different letters are different (P<0.05)

were used. They were individually stabled and randomly allocated in a factorial experiment (2 Se × 2 E levels) with repeated measures. The groups, with 6 experimental units in each one, were: LSeLE, HSeLE, LSeHE, and HSeHE (LSe, 0.1; HSe, 0.3 mg Se/kg DM and LE, 1.6; HE, 2 IU vitamin E/kg BW; NRC, 2007). Se and E were given to supplement the deficient daily ration (Se, < 2μg; E, 14.4IU by kg DM, respectively). The study lasted 77 d distributed in 3 periods: adaptation (d 0 to d 32); moderate exercise (d 33 to d 56) and readaptation (d 57 to d 77). Exercise period consisted of 30 min (5:20:5 min. warm up: gallop: cool down) in 3 consecutive days and 4 d without exercise. At d 64, supplementation was stopped. Once a week, jugular blood samples were taken; during the exercise period it was taken 10 min after activity of the third day. Day zero corresponded to baseline measurement of studied variables. GPx was quantified by spectrophotometry (Randox Daytona) while Se was quantified by hydride generation atomic absorption spectrometry. Data were analyzed by a mixed model (PROC MIXED, SAS 9.1.3) with the design described above. Day, Se, E, and their interactions were the fixed effects, while horse nested in treatment was the random effect. Statistical significance was set at $P < 0.05$. Tukey-Kramer's test was used to compare LSM. The interaction: day × Se × E affected ($P < 0.05$) blood GPx; differences were observed at d 35–49 between HSeHE and LSeHE groups (1915.0 ± 65.9 U/L; 1510.1 ± 54.1 ng/mL, respectively). Day and Se affected blood Se ($P < 0.05$). Values from d 0 to d 14 were not different ($P > 0.05$) from d 63 to 77 (61.4 ± 2.1 ng/mL). Blood Se increased at d 28 (210.8 ± 7.0 ng/L) and decreased again at d 35 (118.38 ± 7.0 ng/L). In general, Se was higher in HSe (97.5 ± 3.8 ng/mL) than in LSe horses (82.01 ± 3.8 ng/mL). Conclusion: supplementation levels of both Se and E affect blood GPx and Se and are closely related to physical activity.

Key Words: selenium, α-tocopheryl, glutathione peroxidase

0819 Age-related changes in select fecal bacteria in foals. M. B. Pyles*[1], A. L. Fowler[1], V. Bill[1], B. E. Harlow[1,2], A. Crum[1], S. H. Hayes[1], M. D. Flythe[1,2], and L. M. Lawrence[1], *[1]University of Kentucky, Lexington, [2]United States Department of Agriculture, Agricultural Research Service, Forage-Animal Production Research Unit, Lexington, KY.*

Adult horses depend on the microbial community in the hindgut to digest fiber and produce VFAs that are utilized for energy. Microbial colonization in the gastrointestinal tract of foals is essential to develop a healthy symbiotic relationship and prevent proliferation of pathogenic bacteria. However, colonization is not well understood. The objectives were to evaluate the age-related changes and effects of maternal diet on select fecal bacterial groups in foals from 1 d to 28 d of age. Thoroughbred foals ($n = 19$) were from dams fed one of two concentrates: an oat-based (OB) or corn and wheat middlings–based (CWB) pelleted concentrate. The mares began the experimental diet at 310 d of gestation and remained on the assigned diets until 28 d postpartum. The foals had access to assigned concentrates, and a mixed grass and alfalfa hay and cool-season grass pasture were available ad libitum. Fecal samples were collected from foals at 1 d (14–36 h), 4 d, 14 d, and 28 d. Foals were continuously monitored on sample days to collect fecal samples immediately after defecation by catch into sterile specimen cups or from the center of the pile using sterile gloves. Fecal samples were transported to the laboratory in an insulated cooler (37°C) under CO_2. Samples were serially diluted 10-fold before inoculation of selective media. Enumerations were performed for *Lactobacillus* spp., total starch utilizing bacteria (TSU), and cellulolytic bacteria (CB). Enumeration data were log transformed then analyzed with PROC MIXED (SAS 9.3) to test the main effects of maternal diet (OB or CWB), time of sample, and interaction between maternal diet and time. Results were considered significant when $P < 0.05$. There was no effect of maternal diet on bacterial enumerations ($P > 0.05$). There was an interaction between maternal

diet and time in *Lactobacillus* spp. with CWB foals having more lactobacilli than OB at 1 d and 4 d ($P < 0.05$); however, there were no differences observed at 14 d ($P > 0.05$). These results indicate that maternal diet may influence some bacteria in foals. Fecal lactobacilli, TSU, and CB increased with age in foals ($P < 0.05$) with CB first appearing between 4 d and 14 d. It is evident that colonization of the hindgut is a sequential process beginning early in the foal's life.

Key Words: bacteria, maternal diet, foal

0820 Changes in equine hindgut fermentation and carbohydrate digestion in response to varying sources of nitrogen. M. O. Lass*, J. S. Drouillard, J. M. Kouba, C. I. Vahl, Y. Wei, and T. L. Douthit, *Kansas State University, Manhattan*.

Casein or urea were administered as dietary N sources in a replicated 3 × 3 Latin square experiment to evaluate impact on hindgut fermentation and carbohydrate digestion in the horse. A basal diet consisting of native prairie hay (5.9% CP; 72.7% NDF) was fed to 9 cecally cannulated horses (469 ± 109 kg BW) at 0.6% of BW DM basis every 8 h for 6 wk. Periods consisted of a 7-d acclimation to the basal diet and a 7-d dosing phase. Horses were dosed via the cecal cannula 3×/d at the time of feeding for 7 d with 200 mL of water (W), or with 200 mL of water containing casein (C) or urea (U) to provide 1.12% N in the diet. During the final 4 d of each dosing phase, total fecal output was collected, and cecal digesta was collected 4 h after each feeding. Cecal digesta and feces were analyzed for pH and concentrations of ADF, NDF, ADIA, total VFA, and ammonia. Dosing with U resulted in greater concentrations of cecal ammonia (3.00 mM, $P < 0.05$) compared to horses dosed with W (1.69 mM), or C (2.01 mM). Cecal pH increased ($P < 0.01$) in horses dosed with C (7.72) or U (7.85) compared to W (7.45), but fecal pH was not different between treatments ($P > 0.05$). Total VFA concentrations in cecal digesta were greater ($P < 0.01$) for horses dosed with U (50.27 mM) compared to those dosed with W (32.17 mM) or C (32.17 mM). Fecal NDF and ADF were decreased ($P < 0.05$) in horses dosed with U (63.07% NDF, 52.78% ADF) or C (59.68% NDF, 49.98% ADF) compared to those treated with W (66.50% NDF, 54.49% ADF), but ADIA content was not different ($P > 0.05$). Taken together, differences in cecal ammonia, pH, and total VFA, along with changes in fecal NDF and ADF as a result of treatment, indicate that protein and non-protein N sources introduced directly into the cecum lead to changes in microbial fermentation in the hindgut that increase fiber digestion in the horse.

Key Words: equine, fiber digestion, nitrogen

0821 Effects of meal size and frequency on the equine cecal microbiota. E. B. Venable*[1], S. S. Bland[1], H. Holscher[2], T. W. Liu[2], and K. S. Swanson[2], [1]*Southern Illinois University, Carbondale,* [2]*University of Illinois, Urbana*.

The effects of meal size and frequency on the equine cecal microbiota are not well documented. We hypothesized that meal size will alter the profile of the microbiota present in the equine cecum. Southern Illinois University Institutional Animal Care and Use approval (#13–070) was obtained before the initiation of this research. Cecally cannulated horses ($n = 6$) with a BCS of 5 (± 0.5) were utilized in this replicated Latin Square (3 × 3) design. All horses received group pasture turnout daily for approximately 6 h and were stalled overnight in identical box stalls (3 × 4 m). Treatment diets of Strategy® pelleted grain-based concentrate were as follows: A = one meal, 2.72 kg, 0600 h; B = two meals, 1.36 kg, 0600 and 1600 h; C = three meals, 0.91 kg, 0600, 1200, and 1600 h. Each treatment period consisted of 8 d of acclimation followed by 3 d of collection. All horses received ad libitum access to water, a white salt block, and 3 kg of mixed alfalfa/grass hay offered overnight. Body weight was recorded weekly and data were analyzed using a Latin square design with the proc MIXED procedure of SAS and was not affected by treatment ($P > 0.05$) Cecal samples (216 total) were collected four times daily over a three-day collection within each period. Cecal bacterial DNA was extracted, and 16S rRNA amplicon sequencing using Illumina technology was followed by analysis using QIIME 1.8.0 and proc MIXED. Significance was set at ($P \leq 0.05$). Weighted principal coordinates analysis (PCoA) of UniFrac distances between samples based on their 97% OTU composition indicated that Treatment A was different than Treatment C ($P = 0.028$). In addition, PCoA also revealed a significant difference associated with breed ($P < 0.05$) for both weighted (abundance) and unweighted (community composition) measures. Alpha diversity measures indicated that bacterial diversity is higher in geldings as compared to mares ($P < 0.01$). Predominant bacterial phyla included Firmicutes (58.8–63.2%); Bacteroidetes (28.78–34.2%); Proteobacteria (2.2–2.8%); and Spirochaetes (2.5–2.7%) for all treatments. Furthermore, when treatment effects were examined at the genus level, six different genera were significantly affected by treatment (*Prevotella*, *YRC22*, *Lactobacillus*, *Streptococcus*, *Coprococcus*, and *Phascolarctobacterium*). These data demonstrate that size and frequency of pelleted concentrate meals affect both the abundance and the composition of the bacteria present in the equine cecum.

Key Words: horse, microbiota, meal size

HORSE SPECIES SYMPOSIUM: URBAN STUDENTS IN ANIMAL SCIENCE AND THE IMPACT OF EQUINE PROGRAMS

0822 Making animal sciences relevant to the urban student: Connecting to the real world.
J. J. Parrish*, *University of Wisconsin, Madison*.

The current Animal Science student is not from an agricultural background and is female. Learning requires information be assimilated onto a conceptual framework. Coming from nonagricultural backgrounds makes it more difficult for students to create the conceptual framework around animals and livestock on their own without help from the instructor. Both experiential and active learning approaches are needed to create context. For example, we can use laboratories, simulations/case studies, writing exercises and international activities in or outside of the classroom. Laboratories in Animal Sciences have the opportunity to utilize animals, tissues, or forages to demonstrate how lecture connects to the real world. For students who do not have a connection with livestock, the chance to interact with cattle, sheep, pigs, or horses may be their first experience with a large animal. Any exposure to or contact with animals in the context of learning is experiential and a profound life-changing event for most students. Laboratories also ensure students learn how to interact as a team to achieve some outcome. The interplay between students in these teams allows the construction of new contextual information so critical in long-lasting learning. Simulations and case studies provide an increase in student motivation to learn by creating a "need to know" situation. While expensive initially, simulations and cases can be used in subsequent years without the initial investment or need to maintain animals. Writing exercises as a required skill in any occupation can also provide a means for students to think more deeply on a subject and create their own connections to the real world. International agriculture increasingly is becoming the focus of not only commodity sales but also direct competition for the US agriculture economy. The classical method of travel to an international destination is out of the economic reach of many Animal Science students. Case studies can have students solve problems in a foreign culture/environment and so gain novel solutions but also international competency. A key impediment to learning is not seeing anyone who connects with them as a role model or presents a point of reference for them to aspire to or that is even relevant. Female students may not see themselves as animal scientists as they only see and hear male instructors. Animal Science must remain sensitive to the needs of society and Animal Science students if it is to retain relevance in the future.

Key Words: experiential, active, learning

0823 Creating hands on learning opportunities for inexperienced equine students.
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Universities across the country offer equine-related classes to a diverse population of students. National trends indicate that 80–85% of these enrolled students are female, and more than 50% are from suburban or urban backgrounds. Career goals for most of these students require firsthand experiences with animal care, behavior, and management. Students interested in marketing and sales of animal health-care products or retail merchandise also require knowledge of animal husbandry. Approximately 65% of students in Animal Science programs, particularly those of urban backgrounds, have little to no experience with horses and thus require experiential learning opportunities.

The Animal and Veterinary Sciences Department at Clemson University offers Pre-Veterinary Sciences (60%), Animal Agribusiness (20%), and Equine Business (EQUI; 20%) concentrations. The latter two require a minor in Business Administration, therefore combining a foundation in animal science with business courses. EQUI is aimed at students who wish to enter any facet of the horse industry that typically does not require an advanced degree. Most students enter the work force directly onto a horse farm or indirectly in allied animal health industries, marketing positions for manufacturing, feed mills, or pharmaceutical companies or through supporting careers such as lawyers, horse associations or councils, public and higher education, and more. Students enrolled in EQUI have a diverse background; some have substantial horse experience and others have none. Therefore, it is important for faculty to provide the much-needed experiences required for successful job placement.

Courses required to meet these needs should be founded in experiential learning, utilizing live animals to provide these hands-on experiences. Formal courses and laboratories, volunteering, interning or working at a horse farm, being a working student, or enrolling in a farm immersion practicum are options. Faculty must learn their students' strengths and weaknesses to offer suggestions on the types of experiences that are required to strengthen their resumes and gain more horse experience. From basic horse handling and health care skills to working with a wide variety of production phases, creating unique individualized experiences is a must. To be successful in doing this, faculty need an organized system of integrating students from a varied background and have a diverse teaching style to cater to all students. Faculty are encouraged to develop efficient and achievable goals for students who have very little experience to provide relevant and less overwhelming experiences that align with their goals.

Key Words: horses, experiential learning

0824 Retaining urban students in animal science: The role of equine programs. J. A. Sterle* and H. D. Tyler, *Iowa State University, Ames*.

The influx of non-traditional, urban students into Animal Science programs in recent years is well documented. While there are slight differences in the percentages of urban students between programs, the trend has been steadily increasing and is often the cause of increased enrollment in Animal Science programs across the country. Many of these students also indicate a primary interest in veterinary medicine. Sometimes, once exposed to the realm of Animal Science, these students are lost to other majors. Many leave because they do not find a "home" in Animal Science; for others, it may be too much emphasis on the traditional livestock species for their liking. However, for those who remain, opportunities abound. Current placement rates of Animal Science graduates at ISU are 98% within 6 mo of graduation. So, the question is: How can we convince urban students, many of whom are high achieving, driven, and intelligent, to remain in Animal Science and one day contribute to the Animal Science industry (even in other species)? The most obvious answer is to make Animal Science more relatable to their interests early in their academic career, and one bridge for that may be equine courses and activities. Freshmen entering Iowa State University's Animal Science program in the fall of 2015 ranked horses second out of all species, with 30% (of 315 responding) citing equine as the primary or secondary interest. The species with the most initial interest from this group was companion animals/household pets (54% ranked companion animals first or second). Anecdotally, it is the urban students who list companion animals first and often list equine second and vice-versa. The current Animal Science curriculum at ISU requires sophomore students to choose three courses from a directed list representing each species (Beef Cattle Science, Swine Science, Equine Science, Sheep Science, Poultry Science, Dairy Cattle Science, Companion Animal Science, or Foods of Animal Origin; with Lab Animal Science to be added in fall 2016). Requiring the third three-credit course on another species often sparks interest in the additional area. Offering these type of courses early in the curriculum allows students to further define their interests while exposing them to a potential new area early enough to explore it further. Allowing students to take in-depth courses on their species of interest early in their academic career keeps them interested in their major and increases retention.

Key Words: equine, undergraduates, urban

0825 Prolonged head elevation causes mucosal IgA fluctuation in horses. J. M. Bobel*, M. R. Di-Lernia, J. R. Abbott, M. T. Long, and L. K. Warren, *University of Florida, Gainesville*.

Stress has a pronounced effect on immune cells and their ability to mount an effective defense against pathogens. Prolonged head elevation is thought to be a major contributor to the increased risk of respiratory disease associated with transportation in horses. Elevated cortisol and changes in leukocyte populations in response to transportation stress are well documented in horses. Few studies have investigated other aspects of immune function that may predispose horses to respiratory disease following head elevation. The objective of this study was to determine if prolonged head elevation affects mucosal IgA secretions and to evaluate the potential use of mucosal IgA as indicators of stress. Twelve horses (mean ± SEM, 552 ± 10 kg; 11.5 ± 1.4 y) were tethered for 12 h with their heads elevated at a height of 1.5 m to induce physiological stress. While tied, horses had unlimited access to bermudagrass hay and were offered water every 2 h. Each horse underwent head elevation on 4 occasions, each separated by 30 d. When not tied, horses were maintained on pasture forage. Nasopharyngeal flush (NPF), whole blood, saliva, and fecal samples were obtained before head elevation (Pre), immediately after (0 h), and 12, 24, and 72 h post head elevation. Cortisol concentration was measured in serum and saliva and IgA concentration was measured in NPF, saliva, and fecal water. Data were compared using mixed model ANOVA with repeated measures. Both serum and saliva cortisol were elevated after head elevation ($P < 0.0001$) and returned to baseline by 12 h post. Salivary ($P = 0.0005$) and fecal water ($P = 0.01$) IgA were elevated above Pre at 0 h post. At 12 h post, salivary ($P < 0.0001$) and NPF ($P < 0.0001$) IgA were lower than Pre. Fecal water IgA remained elevated above Pre at 12 h post ($P = 0.04$) but dropped below Pre at 24 h post ($P = 0.005$). Salivary IgA remained lower through 72 h post ($P = 0.006$), whereas NPF and fecal water IgA returned to normal by 24 and 72 h post, respectively. Prolonged head elevation induced physiological stress and alterations in protective mucosal secretions. Instability in IgA secretions may partially explain the heightened risk for respiratory disease following transportation. Persistent fluctuations in mucosal IgA suggests the time course of physiological stress may exceed that represented by the transient elevation of cortisol. Mucosal IgA secretions may be good indicators of both acute and chronic stress in horses.

Key Words: stress, immunosuppression, respiratory

0826 Effect of a square-toe or perimeter-fit horseshoe on quality of movement and gait kinematics of the western pleasure horse. P. Q. Underwood[1], L. M. White*[1], K. W. Walter[2], D. Hogue[1], and L. K. Hirtz[2], [1]*New Mexico State University, Las Cruces,* [2]*Truman State University, Kirksville, MO*.

Hoof-care professionals often manipulate the thoracic hooves of the western pleasure horse by squaring the toe and moving the horseshoe caudally on the hoof capsule, which is thought to shorten the point of breakover, allowing for a flatter knee and more extension out of the shoulder during the swing phase. Manipulating the shape of the shoe in this way may compromise hoof capsule integrity and could contribute to chronic lameness. Our objective was to evaluate gait quality and kinematics of the western pleasure horse shod with a square-toe aluminum shoe (ST) in comparison to a perimeter-fit aluminum shoe (PF) on the thoracic digit. Quarter horses (n = 9; 5 geldings, 4 mares; 8.4 ± 1.9 yr; 545.9 ± 34.8 kg) trained in western pleasure were utilized in an 85-d repeated measures study and randomly selected on Day 1 to be shod with either an ST or PF shoe for 6 wk, then reshod with the opposing treatment on Day 43. Horses were videoed being ridden at the walk, jog, extended jog, and lope for 3 repetitions over 50 m on Days 15 and 57 wearing each treatment. EquineTec® software was used to evaluate humeroradial extension measured as the minimal elbow angle (extension out of the shoulder) at the end of the swing phase, metacarpal flexion measured as the minimal carpal angle (knee action), and metacarpalphalangeal flexion measured as the minimal fetlock angle (lower leg action), both at the beginning of the swing phase. Equine judges (n = 11) assessed quality of movement by scoring each gait from −1.5 (extremely poor) to 1.5 (excellent), where 0 was considered average. The PF treatment improved quality of movement for some parameters, including humeroradial extension for all gaits ($P < 0.034$) and metacarpal flexion for all gaits ($P < 0.0132$) except the jog ($P = 0.079$). Metacarpalphalangeal flexion and judge evaluations were not different between treatments ($P > 0.3$). Kinematic evaluation revealed quality-of-movement advantages when the PF treatment was applied by allowing for more ideal western pleasure movement seen as decreased knee action and increased extension out of the shoulder, although professional judges did not score treatments differently. The PF treatment achieves equal or superior quality of movement compared to the ST, thus providing a more appropriate shoe for the western pleasure industry that may amplify the longevity of the western pleasure horse.

Key Words: horse, square-toe horseshoe, perimeter-fit horseshoe, western pleasure

INTERNATIONAL ANIMAL AGRICULTURE

0827 Carcass quality of guinea pigs: Age effects on weights, yields, and linear carcass measurements. R. Remache[1], J. Palmay[2], C. Hernández[1], I. Barba[1], V. Inca Guerrero[1], E. Ureña[2], D. Yumisaca[3], A. J. Morales-delaNuez[4], and D. Sánchez Macías*[2], [1]*Agroindustrial Engineering, Universidad Nacional de Chimborazo, Riobamba, Ecuador,* [2]*Agroindustrial Engineering, Universidad Nacional de Chimborazo, Riobamba, Ecuador,* [3]*Facultad de Ciencias Pecuarias, Escuela Superior Politécnica de Chimborazo, Riobamba, Ecuador,* [4]*Facultad de Ciencias Pecuarias, Escuela Superior Politecnica de Chimborazo, Riobamba, Ecuador*.

Guinea pigs are used for meat production in South America, Africa, and Asia. The increased interest in this product is due to the low production price, their relatively rapid reproduction, and the large litter size. The objective of the present study was to evaluate the effect of age on weight, yield, and drip loss in guinea pig carcasses. Fattening guinea pigs reared to different ages were used: 3 months (3M, n = 48), 4 months (4M, n = 37), and 6 months (6M, n = 41). The animals were fasted for 14 h before slaughter. Live weight at slaughter (LWS), empty body weight (EBW), and hot and cold carcass weights (HCW and CCW) were recorded. The following measurements were also recorded: carcass length (L), loin length (Lo), hind limb length (F), width of the buttocks (G), lumbar circumference (LC), thorax circumference (ThC), and thorax width (ThW). Furthermore, carcass compactness (CarC) was calculated. Hot carcass yield (HCY), cold carcass yield (CCY), yields and drip loss were calculated. LWS values increased as animals got older (888 g, 1060 g, and 1168 g, for 3M, 4M, and 6M, respectively. The gastrointestinal content for the three guinea pig groups was similar, around 90 g. The lowest values of hot or cold carcass yields were observed in 3M guinea pigs (52% and 49%, respectively), and no differences were found between the 4M and 6M groups (55–56% for HCY and 53 to 54% for CCY). With respect to drip losses, expressed as percentages, the 3M guinea pig group had the highest loss (5.8%), while the 4M and 6M groups had the lowest losses (3.7 and 3.8%, respectively). L, Lo, F, LC, ThW, and G increased as guinea pigs were reared for longer times. ThC values were similar (19 cm) in all studied animals. When CarC was analyzed, it was possible to see evidence for an age effect: the 4M and 6M groups, without significant differences between them, showed approximately 30 g cm^{-1} of carcass weight vs. 24 g cm^{-1} in 3M guinea pigs. In conclusion, rearing guinea pigs from 3 to 4 months of age increases not only the LWS but also the carcass yields and compactness. However, rearing the guinea pigs from 4 to 6 months of age does not

improve the productivity of the system.

Key Words: guinea pig, carcass yield, linear carcass measurement

0828 Effect of age on the regional composition of fattening guinea pig carcasses. R. Remache[1], V. Inca Guerrero[1], I. Barba[1], C. Hernández[1], J. Palmay[2], M. Tenelema[3], J. Espinoza[2], A. J. Morales-delaNuez[4], and D. Sánchez Macías[*2], *[1]Agroindustrial Engineering, Universidad Nacional de Chimborazo, Riobamba, Ecuador, [2]Agroindustrial Engineering, Universidad Nacional de Chimborazo, Riobamba, Ecuador, [3]Facultad de Ciencias Pecuarias, Escuela Superior Politécnica de Chimborazo, Riobamba, Ecuador,[4]Facultad de Ciencias Pecuarias, Escuela Superior Politecnica de Chimborazo, Riobamba, Ecuador*

Logically, increasing LWS could increase a farmer's profit margin by maximizing meat production. Quantification of the growth of the carcass parts is essential prerequisites of Integrated Management Systems. Guinea pigs are used for meat production in South America, Africa, and Asia, but little information is available in the literature. The objective of this work was to determine the effect of guinea pig age on the regional composition of the carcasses. Fattening guinea pigs reared to different ages were used: 3 months (3M, n = 48), 4 months (4M, n = 37), and 6 months (6M, n = 41). The animals were fasted for 14 h before slaughter. Live weight at slaughter and cold carcass weights (CCW) were recorded. Each carcass was divided into two half carcasses; the left half carcass was jointed in four cuts following anatomical points (neck, shoulder, hind leg, and ribs). Data were recorded in grams and in percent with respect to the left half carcass. ANOVA procedure was used with the statistical program SAS (v. 11). In terms of weights, neck cuts ranged from 18 to 31 g, shoulder cuts ranged from 35 to 49 g, long leg cuts ranged from 78 to 117 g, and ribs ranged from 82 to 117 g. In all cuts, the 3M animal group had the lowest weights and the 6M group the highest. When means are shown as percentages for neck and long leg cuts, the 3M guinea pig group had the lowest values (neck 8.4%), and the 4M and 6M groups the highest without significant differences (9.5–9.9%). For the shoulder, the 3M group had a higher percentage (16.3%) than the 4M and 6M groups (15.2% and 15.5%, respectively). For long leg cuts, the 3M and 4M animal groups did not differ (35.9% and 35.7%), but the results were significantly lower than obtained for the 6M guinea pig group (36.8%). And for ribs, in the 3M and 6M groups the percentages were 37.4% and 36.8%, respectively, without significant differences; these means were lower than the percentage for rib cuts in the 4M group. In conclusion, when animals are older, the cut weights are higher; however, when the results are presented as percentages, there is no linear allometric growth of the different parts of the guinea pig in carcasses.

Key Words: guinea pig, carcass, regional composition

0829 Inulin and flavomicine as growth promoters in rabbit diets: Effects on animal performance, cecum crypt depth, and serum-bone macrominerals (Ca, P, Mg). M. E. Juárez Silva, M. Cuchillo Hilario*, I. Torres Acosta, E. L. Villarreal Delgado, and R. M. Castillo Domínguez, *National Institute of Medical Science and Nutrition Salvador Zubiran, Mexico City, Mexico*.

Concern about the utilization of antibiotics in animal feeding is rising because overuse may cause bacterial and microorganism resistance. Also, the use of probiotics and antibiotics to increase animal productivity and the effects on the cecum crypt depth, mucus layer thickness, and bone macromineral metabolism are still not clear. Therefore, sixty New Zealand rabbits (female = 30/male = 30) of 40 d age (790 ± 150 g) were randomly arranged into four treatments of 15 animals each. All groups were fed with the same protein, energy, crude fiber, and ether extract content (16.9%, 13.80 KJ/g, 12.5%, and 3.9%, respectively). The study lasted 57 d, the first 15 d of which were for adaptation. Weekly weights were registered during the experiment. Basal diet consisted of alfalfa hay (43.8%), wheat bran (25.1%), soybean meal (12.9%), corn (11.6%), soybean oil (3.1), carboxymethyl cellulose (2%), calcium phosphate (1.0), sodium chloride (0.5%), and vitamins and minerals (0.1%). The control group (CG) did not receive either antibiotic (Flaveco40 ECO-Animal Health) or inulin (IPS Raftifeed, Megafarma-Orafti) supplementation. The second group (I+) was supplemented with 2.5 g of inulin/kg of feed. The third group (F+) received 0.1 g of flavomicine/kg of feed. To evaluate possible interactions, the fourth group (IF) received both inulin and flavomicine doses as discussed previously. One-way analysis of variance (ANOVA) and the Tukey test ($P < 0.05$) were employed using SPSS (15.0). Kruskal–Wallis and Mann–Whitney tests were used when the samples showed no normal distribution. Rabbit final weight was greater in CG ($P < 0.05$) than I+, F+, and IF (2269 g, 1938 g, 2036 g, and 2170 g, respectively). The cecum crypt depth and mucus layer thickness were significantly larger in rabbits with I+ ($P < 0.001$). Rabbits supplemented with inulin showed the least triglyceride level in comparison to CG and F+ ($P < 0.05$). In the same line, blood glucose in I+ was less than F+ ($P < 0.05$). In contrast, serum concentrations of calcium and magnesium were greater in I+ ($P < 0.05$). Additionally, calcium, phosphorus, and magnesium values in femur bone from I+ were greater than CG ($P < 0.05$), whereas only phosphorus and magnesium values from I+ were greater than F+ ($P < 0.05$). Nevertheless, the magnesium concentration in bone from IF was greater than CG ($P < 0.05$). Despite the slightly lesser final weight of rabbits with I+, the inclusion of inulin

has positive effects; e.g., cecum crypt depth and mucus layer thickness increased. Likewise, inulin supplementation augmented calcium, phosphorus, and magnesium in serum and in femur bone. Furthermore, inulin is capable of depressing serum triglycerides and glucose, while increasing bones mass.

Key Words: probiotics, crypt depth, bone mineralization

0830 Increased body condition during lactation increases milk production and pre-weaning growth of Bali cattle. D. Dahlanuddin*[1], M. Supriyadi[1], T. S. Panjaitan[2], D. P. Poppi[3], and S. P. Quigley[3], *[1]Faculty of Animal Science, University of Mataram, Mataram, NTB, Indonesia, [2]Assessment Institute for Agricultural Technology, Narmada, NTB, Indonesia, [3]School of Agriculture and Food Sciences, The University of Queensland, Gatton, Qld, Australia*.

Bali cattle (*Bos javanicus*), the main cattle species in eastern Indonesia, have high rates of calf mortality (up to 48%, Talib et al., 2003) and low average daily gain (ADG) (< 0.2 kg, Dahlanuddin et al., 2012). The objective of this experiment was to determine the effect of body condition score (BCS) of heifers throughout pregnancy and lactation on milk production and ADG of calves up to 6 mo of age. Non-pregnant Bali heifers [n = 24, 3.2 ± 0.1 BCS (1 to 5 scale), mean ± s.e.m.] were ranked on body weight (BW; 217 ± 6 kg) and allocated to treatments that would result in high (4.0) and low (2.5) BCS at parturition and throughout lactation. Heifers were maintained in individual pens and fed a mixture of tree legumes (*Leucaena leucocephala* and *Sesbania grandiflora*) ad libitum and 10 g maize grain DM/kg LW.day (HighBCS, 164 g CP and 8.9 MJ ME/kg DM) or King grass (*Pennisetum purpureum*; LowBCS, 75 g CP and 7.8 MJ ME/kg DM) ad libitum throughout pregnancy and lactation. Heifers observed to be in oestrus were mated with a single bull. Heifer BW was measured every week, BCS was measured every month, milk production was estimated by the weigh-suckle-weigh technique, calf BW was measured at birth and every week until weaning at approximately 6 mo of age. At parturition HighBCS heifers were heavier (292 ± 15 vs. 226 ± 10 kg) and in a higher BCS (4.2 ± 0.1 vs. 2.8 ± 0.1) than LowBCS heifers (P < 0.01). At weaning HighBCS heifers were heavier (276 ± 3 vs. 181 ± 12 kg) and in a higher BCS (4.2 ± 0.1 vs. 2.3 ± 0.1) than LowBCS heifers (P < 0.001). Calf birth weight (13.5 ± 0.2 kg) was unaffected by maternal BCS (P > 0.1). HighBCS heifers produced more milk than LowBCS heifers at each measurement during lactation and overall (2.1 ± 0.1 vs. 1.0 ± 0.1 kg/day, P < 0.001). ADG of calves between birth and 6 mo for age was higher for calves born to HighBCS heifers than those born to LowBCS heifers (0.37 ± 0.02 vs. 0.16 ± 0.02 kg, P < 0.001). In conclusion, milk production of Bali cows and pre-weaning ADG of Bali calves are influenced by BCS during lactation. Strategies to increase BCS during lactation will increase calf growth and potentially reduce calf mortality.

Key Words: Bali cattle, calf growth, milk production

0831 Alpaca and llama fiber quality comparison in Ecuadorian Andes. L. Cordova, A. J. Morales-delaNuez, M. Vaca-Cardenas, and N. F. Rodriguez Gonzalez*, *Facultad de Ciencias Pecuarias, Escuela Superior Politecnica de Chimborazo, Riobamba, Ecuador*.

The fiber quality from ten body regions (dorsal neck, RC1; wither, RC2; middle loin, RC3; rump, RC4; ventral neck, RC5; ribs, RC6; flank, RC7; caudal thigh, RC8; forearm, RC9; and dorsal to hock, RC10) of 35 alpacas (*Vicugna pacos*) and 45 llamas (*Lama glama*) were evaluated. Samples were collected from the left side of the animals before shearing. Animals belonged to the Tourism Project of Palacio Real Community (Chimborazo province, Ecuador). Length (L), number of crimps (NR), diameter (D), and medullation rate (M) were measured in ten randomly selected fibers from each body region. Repeated measures ANOVA was performed to evaluate the effects of body region, as repeat measure, and sex and species, as independent factor. Additionally, Pearson's coefficient was used to calculate correlations between parameters. No differences in NR, D, and M due to species or sex in any of the studied body regions were observed. Differences in LA from RC4 between females were observed, where alpacas had longer LA than llamas. In RC5 llama males showed longer LA than llama females, while both sexes of alpacas presented intermediate values. RC6 (ribs) was the body region with better fiber quality, while RC10 (dorsal to hock) showed the worse quality fiber. A significant high correlation (0.64) was found between M and D. In conclusion, the best quality fiber was found in RC6 for both species, whereas the worst was found in RC10. Finally, D and M were highly correlated.

Key Words: *Lama glama*, *Vicugna pacos*, Ecuador

0832 Alpaca fiber quality in Ecuadorian Andes. J. C. Simbaina-Solano, B. Aucancela, A. J. Morales-delaNuez, M. Vaca-Cardenas, and N. F. Rodriguez Gonzalez*, *Facultad de Ciencias Pecuarias, Escuela Superior Politecnica de Chimborazo, Riobamba, Ecuador*.

Nowadays, the importance of fiber from alpaca is increasing worldwide. Therefore, studies about the fiber quality from those animals is requested. To analyze the alpaca fiber quality in Ecuador, 143 alpacas from 3 rural communities from Chimborazo province and 223 alpacas from 7 rural communities from Cañar province were sampling on the middle rib area. Samples were evaluated with a wool-meter and calibrated ruler. Fiber quality was established based on four variables: diameter (D), number of crimps (NR), length (L),

and medullation rate (M). These characteristics were analyzed according to sex and age. Multifactorial ANOVA method was applied with Tukey-Kramer adjustment. Values were considered significant when $P < 0.05$. Furthermore, to establish correlations between parameters, the Pearson correlation coefficient was utilized. In Chimborazo provinces, the following averages were obtained: D: 21.75 μm, NR: 2.12 crimps/cm, L: 11.97 cm, and M of 35.3%. For D, young animals presented finer fiber than old animals. Similarly, males showed finer fiber than females. For NR, older females showed fewer crimps per cm than other groups. Older males presented the longest fiber (L). No effect of sex or age was found in M. In Cañar province, the following averages were obtained: D 21.72 μm, NR: 2.78 crimps/cm, L: 15.16 cm, and M of 53.9%. For D, young animals presented finer fiber than old animals, and sex had no effect on this variable. For NR, older animals showed fewer crimps per cm than young animals, while males had fewer crimps than females. Older animals presented longer fiber than young animals, while males showed shorter fiber than females. No effect of sex or age was found in M. Furthermore, in both provinces the diameter and medullation were strongly correlated. In conclusion, the alpacas raised in the Ecuadorian Andes have a good fiber quality, but it is necessary to improve it to increase the fabric craft quality. Sex and age must be considered for fiber quality.

Key Words: *Vicugna pacos*, South American camelids, Ecuador

0833 Guinea pig carcass quality: Traditional diet vs. high quality diet.

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Guinea pig meat production provides a good and low-cost source of proteins. In Africa, Asia, and South America meat production from this species is common and ensure the food security in many rural communities. Traditionally, in Andean areas, guinea pigs are raised with low quality grass and kitchen waste. Few data is available about the carcass quality in guinea pigs fed in this way. The aim of this study was to evaluate the carcass quality of guinea pigs fed with high quality and low quality feed. In this study, 60 improved guinea pigs (30 males and 30 females) were divided into 3 groups (10 males and 10 females per group). One group was fed with fresh lucerne and concentrate (ASI). Another group of animals was fed with agriculture waste and concentrate (DSI). Finally, the last group was only fed with agriculture waste (DNO). All animals were slaughtered with 120 d, after a fast of 12 h. Weight before slaughter, different carcass weights, non-carcass components, and carcass measurements were recorded and different carcass yields were calculated. Results showed that guinea pigs fed with agriculture waste (DNO) had decreased carcass quality compared to animals fed with concentrate feed. Few differences were found when animals fed with Lucerne (ASI) were compared to those fed with agriculture waste and concentrate (DSI). In conclusion, guinea pigs fed with agriculture waste and concentrate had similar carcass quality as those fed with high quality forage, so guinea pigs are able to use a low quality forage.

Key Words: *Cavia porcellus*, meat quality, nutrition

0834 Do buffaloes have better milk fat profile than cows? Where does the evidence stand in 2016?

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The objective of the present study was to document a comprehensive comparison between the milk fat profiles of buffalo and cattle. Data on milk fat profiles of buffalo were retrieved from nine published studies on different breeds of buffalo (Nili-Ravi, Kundi, Murrah, Egyptian, Italian, Romanian), and values/proportions of individual/groups of fatty acids (FA) were averaged across breeds. Data on milk fat composition of cow milk was obtained from a recent study on Canadian Holstein cows using large gas chromatography data. Milk fat profiles (means of 29 variables each) of the buffalo and the cow were compared using Student's *t*-test. Overall, Holstein cows had approximately 3–4 times higher daily milk yield than buffalo. Buffalo milk had greater total solids (17.76% vs. 13.94%) and a higher fat percentage (7.02% vs. 3.86%) than cow milk, indicating more value for buffalo milk. Buffalo milk fat had slightly higher proportions of total saturated, total trans, and total mono-unsaturated FA but similar proportions of total polyunsaturated FA than that of cow; although differences in these groups of FA were statistically nonsignificant. Buffalo milk fat had higher proportions of human-health-related beneficial fatty acids (comparing one fatty acid at a time) such as oleic acid, CLA, cis-9 trans-11, and two omega-3 FA (C18:3 cis-9, 12, 15 and C20:5n3). Additionally, buffalo milk had relatively lower proportions of potentially undesirable (from human health standpoint) saturated FA (C12:0, C14:0, and C16:0) than cow's milk. Although the present study did not correct the data for various background effects involved in each of the reported studies, it provides a comprehensive comparison between buffalo and cow milk fat and is likely to have useful implications for the promotion of buffalo as a dairy animal from the human health point of view.

Key Words: buffalo, cattle, milk fat profiles

INTERNATIONAL ANIMAL AGRICULTURE SYMPOSIUM: THE FUTURE OF PASTORAL PRODUCTION SYSTEMS

0835 Contribution of pastoral systems to global food security and potential for sustainable intensification. A. Mottet*, F. Teillard, G. Cinardi, and G. Velasco Gil, *Food and Agriculture Organization of the United Nations, Rome, Italy*.

Pastoralists produce food in the world's harshest environments, converting scarce resources from nonarable land into edible products. Pastoral production supports the livelihoods of rural populations on almost half of the world's land and is making a growing contribution to feeding also urban populations. Though many pastoralists can be found in Africa, pastoralism is also practiced in dry and sub-humid lands in the Middle East, South and East Asia, South America, and Europe. While the global livestock sector is expected to grow by 70% between 2005 and 2050 to feed a growing population, urbanized and with higher incomes, pastoral systems are also following this trend but are submitted simultaneously to a number of major socioeconomic, agro-ecological and institutional changes such as climate change, market globalization, population migrations, changes in animal products due to urban demand, and political instability. These changes can result in higher competition between extending croplands and increasing herds for access to natural resources, a decline in cropland fertility and a degradation of pastoral resources. In addition, extensive ruminant systems are often pointed out for having high greenhouse gas emission per unit of product because of their low levels of productivity. Detailed and reliable information is essential to monitor these trends in pastoral areas and provide adequate support to the public policy planning process and to the development of strategies designed to meet the specific needs of pastoral communities and stakeholders. This communication reviews the information and knowledge available about pastoralist systems and their actual contribution to food security and livelihoods, through the production of a range of direct goods and services, such as meat, milk, fibers, hides, income generation, transport, savings and insurance, but also indirect ones, such as ecosystem services. It also explores their vulnerability and adaptive capacity to climate change and discusses possible ways for future development of the sector through sustainable intensification, including increased productivity, better resilience to climate shocks and mitigation of greenhouse gas emissions.

Key Words: pastoralist systems, food security, demand for livestock products, sustainable intensification, climate change, ecosystem services

0836 Opportunities for international research and development through the Feed the Future Innovation Lab for Livestock Systems. A. T. Adesogan*, *Dep. of Animal Sciences, IFAS, University of Florida, Gainesville*.

The U.S. Agency for International Development (USAID) awarded the University of Florida (UF) Institute of Food and Agricultural Sciences (IFAS) a $49 million, 5-yr cooperative agreement to establish the Feed the Future Innovation Lab for Livestock Systems. The grant supports USAID's agricultural research and capacity building work under Feed the Future, the U.S. Government's global hunger and food security initiative. The Livestock Systems Innovation Lab is led by UF/IFAS in partnership with the International Livestock Research Institute (ILRI). The objective of the Livestock Systems Innovation Lab is to achieve sustainable improvements in livestock productivity and marketing to increase the incomes, nutrition, and health of vulnerable livestock holders. The Livestock Systems Innovation Lab will design, lead, and implement a program of livestock research for development and capacity building aimed at addressing key opportunities in the livestock sector, including those created from the increasing demand for animal-source foods due to population growth, urbanization, and rising incomes. The primary focus of the Livestock Systems Innovation Lab will be in in East Africa, West Africa, and South Asia. The four Areas of Inquiry (AOI) of the Livestock Systems Innovation Lab are as follows: Future Livestock Systems; Animal-Source Foods (ASF) Production and Marketing, Livestock Disease Management and Food Safety, and Enabling Policies for Livestock. Across these AOI, the Livestock Systems Innovation Lab will integrate the following cross-cutting themes: The Role of Gender in Livestock Systems Research, Human Health and Nutrition, and Human and Institutional Capacity Development. The Livestock Systems Innovation Lab is led by a Management Entity at UF/IFAS, with Regional Coordinators at ILRI centers in each of the target regions. The research will be mainly conducted through competitive sub-awards. The Management Entity engaged stakeholders in the livestock and public health industries in Nepal, Ethiopia, Tanzania, and Rwanda in a participatory research for development prioritization exercise in Spring 2016 and released a Request for Applications in April 2016. Another Request for Applications will be tentatively released in September 2016 seeking proposals for research for development projects in Mali, Burkina Faso, and Cambodia, subject to USAID approval. These competitions are open to any qualified research, educational, governmental, private sector, or nonprofit institution. The projects selected for funding will fall within the objectives of the Livestock Systems Innovation Lab and contribute to the overall Feed the Future goals of reducing global hunger and improving food security.

Key Words: livestock, research, animal-source foods

0837 Community-based breeding programs: A sustainable solution for livestock keepers?

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In recent years community-based livestock breeding programs (CBBPs) have received some attention and have been considered as a new and more sustainable option to improve livestock production under smallholder conditions and in low-input systems. Most CBBPs are found with livestock keepers owning local breeds of small ruminants. The idea of CBBPs is that livestock keepers with a common interest in improving their genetic resources work together and jointly develop breeding strategies, which are based on their local rules and institutional settings. This bottom-up process ensures that the decision-making power remains with the livestock keepers. However, scientists play an important role as facilitators, moderators, and technical experts and can provide guidance and bring their know-how to the various steps in the design and implementation of a breeding program. Beside the numerous technical challenges, there are also various socio-cultural aspects that have to be addressed and discussed with the participants of the breeding program. Enough room for reflection and discussion on traditional norms and values and possible changes has to be provided. In some cases changes can maybe more easily proposed and initiated by scientists as they are outsiders of the communities. The important role of women in the different aspects of livestock management is indisputable, but their participation in decision-making processes not only in households but also at a breeders' association or at the community level is often neglected. Therefore, new forms of cooperation and modification of traditional roles of disadvantaged groups should be considered. Exclusion of women impoverishes the knowledge base, so that future adaption options might be overlooked. In addition, excluding women undermines the legitimacy of the institutions, thus threatening the whole management system. Inclusion of different viewpoints of concerned actors leads to more sustainable solutions and makes a production system more resilient.

Key Words: community-based breeding programs, gender, resilience

0838 Innovative dissemination of small ruminant genetic improvement by a non-government institute in India.

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This report describes the dissemination methods of superior genetic material from sheep and goat breeding programs established by the Nimbkar Agricultural Research Institute (NARI) in Maharashtra State of India. The *FecB* gene carrier, moderately prolific NARI Suwarna breed of sheep developed by NARI has been disseminated since 2014 in village flocks in 7 districts of Karnataka State by the State Government. The first 20 sheep owners who received breeding rams were trained at NARI in the management of multiple-born lambs and their dams. Out of a total of 425 rams and 620 ewes sold for breeding so far, 167 rams and 128 ewes have been distributed in Karnataka. Seventy-three lambs born in these flocks were genotyped at the *FecB*locus at NARI and 19 good quality homozygous ram lambs were purchased by the State Government for dissemination to more flocks. The average litter size of NARI Suwarna ewes in these flocks is 1.8 with around 15% mortality in multiple-born lambs, leading to about 1.5 lambs weaned per ewe per lambing. Local ewes usually wean less than one lamb per ewe on average. The revenue generated by the sale of breeding animals has made the nucleus flock at NARI self-sustaining. NARI selects buck kids of the Osmanabadi goat breed from villages in four districts of Maharashtra State where performance recording is performed under the All India Coordinated Research Project on Goat Improvement of the Indian Council of Agricultural Research. NARI purchases from goat keepers 6-month-old, twin-born male kids with high growth rates, born to dams with a high milk yield. They are reared on NARI's farm and their semen is frozen after they attain sexual maturity. Each dose contains 100 million spermatozoa and the post-thaw progressive motility is more than 60%. Private Artificial Insemination (AI) technicians purchase buck semen straws (3800 so far) and provide cervical insemination to does in natural oestrus in the villages they visit. Village women trained by NARI under a collaborating NGO program have been found to be honest, hard-working, sincere, and skillful in goat AI. The same AI gun used with cows can be used with goats. Since 2009, NARI has made available frozen semen of Boer (10,000 straws) and Damascus (2000 straws) breed bucks from its nucleus flocks. Conception rates have been found to be about 50%. Dissemination methods that fit into the existing ethos and circumstances are likely to be more successful.

Key Words: dissemination methods, goats, sheep

0839 Pastoral systems in the developing world: Trends, needs, and future scenarios.

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Developing-country rangelands are vast and diverse. They are home to millions who are often poor, politically marginalized, and dependent on livestock for survival. Here we summarize experiences from six case-study sites across sub-Saharan Africa, central Asia, and Latin America generally covering the past 25 yr. We examine issues pertaining to population, natural resource management, climate, land use, livestock marketing, social conflict, and pastoral livelihoods. The six study sites differ with respect to human and livestock population dynamics and the resulting pressures on natural resources. Landscape degradation, however, has been commonly observed. Climate change is also having diverse systemic effects often related to increasing aridity. As rangelands become more economically developed pastoral livelihoods may diversify, food security can improve, commercial livestock production expands, but wealth stratification widens. Some significant upgrades in rural infrastructure and public service delivery have occurred; telecommunications are markedly improved due to widespread adoption of mobile phones. Pressures from grazing, farming, mining, and other land uses—combined with drought—can ignite local conflicts over resources, although the intensity and scope of conflict markedly varies across case-study sites. Pastoralists and their herds have become more sedentary overall due to a wide variety of factors, and this can undermine traditional risk-management tactics based on mobility. Remote rangelands still offer safe havens for insurgents, warlords, and criminals, especially in countries where policing remains weak; the resulting civil strife can undermine commerce and public safety. There has been tremendous growth in knowledge concerning developing-country rangelands since 1990, but this has not often translated into improved environmental stewardship or an enhanced well-being for rangeland dwellers. Some examples of demonstrable impact are described, and these typically have involved longer-term investments in capacity building for pastoralists, local professionals, and other stakeholders. Research is shifting from ecologically centered to more human-centered issues; traditional academic approaches are often being augmented with participatory, community-based engagement. Building human or social capital in ways that are integrated with improved natural-resource stewardship offers the greatest returns on research investment. Our future research and outreach priorities include work that fortifies pastoral governance, enhances livelihoods for a diverse array of rangeland residents, and improves land and livestock management in a comprehensive social-ecological systems approach.

Key Words: Bolivian Altiplano, Borana Ethiopia, Kuchi Afghanistan, northern Mexican rangelands, Mongolia, Peruvian Altiplano, Sahelian Zone

LACTATION BIOLOGY

0840 Duration of lactation in first-parity sows: Does it affect piglet growth in second parity?

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It was recently shown that a teat which is not used in first lactation will have reduced development and milk yield in second lactation. This leads to the question of the minimum duration of suckling required in first parity for milk yield not to be hindered in second parity. The goal of the present study was to determine the impacts of a 2 d, 7 d or 21 d suckling period in first lactation on piglet growth, milk composition, and endocrine status of sows in second lactation. Pregnant Yorkshire gilts were divided into 3 groups according to lactation length: 1) 2 d (2D, $n = 20$), 2) 7 d (7D, $n = 20$); and 3) 21 d (21D, $n = 21$). After weaning, sows were bred and kept for a second parity. In both lactations, litters were standardized to 12 piglets with 12 functional teats and surplus teats were sealed with tape. During the second lactation, piglets were weighed on d 2, 7, 14, 21(weaning), 31, and 56 postpartum, and sow feed intake was recorded. Milk samples and jugular blood samples were obtained from sows on d 21 of the second lactation. Concentrations of prolactin, IGF-1, glucose, and urea were measured in blood. The MIXED procedure of SAS using a univariate model (3 levels) was used for statistical analyses and means were compared using Tukey's test. There was a tendency for 21D sows to consume more feed than 2D or 7D sows during the first week of lactation ($P < 0.10$). There was no treatment effect on BW of piglets at any time until d 56 ($P > 0.10$). Concentrations of prolactin, IGF-1, urea and glucose in sows on d 21 of lactation were not affected by treatment ($P > 0.10$). Furthermore, dry matter, fat, protein, and lactose contents in milk were not affected by treatment ($P > 0.10$). Results indicate that increasing the duration of lactation from

2 d to 7 d, or to 21 d in first-parity sows, does not improve growth rate of their piglets in the subsequent lactation. This suggests that suckling of a teat for 2 d during the first lactation is sufficient to ensure optimal mammary development.

Key Words: lactation length, parity, piglet growth

0841 Effects of glucose and amino acids on casein synthesis via JAK2/STAT5 signaling pathway in bovine mammary epithelial cells.

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Studies confirmed that glucose and amino acids (AAs) could be used as signaling factors to regulate milk protein gene transcription and translation through signaling cascade pathways in the mammary gland that affect milk protein synthesis. Some signaling pathways, like Janus kinase-signal transducer and activator of transcription (JAK-STAT), may play a role in the process of milk protein gene transcription. This study employed bovine mammary epithelial cells (BMEC) as a model to investigate the effects of glucose and AAs on β-casein and κ-casein gene transcription, and to determine if effects are mediated through the JAK-STAT signaling pathway. BMEC cells were cultured in specific medium (without D-glucose and AAs), starved overnight, and then subjected to 3 levels of D-Glu (0, 2.5, or 17.5 mmol/L) and 3 levels of AAs (0, 1, or 7.2 mmol/L) in a 3 × 3 factorial arrangement of treatments. After 6 h of culture, the mRNA abundance of *CSN2, CSN3, JAK2,* and *STAT5* genes were measured by qRT-PCR. Statistical analysis of data was performed using SAS 9.2 statistical software package. Differences between experimental groups were considered significant at $P < 0.05$. The results showed that, at the same level of D-Glu or AAs, increasing the concentration of the other to the medium level or higher, substantially increased the mRNA abundance of *CSN2, CSN3, JAK2,* and *STAT5* genes. These results demonstrated that D-Glu or AA supplements could promote transcription of casein genes (β-casein, κ-casein), and that process might be related to JAK-STAT signaling in the bovine mammary epithelial cell. In conclusion, our results provide basic information for the further study of the mechanisms by which glucose or AAs affect casein expression in the bovine mammary epithelial cell.

Key Words: amino acids, glucose, JAK2/STAT5

0842 Repeated mammary tissue collections during lactation have no impact on cow performance.

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Mammary biopsy (MB) collection is a necessary and valuable approach for studies in mammary gland biology, but it is not known if repeated MB impair performance of the lactating cow. Our objective was to examine the effect of multiple MB during lactation on udder health, DMI, and milk yield of dairy cattle. Sixty-four multiparous, mid-lactation Holstein cows were enrolled in a trial and 32 cows were randomly selected for repeated MB. The MB and non-MB cows had similar parity (2.6 ± 0.9, $P = 0.13$) and DIM (96.5 ± 56.3 d, $P = 0.13$) at enrollment. All animals were housed in the same barn and fed the same diet. Cows were milked three times a day and milk yield was recorded at each milking. Milk composition was measured weekly and DMI was recorded daily. Three MB were performed per cow: at enrollment and at 3 and 5 mo post-enrollment. The first and third MB were taken from the left rear quarter whereas the second MB was from the right rear quarter. The experimental procedures were approved by the Institutional Animal Care and Use Committee of the University of Georgia. Before MB, cows were mildly sedated through i.v. injection of xylazine HCL (20 μg/kg of BW). Briefly, the MB was performed using a rotating stainless steel cannula with a retractable blade at the cutting edge connected with a cordless drill. After sanitation with iodine and ethanol, an incision was made through the skin and connective tissue in the middle of the quarter and a core of mammary tissue (0.75 to 1 g) was extracted. The incision was closed using stainless wound clips and sprayed with an antiseptic dressing to avoid infection. After MB, udder health, wound healing of incisions, and appearance of blood in milk were visually examined at each milking. All bloody milk was discarded and blood was cleared from milk 3.86 ± 2.0 d after MB. During the experiment, four MB quarters and 14 non-MB quarters were diagnosed and treated for clinical mastitis. Compared with non-MB cows, MB cows had similar ($P > 0.1$) DMI, milk yield and percentage of fat, lactose, protein, solids-not-fat, and somatic cell score. In conclusion, mid- to late-lactation cows recover rapidly from MB and repeated MB have no impact on DMI, milk yield and composition, and udder health

of lactating dairy cows.

Key Words: lactating cow, lactation performance, mammary biopsy, udder health

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0843 Lack of glucose and amino acids suppresses protein synthesis of bovine mammary epithelial cells by activating AMPK and inhibiting mTORC1 signaling pathways. S. Wang[1,2,3,4], S. Zhao[1,2,5], H. Gao[1,2,3,6], M. Zhang[1,2,3], N. Zheng[1,2,5], Y. Zhang[1,2,5], S. Yan[4], and J. Wang[*2,3,5], *[1]Ministry of Agriculture-Milk Risk Assessment Laboratory, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]Ministry of Agriculture-Milk and Dairy Product Inspection Center, Beijing, China, [4]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China, [5]Ministry of Agriculture-Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [6]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China*.

Glucose and amino acids (AA) regulate milk protein synthesis via signaling pathways involving AMP-activated protein kinase (AMPK) and mammalian target of rapamycin (mTOR) in current nutrient requirement models. The objective of this study was to investigate the effects of nutritional stress due to lack of glucose and/or AAs and determine the sensitivity of bovine mammary epithelial cells to each stress by measuring cell proliferation and expression of β-casein and signaling proteins. Bovine mammary epithelial cells were cultured in specific medium (without glucose and AAs) and starved overnight, then three levels of glucose (0, 2.5, or 17.5 mmol/L) and AAs (0, 1.03, or 7.2 mmol/L) in a 3 × 3 factorial design were added to the medium. The proliferation of bovine mammary epithelial cells was detected by the thiazolyl blue (MTT) method, and the expression of β-casein and phosphorylation of signaling proteins were detected by Western blot. The results showed that proliferation of bovine mammary epithelial cells and their expression of β-casein was decreased under stress due to lack of glucose and/or AAs. When the concentration of AAs was 7.20 mmol/L and the glucose levels 17.5 and 2.5 mmol/L, cell proliferation and β-casein expression were downregulated 9.44% and 37.53%. When the concentration of glucose was 17.5 mmol/L and the AA levels 7.2 and 1.03 mmol/L, cell proliferation was downregulated 6.67% and 21.98%. Further experiments validated that the phosphorylation of AMP-activated protein kinase (AMPK, $Thr^{183/172}$) was upregulated under glucose and/or AA stress. When the AA level was 7.2 mmol/L and glucose levels were 17.5 and 2.50 mmol/L, the expression of P-AMPK($Thr^{183/172}$) was upregulated 210%. When the concentration of glucose was 17.5 mmol/L and AAs 7.20 and 1.03 mmol/L, the expression of P-AMPK($Thr^{183/172}$) had no effect. In contrast, the phosphorylation of the mammalian target of rapamycin (mTOR, Ser^{2481}), the regulatory associated protein of mTOR (Raptor, Ser^{792}), the ribosome protein subunit 6 kinase 1(S6K1, Thr^{389}), the 4E binding protein 1 (4EBP1, Thr^{37}), and the content of ATP were downregulated under glucose and/or AAs stress, and we also find that these phosphorylation proteins and ATP content are more sensitive to glucose than AAs. Results from this study suggest that stress due to lack of glucose and/or AAs can influence the energy and protein supplies in mammary epithelial cells, causing downregulation of proliferation, activating the fuel sensor AMPK, and suppressing the mTOR signaling pathway, which may lead to decreased β-casein expression. Bovine mammary epithelial cells are more sensitive to glucose stress than to AAs.

Key Words: amino acids, β-casein, glucose

0844 Genome-wide association analysis and pathways enrichment for lactation persistency in Canadian Holstein cattle. D. N. Do[*1,2], N. Bissonnette[1], P. Lacasse[1], M. Sargolzaei[3,4], F. Miglior[4,5], X. Zhao[2], and É. M. Ibeagha-Awemu[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada, [2]Department of Animal Science, McGill University, Montreal, QC, Canada, [3]Semex Alliance, Guelph, ON, Canada, [4]Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [5]Canadian Dairy Network, Guelph, ON, Canada*.

Lactation persistency (LP), generally defined as the rate of declining milk yield after milk peak, is an economically important trait for dairy cattle. Enhancing LP through genetic improvement is an interesting avenue for increasing overall milk production because it does not cause negative energy balance and related health issues for cows. We performed a genome-wide association study (GWAS) and pathway enrichment to explore the genetic mechanisms underlying LP. A GWAS based on generalized quasi-likelihood score method was performed on LP data of 866 cows and 44,023 single nucleotide polymorphisms (SNPs) with inclusion of a polygenic effect explained by genomic relationship matrix. A total of 29 and 88 SNPs were significantly associated with LP at the adjusted Bonferroni ($P < 2.15 \times 10^{-5}$) and at false discovery rate of 5%, respectively. Important genomic regions that harbored several significant SNPs for LP were: 68.2–71.2 mega base pairs (Mb) on bovine chromosome (BTA) 16, 14–16 Mb on BTA 3, 107–109 Mb on BTA 5, and 133–137 Mb on BTA 1. The most significantly associated SNP (rs41818282) is located in an intronic region of hemicentin 1 gene. Functional annotation of 599 genes in the flanking regions (0.5 Mb) of significant SNPs showed that natural killer cell-mediated cytotoxicity and TGF-β signaling pathways were important for LP. In addition, 8 among 11 gene

ontologies enriched for LP were involved in the immune process. These results suggest that biological processes involving cell death, cell proliferation, and immune response are important in the regulation of LP. However, it is necessary to further characterize the detected regions and enriched pathways for confirmation and validation. In conclusion, this study detected several genomic regions for fine mapping to identify potential markers for LP improvement.

Key Words: cows, genomics, GWAS, lactation persistency, pathways

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0845 Effect of 17β-estradiol on milk production, hormone secretion, and mammary gland gene expression of dairy cows. J. J. Tong[1], I. M. Thompson[2], and P. Lacasse*[3], [1]*Department of Clinical Veterinary Medicine, College of Veterinary Medicine, Northeast Agricultural University, Harbin, China,* [2]*AAFC-Sherbrooke R&D Centre, Sherbrooke, QC, Canada,* [3]*Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada*.

Estradiol inhibits milk production in dairy cows. The present study evaluated the impact of estradiol injections on prolactin (PRL) secretion and mammary gland responsiveness to PRL. Eight mid-lactation cows received either 17β-estradiol (2.5 mg; E2; $n = 4$) or soy oil (2.5 mL; CTL; $n = 4$) injections during 7 d (period 1). After a resting period of 3 wk, a second treatment period was performed where the cows were switched from treatments. For each period, blood and milk samples were collected from d −4 to 14 (relative to the first injection). In addition, blood samples were collected during the a.m. milking on d −4, 2, and 7 to determine the milking-induced PRL release. Mammary gland biopsies were harvested on the last injection day of both periods. Milk fat samples were collected on d 1, 4, 7, and 14. The mRNA levels of genes encoding proteins related to mammary activity (α-lactalbumin, β-casein, and acetyl-CoA carboxylase), apoptosis (Bax, Bcl2, and caspase-3), PRL receptors (PRLR, long and short forms), LIF, and suppressors of cytokine (SOCS1, 2, and 3) were measured by real-time RT-PCR using RNA extracted from milk fat and mammary gland. Injections of E2 decreased moderately milk production during the treatment period (36.70 ± 0.45 kg/d and 39.74 ± 0.45 kg/d, respectively; $P = 0.01$). The E2 treatment tended to increase fat ($P = 0.08$), increased lactose ($P = 0.04$), and increased protein ($P = 0.03$) content of milk. Serum PRL concentration was increased by E2 injections during the treatment ($P = 0.04$) and the post-treatment ($P = 0.01$) periods. Accordingly, milk PRL concentration tended to be increased by E2 ($P = 0.09$). Milking-induced PRL release was also increased by E2 injections ($P = 0.03$). Injections of E2 increased plasma concentrations of IGF-1 ($P < 0.01$) and estradiol ($P < 0.01$) during the treatment period. Milk BSA was not affected by treatments, suggesting that mammary tight junctions were not impaired by E2. In mammary tissue, the LIF mRNA level tended to be lower during the E2 treatment ($P = 0.09$). In milk fat, PRLRL mRNA level tended to be decreased ($P = 0.07$), and PRLRS mRNA level was decreased ($P = 0.04$) by E2 injections. No difference in expression was observed for the other genes in mammary tissue and milk fat. These results suggest that a decrease of mammary gland responsiveness to PRL may be involved in the estradiol-induced inhibition of milk production.

Key Words: estradiol, gene expression, prolactin

0846 Estimation of quarter vs. composite colostrum composition via Brix refractometry, specific gravity, and visual color appearance in dairy cows. J. J. Gross*, E. C. Kessler, and R. M. Bruckmaier, *Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland*.

The control of colostrum quality is essential for successful calf rearing. Instruments for on-farm colostrum quality determination are widely used in dairy practice. However, composite colostrum samples have predominantly been considered so far, thereby not taking potential variation between quarters into account. In cases of low quality of composite colostrum, feeding a better quality colostrum from individual quarters might be beneficial. The objective of the present study was to identify relationships between colostrum color, quality (assessed by a colostrometer and a Brix refractometer), and composition (measured by different laboratory methods) of colostrum at a quarter level, for two types of colostrum sampling. Quarter and composite colostrum samples from 17 primiparous and 11 multiparous Holstein cows were analyzed for total IgG, fat, protein and lactose contents, and color was measured by a spectrophotometer. In the present study, an IgG concentration below 50 g/L, as determined by ELISA, was found in 14.3% of the analyzed quarter samples. Concentration and total mass of IgG in composite colostrum samples were greater in multiparous compared with primiparous cows ($P < 0.05$). Specific gravity (SG) of colostrum from individual and composite samples was lower in primiparous than in multiparous cows ($P < 0.05$). Milk fat content was greater in quarter and composite colostrum samples of primiparous compared with multiparous dairy cows ($P < 0.05$). Neither in primiparous nor in multiparous dairy cows were there clear relationships between IgG content and SG, Brix, and the color space coordinates L^*, a^*, and b^*. Interestingly, results indicate that despite a similar range of the variables investigated, correlations between those variables can differ between the quarter and the composite samples. Correlation coefficients with IgG concentration of the respective samples were greater using a composite compared with an individual quarter sample. This was true for SG and Brix determination, and also for the color space coordinates measured. Due to the variation in milk composition between individual quarters of a cow, correlation coefficients between colostral IgG concentration, SG, Brix-values, and colostrum

color were poorer in quarter compared with composite samples. In conclusion, both accuracy and limitations of on-farm instruments estimating colostrum quality apply for quarter colostrum samples as well as composite samples.

Key Words: colostrometer, immunoglobulin G, refractometer

0847 Effects of increasing residual milk on milk yield and composition. L. L. Hernandez[1], V. J. McKeon[*2], E. L. Endres[2], A. de Bruijn[2], A. Kleinhans[2], and D. J. Reinemann[2], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]University of Wisconsin, Madison.*

The future profitability of the dairy industry depends, in part, on faster milking time and increased milk yield. Currently, milking machines detach from the udder when milk flow decreases to a specified amount. Due to variability in quarter-level milk yield, conventional practice may result in over-milking of up to three quarters and a variable amount of over-milking of the fourth quarter. The objective of this research was to evaluate the effect of residual milk on milk yield and composition. Twelve multiparous (avg. lactation 2.83 ± 0.99) Holstein cows were milked twice daily with a quarter milking machine for 42 d beginning 5 d post calving. Twice-daily quarter milk weights were recorded. Cows were assigned alternating control and treatment half udders depending on calving order, resulting in 12 control (CON; 0% residual milk) and 12 treatment (RES; 30% residual milk) quarters. Milk removed from RES quarters was recalculated weekly to account for an increase in milk production. Milk yield was affected by treatment ($P < 0.001$; 87.64 ± 5.20 kg for CON vs. 63.25 ± 5.20 kg for RES), quarter ($P < 0.001$; 67.10 ± 4.68 kg for front vs. 83.79 ± 4.68 kg for rear), and the treatment by week interaction ($P < 0.01$). Milk samples were collected weekly starting on d 5 and ending on d 47. Milk samples were analyzed for SCC, SNF, protein, MUN, and lactose. There was a week effect for SNF, butterfat, protein, MUN, and lactose ($P < 0.001$). There was a treatment by week by quarter effect on SNF ($P < 0.05$). Milk lactose concentrations were decreased by treatment ($P < 0.05$; 4.86 ± 0.07 kg for CON vs. 4.66 ± 0.07 kg for RES), differed among quarters ($P < 0.05$; 4.81 ± 0.07 kg for front vs. 4.71 ± 0.07 kg for rear), and there was a treatment by quarter interaction ($P < 0.05$; 4.96 ± 0.08 kg for CON front, 4.76 ± 0.08 kg for CON rear, 4.67 ± 0.08 kg for RES front, and 4.66 ± 0.08 kg for RES rear). Treatment increased SCC ($P < 0.05$; 42.78 ± 14.75 kg for CON vs. 89.60 ± 14.75 kg for RES). A treatment by quarter interaction was present for SCC ($P < 0.05$; 40.75 ± 16.58 kg for CON front, 44.82 ± 16.58 kg for CON rear, 111.26 ± 16.58 kg for RES front, and 67.94 ± 16.58 kg for RES rear). Results suggest that leaving 30% residual milk in the udder suppresses milk yield, increases SCC, and decreases milk lactose content. Future research should explore optimal take-off settings of milking machines at the quarter level.

Key Words: quarter variability, residual milk

0848 Nutrient composition of milk from great apes throughout lactation. M. Garcia[*1], M. Power[2], and K. M. Moyes[1], *[1]Department of Animal and Avian Sciences, University of Maryland, College Park, [2]Smithsonian Conservation Biology Institute, Washington, DC.*

For great ape infants, milk is the primary, if not sole, food providing the only supply of water, organic nutrients, and minerals during the first 12 to 18 mo of life. Moreover, when mother's milk is not available to a great ape infant (e.g., maternal death or infant rejection), zoo nutritionists/veterinarians formulate a milk replacer to maximize the chances of neonate survival. However, very limited information on milk composition from non-human apes is currently available. This study aimed to identify the nutrient composition of milk from gorillas and orangutans throughout lactation. Fifty three milk samples from 4 gorillas and 3 orangutans were collected throughout 48 and 22 mo in milk (MIM), respectively. Samples were grouped into 5 stages of lactation (i.e., 0 < MIM = 6, 6 < MIM = 12, 12 < MIM = 18, 18 < MIM = 36, and 36 < MIM = 48). Data were analyzed as a complete randomized design. The analysis to compare gorilla with orangutan included only 4 stages of lactation. Across MIM, protein was greater in gorilla than in orangutan milk (1.27 vs. 0.85%, respectively; $P < 0.01$). Protein, fat, lactose, and gross energy were affected by the interaction of species by MIM ($P < 0.05$). For gorilla milk, all components changed with MIM, whereby protein content was greatest by 48 MIM (1.91%, $P < 0.01$) and lactose was lower by 6 MIM, reaching a nadir by 48 MIM (4.95%, $P < 0.01$). Moreover, fat and gross energy contents followed a similar pattern to that of DM, with the highest content by 36 MIM ($P \leq 0.01$). For orangutan milk, protein, DM, and fat were unaffected by MIM. However, gross energy and lactose contents were steady during the first 18 MIM (7.51% and 0.36 Kcal/g, for lactose and gross energy, respectively) and decreased (lactose, 6.67%, $P < 0.05$) or tended to decrease (gross energy, 0.39 Kcal/g, $P < 0.10$) by 36 MIM. Major macronutrients in milk were similar between orangutan and gorilla, except for a lower protein content in orangutan milk. There was some change in milk composition over lactation. Mean values for mature milk between 6 and 18 MIM are the best values to consider when formulating milk replacers (protein 1.05%, fat 2.12%, and lactose 7.21%). Coupled with immune parameters, these results provide useful information to assist professionals caring for non-human great apes under captivity.

Key Words: gorilla, milk components, orangutan

0849 Milk fat globules as a source of mammary microRNA. D. Lago-Novais[1,2], K. Pawlowski[1], J. A. A. Pires[*1], L. Mobuchon[1,3], S. Bes[1], P. Martin[3], and C. Leroux[1], *[1]UMR1213 Herbivores, INRA, VetAgroSup, Saint-Genes-Champanelle, France, [2]Universidade Federal da Bahia, CEP, Salvador-BA, Brazil, [3]UMR1313 Gabi, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France*.

Tissue for research on mammary gland (MG) gene expression is obtained via invasive and expensive methods (biopsy or post-mortem) that limit high throughput analyses. Milk fat globules (MFG) have been used to assess the mRNA content of the mammary epithelial cells in the bovine and goat (Brenaut et al., 2012; Canovas et al., 2014) for gene expression studies. MFG is therefore a satisfactory alternative source of mammary mRNA. MicroRNAs (miRNA) are small stable noncoding RNAs involved in multiple aspects of mammary gland physiology. Whereas the use of MFG was reported in humans (Munch et al., 2013), until now MFG as the source of miRNA has not been studied in the bovine. The objective of this study was to assess MFG as a source of miRNA, and whether the latter are representative of MG miRNA expression, by comparing targeted miRNA in MFG and MG sampled from mid-lactation Holstein cows. Total RNAs were extracted from MFG (n = 6) and MG (n = 6) using TRIzol (ThermoFisher, Inc, USA). Nine miRNA (*miR-29a*, *miR-125*, *miR-126*, *miR-141*, *miR-148a*, *miR-204*, *miR-223*, *miR-320*, and *miR-494*) were studied by RT-qPCR. The results are expressed as fold change of MFG data relative to MG data using the 2-ΔΔCt method and *U6* as internal reference. Statistical analyses were performed using a t test (DataAssist™ software) and $P < 0.05$ considered as significant. Among the nine miRNA chosen on the basis of the expression in MG, two were not detected in MFG whereas they were highly abundant in MG (*miR-126* and *miR-204*), and three were significantly more abundant in MG than in MFG (*miR-29a*, *miR-125b*, and *miR-148a*, presenting a fold change value of 23.2, 13.9, and 8.7, respectively). Four miRNA were detected at the same level in both MFG and MG. Our results suggest that there are different mechanisms of miRNA transfer to milk. Nevertheless, it is possible that miRNA not present in MFG are not expressed in epithelial cells, but are present in other MG cell-types, and therefore not transferred to milk. In conclusion, MFG can be used as a non-invasive source of microRNA but do not reflect exactly the MG miRNome. Further research is warranted on the composition of MFG miRNome and modulation of their secretion in milk.

Key Words: bovine, microRNA, milk fat globule

0850 Consumption of endophyte-infected fescue seed during the dry period and lactation affects mammary gland gene expression in dairy cows. R. L. Baldwin[*1], C. Li[1], D. M. Bickhart[1], C. M. Evock-Clover[1], P. Grossi[2], R. K. Choudhary[3], T. H. Elsasser[4], G. Bertoni[5], E. Trevisi[6], G. E. Aiken[7], K. R. McLeod[8], and A. Capuco[1], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]Università Cattolica del Sacro Cuore, Piacenza, Italy, [3]School of Animal Biotechnology, GADVASU, Ludhiana, Punjab, India, [4]USDA-ARS, Animal Biosciences and Biotechnology Laboratory, Beltsville, MD, [5]Istituto di Zootecnica, Università Cattolica del Sacro Cuore, Piacenza, Italy, [6]Università Cattolica del Sacro Cuore, Piacenza, Italy, [7]USDA-ARS, Lexington, KY, [8]University of Kentucky, Lexington*.

Ergot alkaloids in endophyte-infected grasses inhibit prolactin secretion and reduce milk production when fed to lactating cows. However, we have shown this effect is temporal in that prepartum consumption of infected seed throughout the dry period does not inhibit subsequent milk production and, in fact, prior exposure to bromocriptine (ergot peptide) actually increases production. To identify changes in the transcriptome and pathways mediating the mammary gland's response to ergot alkaloids in the diet, RNA sequencing (RNA-Seq) was performed on mammary tissue obtained from 24 multiparous Holstein cows exposed to 1 of 3 treatments. Starting at 90 ± 4 d prepartum, cows were fed endophyte-free fescue seed (control, C), endophyte-free fescue seed plus 3×/wk subcutaneous injections of bromocriptine (0.1 mg/kg BW, B), or endophyte-infected fescue seed (I), as 10% of the diet on an as-fed basis. Mammary biopsies from 4 or 5 cows/treatment at each of 3 distinct phases were obtained: 7 d before dry off during the initial lactation (L1), mid-dry period (D), and 10 d postpartum (L2). Biopsy samples from each treatment group and phase of lactation were used to generate individual RNA-Seq libraries. Normalized reads of the RNA-Seq data were organized into technical and biological replicates before processing with the RSEM software package. Each lactation phase was processed separately with the "rsem-run-ebseq" pipeline, and genes that differed between any of three treatments were identified from program output. A large proportion of genes considered to be differentially expressed in at least one treatment with a posterior probability of differential expression greater than 90% (n = 866) were found to be similarly expressed in B and I treatments, but differentially expressed from C (n = 575, total for all three phases). When phases were compared, 104 genes that were differentially expressed compared to C were found to be common to the L1 and L2 phases. Consistent with the production findings, networks most affected by treatments in L1 and L2 include lipid metabolism, small molecule biochemistry, and molecular transport, while in D networks relate more to

developmental and cellular functions and maintenance. The strong similarity in pattern of expression in B and I treatments during both late and early lactation suggests, at least in part, the involvement of similar cell signaling pathways or mechanisms of action for both B and I and the importance of prolactin messaging pathways.

Key Words: ergot alkaloids, prolactin, RNA sequencing

0851 Intravenous infusion of 5 hydroxy-L-tryptophan, a serotonin precursor, to transition dairy cows pre-calving affects GH-IGF axis gene expression in the mammary gland and liver post-calving.

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The role of the monoamine serotonin in the regulation of growth hormone (GH) and insulin-like growth factor-1 (IGF1) is controversial. Most studies have focused on serotonin produced in the brain. Given that the majority of total-body serotonin is produced outside of the central nervous system, we set out to determine whether infusing a serotonin precursor, 5 hydroxy-L-tryptophan (5-HTP) intravenously would impact the somatotropic axis in transition dairy cows. Multiparous Holstein cows were intravenously infused once daily for approximately 6 d pre-calving (−6 to −1), with either 1 L of saline ($n = 6$) or 1.0 mg/kg BW of 5-HTP ($n = 6$). Blood was collected before and after infusion, and at 2, 4, and 8 h post-infusion, at calving, and on d 3, 5, 7, and 14 post-calving to measure serotonin and IGF1 concentrations in serum. Mammary gland and liver biopsies were collected on d 1 and 7 post-calving to assess gene expression of the somatotropic axis. Gene expression data was analyzed using the DDCt method, using d 1 saline-infused cows as the control. Blood variables were analyzed with a two-way ANOVA (pre- and post-calving separately). Overall, 5-HTP-infused cows had greater serotonin and lower IGF1 concentrations than controls. Specifically, 5-HTP-infused cows had greater serotonin concentrations pre-calving (all days except d −2), at calving (d 0), and post-calving only on d 1 of lactation ($P < 0.05$). Infusion of 5-HTP decreased IGF1 concentrations pre-calving, particularly on d −6 and d −5, and only during the first and second hour post-infusion ($P < 0.05$). No differences in IGF1 were detected on d −4 to d −1 of infusion pre-calving. Post-calving, IGF1 concentrations markedly decreased, compared with pre-calving levels, but there were no differences between treatments on d 3, 5, or 7. On d 14, IGF-I concentrations increased to pre-calving levels only for the saline-infused cows and remained low in the 5-HTP-infused cows ($P < 0.05$). In the liver, 5-HTP treatment upregulated the mRNA expression of IGF1, IGF1-receptor and GH-receptor and IGF1-binding protein 3 on d 1 post-calving ($P < 0.01$), and no differences in gene expression were observed on d 7. In the mammary gland, 5-HTP treatment upregulated the mRNA expression of IGF1 and IGF1-binding protein 2 on both d 1 and 7 post-calving ($P < 0.05$). Regardless of the relative steadiness of circulating IGF1 concentrations post-calving, these data imply a potential benefit of 5-HTP administration pre-calving to improve the expression of genes related to the somatotropic axis in the liver and mammary tissue at the onset of lactation in dairy cows.

Key Words: lactation, serotonin, somatotropic axis

0852 Effect of cortisol on mammary epithelial cell Bax and Bcl-2 gene expression at lactation peak of goats.

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Cortisol is one of the main hormones that characterize stress, and chronically elevated cortisol can induce apoptosis, as well as expression of Bax (pro-apoptotic), which, in high levels, signals to cellular mitochondria causing cell apoptosis. In contrast, Bcl-2 (anti-apoptotic) acts as a "protector" of cells. Thus, the aim of this study was to analyze the effects of different levels of cortisol on Bax and Bcl-2 expression in mammary epithelial cells. Twenty-four Saanen goats were distributed in two groups: ACTH administration (cortisol group) or placebo (control group), during the lactation peak, i.e., 60 d of lactation. Four goats from each group were submitted to a biopsy of mammary gland after 1 h of treatment administration. Epithelial cells were isolated and four different concentrations of cortisol were added to this culture: 0.0 (control), 10, 100, or 1000 ng/mL. After 5 d, mRNA was extracted and Bax and Bcl-2 gene expression was measured by RT-PCR. Statistical analysis was performed using ANOVA, and significance was declared at $P \leq 0.05$. In the cortisol group, there was no effect of pre-treatment on expression of Bax and Bcl-2 in cell culture. However, in the placebo group, there was a significant difference ($P < 0.05$) in Bax expression, such that at higher levels of cortisol in the culture, Bax expression was lower (2.28 ± 0.58 and 2.01 ± 0.4, respectively, for 100 and 1000 ng/mL), compared to the control (4.38 ± 1.1, 0.0 ng/mL). For Bcl-2 there was no significant difference ($P > 0.05$). In summary, high levels of cortisol in mammary epithelial cells can interfere with Bax gene expression.

Key Words: apoptosis, cortisol, mammary gland, stress

0853 Interactions among serotonin and circadian systems in the mammary gland. A. Suárez-Trujillo[1], J. S. Crodian[2], A. M. Shamay[3], S. J. Mabjeesh[*4], K. Plaut[5], and T. M. Casey[6], *[1]Department of Animal Science, Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Purdue University, West Lafeyette, [3]Agriculture Research Organization, Volcani Center, Bet Dagan, Israel, [4]Department of Animal Sciences, The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University, Rehovot, Israel, [5]Department of Animal Sciences, Purdue University, West Lafayette, [6]Department of Animal Sciences, Purdue University, West Lafayette*.

The circadian and serotonin systems are reciprocally regulated in the brain and function to maintain homeostasis and respond to internal and external stimuli. Both systems play regulatory functions throughout the lactation cycle in the mammary gland. We hypothesized that the serotoninergic and circadian systems are reciprocally regulated in the mammary gland to mediate mammary homeostasis and respond to metabolic demands of milk synthesis. The objective of this study was to determine whether there is reciprocal regulation among the systems using approaches that encompassed bioinformatics analysis, mammary cell and tissue culture, and temporal expression analysis of mammary gene expression using sheep milk. Bioinformatics analysis of the 2000-bp upstream region of the *SLC6A4* (serotonin reuptake transporter, SERT) gene revealed the presence of a canonical E-box sequence (CACGTG) that circadian transcription factor CLOCK:BMAL1 binds. qPCR analysis of steady-state *SLC6A4* mRNA in samples isolated from sheep milk fat globules showed that this gene exhibits a circadian rhythm of expression. *SLC6A4* pattern of expression was similar to *PER2,* a core clock gene that is a transcriptional target of CLOCK:BMAL1. Moreover, comparison of *PER2* and *SLC6A4* temporal expression in wild-type HC11 cells also showed similar expression patterns in this mammary epithelial cell line. In HC11 cultures that carry shRNA that targeted *CLOCK, SLC6A4* expression was decreased across all time points ($P < 0.05$), supporting that the mammary clock regulates this serotonergic factor. To study the effect of serotonin (5-HT) on the mammary clock, mammary explants were prepared from lactating mice and divided into two treatments: control (lactogenic culture media–prolactin, glucocorticoids, and insulin) and 5-HT (lactogenic culture media and 200 μM of 5-HT). Samples were collected every 4 h over a 24-h period. One-way ANOVA of temporal variation within treatments found time had a significant ($P < 0.05$) impact on *BMAL1* expression in the control, but not the 5-HT treated samples, indicating that 5-HT attenuates *BMAL1* expression rhythm. *PER2* temporal variation was significant in both treatments ($P < 0.001$), but the differences were due to different time points, indicating that 5-HT shifted the phase of expression rhythm. Together, these data support that circadian and serotonergic systems interact in mammary gland. Further studies are needed to understand the significance of these interactions and how they may affect productivity.

Key Words: circadian clocks, mammary gland, serotonin

0854 Effects of stress on IGF-1 plasma concentrations and on expression of GH and IGF-1 receptors in mammary glands. G. F. Bomfim*, *Faculty of Animal Science and Food Engineering–FZEA/USP, Pirassununga/Sao Paulo, Brazil*.

Growth hormone (GH) and insulin-like growth factor-1 (IGF-1) have positive effects on lactation. The action of these hormones on mammary tissue can be regulated by their respective receptors, GHR and IGF-1R. When females undergo a situation of stress during the lactation period, its influence on the expression of these receptors, as well as on concentrations of IGF-1 in the blood, is unknown. The objective of this study was to evaluate the effects of cortisol on IGF-1 plasma concentrations and on the expression of IGF-1R and GHR at the peak and end of lactation. Thirty Saanen goats were distributed in two groups: ACTH administration to induce stress (cortisol group) or placebo (control group), at peak (60 d) and end (180 d) of lactation. Four goats from each group were submitted to a mammary biopsy after 60 min of treatment administration. Mammary tissue was collected to measure mRNA levels for IGF-1R and GHR via RT-PCR, and IGF-1 plasma concentrations were measured (EIA method) in blood samples of goats collected at the time of biopsy. Statistical analyses were performed using ANOVA. There was no treatment effect ($P > 0.10$) on GHR or IGF-1R gene expression or on IGF-1 plasma concentrations at 60 d and 180 d of lactation. These results suggest that an increase in concentrations of cortisol in the bloodstream does not influence GHR and IGF-1R expression in the mammary gland. In addition, IGF-1 plasma concentrations remained constant in both groups during lactation.

Key Words: ACTH, hormones, lactation

0855 Extracellular matrix molecule d*Eco*RIn signaling pathway gene expression in two bovine mammary cell lines. H. L. M. Tucker*, C. L. M. Parsons, and K. M. Daniels, *Virginia Polytechnic Institute and State University, Blacksburg.*

Previously we showed that d*Eco*RIn, an extracellular matrix (ECM) proteoglycan, is primarily located in mammary stroma and localization depends on physiological stage. Because the mammary gland is a heterogeneous tissue, the primary d*Eco*RIn producing cell populations and primary d*Eco*RIn responsive cell populations have not been identified; knowing this will advance our understanding of mammary ECM remodeling during mammary growth and involution. Our

objective was to characterize known d*Eco*RIn pathway genes in two immortalized bovine cell lines. These were bovine mammary epithelial cells (BME) and mammary fibroblasts (MF-T2). BME and MF-T2 were each grown on 6-well plastic dishes with Dulbecco's Modified Eagle Medium (DMEM) plus 10% fetal bovine serum. Initial densities were 5×10^5 cells/well for BME and 1×10^6 cells/well for MF-T2. After 16 h, media was changed to 100% DMEM. Cell lysates were collected after 16 h of DMEM incubation; total RNA and DNA were quantified. Total RNA was converted into cDNA and used in real-time quantitative PCR (qPCR). Genes of interest were: d*Eco*RIn, transforming growth factor β 1, transforming growth factor receptor 1, insulin-like growth factor 1, insulin-like growth factor receptor 1, epidermal growth factor, epidermal growth factor receptor, hepatocyte growth factor, hepatocyte growth factor receptor, and insulin receptor. Before data analyses, genes of interest were normalized to the average of three internal control genes and the final DNA content of each cell culture well. Triplicate cell culture wells were used and qPCR performed in duplicate. Separate immunocytochemistry experiments were conducted with the similar culture conditions to show cellular localization of the d*Eco*RIn core protein in BME and MF-T2 using a rabbit polyclonal d*Eco*RIn primary antibody (1:50; SC22753) and AlexaFluor 594 goat anti-rabbit secondary antibody (1:200; A11012). MF-T2 produced relatively more d*Eco*RIn core protein mRNA (31× more abundant) and protein than BME when both cell types were cultured under basal conditions. All other genes of interest were detected in both cell types, with transforming growth factor β 1 mRNA also being relatively more abundant in MF-T2 (9× more abundant). Because d*Eco*RIn has known growth regulatory properties, resultant findings will be used to design mechanistic cell culture studies. In the future, d*Eco*RIn signaling pathways may be manipulated in vivo in efforts to increase milk production efficiency via increased epithelial cell proliferation or decreased apoptosis during growth and involution.

Key Words: cell culture, ECM, gene, mammary gland

0856 Associations between quarter-level inflammation status across the dry period and health outcomes in the subsequent lactation. S. A. Metzger*[1], L. L. Hernandez[2], and P. L. Ruegg[1], [1]*Department of Dairy Science, University of Wisconsin-Madison, Madison, WI,* [2]*Department of Dairy Science, University of Wisconsin, Madison.*

The objective of this prospective cohort study was to determine associations of inflammation status of individual mammary quarters of dairy cows across the dry period with health status in the first 150 d of lactation. Milk from all mammary quarters ($n = 649$) of all lactating cows at the University of Wisconsin–Madison Emmons Blaine Dairy Cattle Research Center was sampled at dryoff before administration of dry cow antibiotic therapy and twice within the first 2 wk after the subsequent calving. Quarters with a somatic cell count (SCC) < 100,000 cells/mL and no microbiological growth at all three sampling times (low negative, LN; $n = 76$), quarters with SCC ≥ 150,000 cells/mL and no microbiological growth at the first two sample times and a variable third sample (high negative precalving, HNPre; $n = 17$), quarters with a variable first sample and SCC ≥ 150,000 cells/mL and no microbiological growth at the second and third sample times (high negative postcalving, HNPost; $n = 6$), and quarters with SCC ≥ 150,000 and positive microbiological growth at all three samples (high positive, HPos; $n = 3$) were followed until 150 d in milk (DIM). Foremilk samples were collected weekly for SCC analysis and monthly for microbiological analysis. Log-rank tests were performed to analyze survival to clinical mastitis (CM) and growth in monthly culture and SCC was analyzed with repeated measures analysis. The SCC of LN quarters was lowest throughout the first 150 DIM ($P < 0.001$) and LN quarters were least likely to experience a case of CM ($P < 0.001$). Fifty percent of HNPost quarters experienced CM, as compared to 1 of 3 HP quarters, 3 of 17 HNPre quarters, and only 2 of 76 LN quarters. LN quarters were also least likely to have bacterial growth in monthly samples ($P < 0.001$). All HP and HNPost quarters had bacterial growth in one or more monthly milk samples, while 36% of HNPre quarters and 9.7% of LN quarters had bacterial growth in one or more monthly milk samples. The most common bacteria isolated from monthly aseptic milk samples ($n = 383$) were coagulase-negative *Staphylococcus* species ($n = 22$), followed by streptococcus-like species ($n = 12$), *Corynebacterium bovis* ($n = 4$), yeast species ($n = 3$), and *Klebsiella*species ($n = 1$). Overall, LN quarters had better health outcomes during the first 150 DIM.

Key Words: dry period, inflammation, mastitis

0857 Interaction among energy status, dietary protein, and vitamin A in periparturient dairy cows: Effects on milk fatty acid profile and gross milk yield efficiency. Y. Chen*, K. C. Ramsey, C. Y. Tsai, M. A. McGuire, and P. Rezamand, *University of Idaho, Moscow*.

Diet affects the fatty acid (FA) composition of milk. The objective of this study was to determine the interaction of various rates of dietary protein (11 or 13%), vitamin A (0 or 110 IU/kg BW), and monensin (0 or 400 mg/d per head) fed during the dry period (4 wk before expected calving until calving) on milk FA profiles and feed efficiency of early postpartum dairy cows. Multiparous Holstein dairy cows ($n = 80$ total) were blocked by expected calving date and previous milk yield and randomly assigned to one of eight treatments in a 2 × 2 × 2 factorial arrangement of treatments. Milk yield and composition and feed intake were determined daily from calving (d 0) to 21 d postpartum. Results were analyzed using mixed model repeated measures ANOVA. Significance was declared at $P \leq$

0.05 while $0.05 < P \leq 0.1$ was considered a trend. Dietary vitamin A × monensin affected yield of several FA in milk; cows receiving both vitamin A and monensin during the dry period produced more C18:3 n3 as well as C22:6 compared with other treatment groups ($P = 0.004$ and 0.009, respectively). The interaction of dietary vitamin A × monensin also affected yield of C18:3 n6, sum of saturated FA, sum of unsaturated FA, sum of n3, sum of n6 FA, sum of MUFA, sum of PUFA, and sum of preformed FA. Dietary protein × monensin × vitamin A affected yields of C16:0 + C16:1, C20:4, C20:5, and C22:6 ($P < 0.03$ for all). Furthermore, greater dietary protein reduced the yield of C18:3 n3 and sum of *de novo* FA. Dietary protein × monensin × vitamin A tended to affect yields of C18:1 *cis*, C18:2 *cis*, C18:3 n3, C18:3 n6, sum of n3, sum of n6 FA, and n6:n3. Both energy corrected (ECM) and 3.5% fat corrected milk were interactively affected by dietary protein, monensin, and vitamin A ($P < 0.03$). Gross milk yield efficiency (ECM/DMI) was changed over time but no dietary effect was detected. Overall, diet composition altered the profile and yields of milk FA as well as ECM of early lactating Holstein cows.

Key Words: dairy cow, fatty acids, feed efficiency

0858 Effect of intrammamary infusion of chitosan hydrogels on bovine mammary gland involution after drying-off.

0859 Differences in body condition of gilts that are maintained from mating to the end of gestation affect their mammary development.

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The goal of this project was to determine if different body conditions in late gestation that are due to varying body conditions at mating affect mammary development of gilts. Gilts that were fed ad libitum in the growing period were selected based on their backfat thickness (BF) to form three groups at mating, namely, low (LBF; 12–15 mm, $n = 14$), medium (MBF; 17–19 mm, $n = 15$), and high (HBF; 22–26 mm, $n = 15$) BF. During gestation, LBF, MBF, and HBF gilts were fed approximately 1.25, 1.43, and 1.63 of maintenance requirements to maintain their differences in body condition. Daily feed intake was increased by 1 kg in the last 10 d of gestation. All gilts had their BF measured ultrasonically at mating and every 15 to 20 d thereafter. Blood samples were obtained at mating and on d 109 of gestation to measure concentrations of IGF-1, glucose, insulin, estradiol, urea, FFA, and adiponectin. Gilts were slaughtered on d 110 of gestation to collect mammary glands for compositional analyses and measures of mRNA abundance for selected genes. The MIXED procedure of SAS using a univariate model (3 levels) was used for statistical analyses and means were compared using the Tukey test. Mammary extraparenchymal tissue weight was less in LBF and MBF than in HBF gilts (1259.3, 1402.7, and 1951.5 ± 70.4 g, respectively, $P < 0.01$). Weight of parenchymal tissue was not altered by treatment ($P > 0.10$), but its composition was affected. Concentrations of DNA and RNA decreased as BF increased ($P < 0.01$), whereas percent fat and dry matter increased ($P < 0.01$). Mammary expression of *CSN2* (β-casein) in parenchymal tissue was also lower in HBF than LBF gilts ($P < 0.05$). On d 109 of gestation, concentrations of insulin, IGF-1, and adiponectin were greater ($P < 0.05$) in HBF than in LBF or MBF gilts, whereas those of urea were lower ($P < 0.01$). Maintaining differences in body condition from mating to the end of gestation therefore had an impact on mammary development of gilts. Extraparenchymal tissue mass was affected and, more importantly, composition of parenchymal tissue.

Key Words: body condition, gilt, mammary development

0860 Stem cells and cell hierarchy in the bovine mammary gland.

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Elucidating cell hierarchy and lineage commitment in the mammary gland is fundamental for understanding its development and for establishing methodologies aimed at increased production via stem-cell manipulation. Here, we demonstrate the existence of bovine mammary stem cells and describe enrichment and transplantation methodologies and attempts made to manipulate this population. Lin^- bovine mammary epithelial cells (bMECs) from Holstein heifers were sorted according to CD24 and CD49f expression into four populations. The $CD24^{med}CD49f^{pos}$–enriched population maintained high expression of basal markers. In culture, it generated luminal and basal clones and had high floating-sphere formation and growth rate. Upon transplantation into cleared mouse mammary fat pad, it gave rise to multilayered outgrowths with self-renewing properties. This population was positioned at the top of the cell hierarchy and referred to as the stem cell population. A more committed, bipotent basal population generated both luminal and basal clones in vitro but was almost completely restricted to generating unilayered basal outgrowths. Together with the luminally restricted progenitor population, it may serve as a reservoir for the highly differentiated luminal cells. Two markers, E-cadherin and miR-200c, whose expression levels correlate with differentiation, assisted in more comprehensive delineation of the bovine mammary cell hierarchy. Xanthosine administration did not affect the proportion of stem cells in bovine implants

transplanted into the cleared mouse fat pad. However, it had a latent negative effect on cell proliferation and may, therefore, interfere with mammary gland development and also limit tumor growth. To analyze the development of bovine mammary morphology in the mouse mammary stroma, bMECs were transplanted into the cleared mammary fat pad of immunodeficient mice. Multilayered hollow spheres developed within fibrotic areas. They shared morphological and immunohistochemical characteristics with the heifer gland but did not extend via ductal morphology. Nevertheless, a single case of terminal ductal lobuloalveolar unit (TDLU) development was recorded in mice treated with estrogen and progesterone, implying the feasibility of this representative bovine morphology's development. *In vitro,* paracrine inhibition of bovine epithelial mammosphere development by adipocytes was recorded, and it was antagonized by FGF administration. This indicates an active equilibrium between inhibitory and promotive effects exerted by the adipose and fibrotic regions of the stroma, respectively. Together, these findings imply that unique bovine mammary cell properties are integrated within a conserved mammary cell hierarchy paradigm delineated in their mouse and human counterparts.

Key Words: bovine, cell hierarchy, mammary gland, stem cells

0861 Optimal combination of histidine, lysine, methionine, and leucine affect β-casein synthesis via mTOR signaling pathway in bovine mammary epithelial cells.

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Assessing the regulatory effect of the optimal ratio of the essential amino acids (EAAs) on milk protein synthesis is vital to AA requirement models for lactation. The study employed response surface methodology (RSM) to determine the optimal ratio of histidine, lysine, methionine, and leucine on β-casein expression level in vitro and to clarify the effect of four EAAs on β-casein through mechanistic targeting of the rapamycin (mTOR) signaling pathway. A central composite design containing 5 axial points per EAA, and 28 combinations of the four EAAs was performed for our study. The efficiency of RSM and the changes of the mTOR-related signaling proteins were further verified by western blot. The protein band values from the AA-supplemented cells were related to their AA-deprived controls. The β-casein data from the RSM experimental design were analyzed using a regression model by Design–Expert 8.0.6. The other experimental data were analyzed using Tukey's test for post-hoc multiple comparisons of treatment means by SAS. Differences between experimental groups were considered significant at $P < 0.05$. The results showed that β-casein level was significantly affected by all four EAAs ($P < 0.01$, $R^2 = 0.71$). The optimal conditions for β-casein expression were as follows: His:Lys:Met:Leu = 5:6:1:7. Only a significant interaction of Leu and Met was observed as to β-casein expression ($P < 0.01$). Further experiments validated that under the optimal mixture of four EAAs, the expression of β-casein was 98% as high as the positive control (i.e., media with all AAs). The phosphorylation of mTOR, Raptor, GβL, S6K1, Rps6, and eEF2 was increased with supplementation of either single EAAs or the optimal combination of EAAs. Finding the best combination of these four EAAs promoted β-casein expression, and this appeared to be mediated through activation of the mTORC1 signaling pathway.

Key Words: bovine mammary epithelial cells, optimal ratio of EAAs, mTOR, β-casein

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0862 The goat (*Capra hircus*) mammary gland secretory tissue proteome as influenced by weight loss: A study using label-free proteomics.

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The objective of this work was to study the effect of seasonal weight loss (SWL) on the mammary gland secretory tissue proteome in two goat breeds from the Canary Islands. Two lactating dairy goat breeds from the Canary Islands with different levels of tolerance to SWL were used: Majorera (tolerant) and Palmera (susceptible). Within each breed, goats with the same age and stage of lactation were divided into two groups: control (constant weight) and restricted (15% liveweight reduction). Four groups were established: Palmera control (PC, $n = 6$), Majorera control (MC, $n = 4$), Palmera restricted (PR, $n = 4$), and Majorera restricted (MR, $n = 5$).

Animals on the restricted groups were fed on standard wheat straw, and animals in the control groups were fed on alfalfa hay supplemented with maize, soy, and dehydrated beetroot. At Day 22 of the trial, mammary gland biopsy samples were obtained. Samples (30 mg) were ground in liquid nitrogen with mortar and pestle, added to 500 μL of ammonium bicarbonate 50 mM, urea 8M, and thiourea 2M buffer, homogenized, and centrifuged, and the supernatant recovered. Per sample, 15 μg of proteins were trypsin digested (FASP protocol) and desalted. Peptides were loaded onto reverse-phase C18 columns and analyzed on an LTQ-Orbitrap Velos mass spectrometer. Protein identification and label-free quantification were performed using Mascot (Matrixscience) and Progenesis software (Nonlinear Dynamics). A total of 1010 proteins were identified, from which 96 proteins were considered statistically different among groups (fold change > 1.98 and $P < 0.05$). After SWL, there was an increase of proteins related to apoptosis and stress processes in both breeds. Moreover, both breeds showed a decrease in the number of proteins related to protein, carbohydrate, and fat biosynthesis. When both breeds were compared after SWL, the Majorera breed showed higher expression of immune system related proteins compared to the Palmera breed. In contrast, the Palmera breed showed higher expression of proteins related to apoptosis, ketone body formation (fatty liver), and protein metabolic processes compared to the Majorera breed. In conclusion, the two goat breeds have different metabolic reactions to SWL, highlighting differences particularly related to the immune system (higher expression in the tolerant breed) and apoptosis (higher expression in the susceptible breed).

Key Words: goat, label-free proteomics, mammary gland, seasonal weight loss

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0863 Pre-calving and early lactation factors that predict milk casein and fertility in the transition dairy cow. R. M. Rodney*[1,2], J. K. Hall[3], C. T. Westwood[4], P. Celi[5], and I. J. Lean[1,2], *[1]Scibus, Camden, Australia, [2]University of Sydney, Camden, Australia, [3]Halltech Services, Orange, Australia, [4]Kimihia Research Centre, PGG Wrightson Seeds Limited, Lincoln, Canterbury, New Zealand, [5]Faculty of Veterinary and Agricultural Sciences, University of Melbourne, Parkville, Australia*.

Multiparous Holstein cows ($n = 82$) of either high or low genetic merit (GM) (for milk fat + protein yield) were allocated to one of two diets in a 2 × 2 factorial design. Diets differed in the ratio of rumen-undegradable protein (RUP) to rumen-degradable protein (37% RUP vs. 15% RUP) and were fed from 21 d pre-calving to 150 DIM. This study evaluated the effects of these diets and GM on concentrations of milk casein (CN) variants and aimed to identify pre-calving and early lactation variables that predict milk, CN and protein yield and composition, and fertility of dairy cows. It explored the hypothesis that low milk protein content is associated with lower fertility, extending this to also evaluate the contribution of CN contents. Yields (kg/d) for CN variants were 0.49 and 0.45 of α CN, 0.38 and 0.34 of β CN, 0.07 and 0.06 of κ CN, and 0.10 and 0.09 of γ CN for high and low RUP diets, respectively. Increased RUP increased milk, CN and milk protein yields. Increased GM increased milk and γ CN yields and tended to increase milk protein yield. The effects of indicator variables on CN variant yields and concentrations were largely consistent, with higher body weight and α amino nitrogen resulting in higher yields, but lower concentrations. An increase in cholesterol was associated with decreased CN variant concentrations, while disease lowered CN variant yield. A diet high in RUP increased the proportion of first services that resulted in pregnancy from 41 to 58%. Increased pre-calving metabolizable protein (MP) balance decreased the proportion of first services that resulted in pregnancy when evaluated in a model containing CN %, milk protein yield, diet, and GM. This indicates that the positive effects of a diet high in RUP on fertility may be curvilinear as cows with a very positive MP balance before calving were less fertile than those with a lower, but positive, MP balance. Prepartum MP balance was important to production and reproduction outcomes, while surprisingly, metabolizable energy balance was not. Cows producing the lowest quartile of milk protein percentage were 28% less likely to become pregnant during the first 150 DIM. Milk CN % was similarly positively associated with improved pregnancy at first service. This study demonstrates the importance of protein metabolism to reproductive performance of the dairy cow.

Key Words: casein, fertility, protein degradability

0864 Increasing blood 5-hydroxy-L-tryptophan concentration for prevention of periparturient hypocalcemia in dairy cows. L. E. Hernandez-Castellano*[1], S. R. Weaver[2], L. L. Hernandez[2], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland, [2]Department of Dairy Science, University of Wisconsin, Madison*.

Hypocalcemia in dairy cows is caused by the sudden increase in demand for Ca^{2+} by the mammary gland for milk production after partum and simultaneously the limited ability of Ca^{2+} to be mobilized from bone in a timely manner. Serotonin (5-HT) is a key factor which mediates Ca^{2+} mobilization from bones. Therefore, we hypothesized that administration of 5-hydroxy-L-tryptophan (5-HTP), a 5-HT precursor, would increase 5-HT concentration in blood, and in turn induce Ca^{2+} mobilization from bone. In this study, 20 Holstein dairy cows were randomly assigned to two experimental groups. Ten animals received a daily i.v. infusion of 1 L of 0.9% NaCl (control; C). The other 10 animals received 1 L of 0.9% NaCl containing 1 mg of 5-HTP/kg BW daily (5-HTP group). Infusions were performed beginning on Day 10 before estimated

parturition. Infusions were conducted until the day of parturition, resulting in at least 4 d of infusion. Until parturition, blood samples were collected every morning before the infusions, and after parturition daily until Day 7, and on Day 30. Milk yield was recorded during this period. No differences between groups were observed for blood glucose, Mg^{2+}, β-hydroxybutyrate, and non-esterified fatty acid concentrations. Serum 5-HT concentration was increased until Day 5 after partum in the 5-HTP group compared to the C group. Colostrum 5-HT concentrations were higher in the 5-HTP group than in the controls (37.10 ± 3.12 vs. 25.02 ± 2.75 nM; $P < 0.05$), but differences were undetectable in milk 7 d after partum (13.43 ± 1.12 *vs.* 14.63 ± 1.13 nM; $P > 0.05$). Serum total Ca^{2+} concentrations decreased in both groups around parturition ($P < 0.05$), however, 5-HTP group had higher blood Ca^{2+} concentrations than the controls on Day 1 (1.93 ± 0.06 vs. 1.62 ± 0.09 mM) and Day 2 (2.07 ± 0.04 vs. 1.83 ± 0.07 mM), respectively ($P < 0.05$). Additionally, colostrum yield (first milking) was lower in the 5-HTP group compared to the C group (5.63 ± 0.34 *vs.* 8.56 ± 0.47 kg; $P < 0.05$), but no differences in colostrum IgG concentration were detected (68.41 ± 5.20 vs. 60.70 ± 10.27 mg/mL; $P > 0.05$). Milk yield did not differ between groups during the rest of the experiment. In conclusion, 5-HTP infusions increased blood 5-HT concentration. Moreover, 5-HTP can reduce the decline in blood Ca^{2+} concentration around parturition and hence may influence the occurrence of clinical or subclinical hypocalcemia. Finally, 5-HTP reduced colostrum production without affecting IgG concentrations, suggesting the mass of IgG available from colostrum may be sufficient to fulfill the needs of the offspring.

Key Words: dairy, hypocalcemia, serotonin

0865 Beta-hydroxybutyrate infusion affects glucose metabolism before and after parturition in dairy cows. M. Zarrin[1,2], L. Grossen-Rösti[1], R. M. Bruckmaier[1], and J. J. Gross[*1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland, [2]Department of Animal Science, Yasouj University, Yasouj, Iran*.

Recent studies in mid- and late-lactating dairy cows showed that β-hydroxybutyrate (BHBA) infusion had considerable impact on glucose metabolism and immune response during intramammary lipopolysaccharide challenge. The objective of the present study was to infuse BHBA during the dry period and after parturition to investigate the effects of elevated plasma BHBA concentrations on metabolism and endocrine changes in transition dairy cows. Eight multiparous Holstein cows in wk −2 (a.p.) and wk +2 (p.p.) relative to calving were infused (from 0800 AM to 1200 AM, 4 h) with a BHBA solution to increase plasma BHBA concentrations to 1.5 to 2.0 mmol/L (HyperB). The same period on the next day (without any infusion) was assigned as the control (Control). Blood samples were taken before the start of infusion as reference samples, and every 30 min during the following 6 h (4 h infusion and 2 h after the stop of infusion) in HyperB and on the control day, and were analyzed for glucose, BHBA, insulin, and glucagon. Plasma BHBA concentrations reached 1.7 ± 0.1 mmol/L (a.p.), and 1.6 ± 0.2 mmol/L (p.p.) in HyperB compared with 0.6 ± 0.1 mmol/L, and 0.6 ± 0.0 mmol/L in Control, respectively. The 4-h average BHBA infusion rate was 12.4 ± 1.0 and 13.3 ± 0.9 μmol/kg BW/min in wk −2 and +2, respectively ($P = 0.13$). BHBA infusion caused a decrease of plasma glucose concentrations, compared with pre-infusion levels, both before and after parturition ($P < 0.05$). The glucose response did not differ between a.p. and p.p. infusion even though basal glucose concentrations were different before and after calving (3.7 ± 0.1 vs. 3.2 ± 0.2 mmol/L, $P < 0.05$). BHBA infusion increased plasma insulin a.p. but not p.p. ($P < 0.05$) despite greater basal insulin concentrations before compared with after parturition (29.0 ± 8.4 vs. 5.8 ± 0.8 μU/mL, $P < 0.05$). Though basal glucagon concentrations were not different between wk −2 and +2 ($P = 0.30$), BHBA infusion decreased plasma glucagon only p.p. ($P < 0.05$). These findings show that effects of hyperketonemia on plasma glucose concentrations are independent of lactational stage, but endocrine adaptation to hyperketonemia differs before and after parturition. It can be assumed that BHBA has a glucose sparing effect and is a metabolic key regulator in early lactating dairy cows.

Key Words: β-hydroxybutyrate, glucagon, transition period

0866 Impact of increasing dietary crude protein content on urinary nitrogen excretion and milk nitrogen secretion of lactating sows. T. F. Pedersen[*1], C. Y. Chang[1], T. S. Bruun[2], and P. K. Theil[1], *[1]Aarhus University, Tjele, Denmark, [2]SEGES Pig Research Centre, Copenhagen, Denmark*.

The objective of the current study was to evaluate the effect of increased dietary crude protein (CP) content on urinary nitrogen (N) excretion and milk N secretion during lactation. In total, 36 sows from first to fifth parity were included in the experiment from parturition until weaning at d 28. Sows were allotted to 6 different treatments, with dietary CP contents of 149, 164, 174, 183, 193, and 208 g/kg DM, while dietary contents of SID lysine, methionine, threonine, and tryptophan were kept constant by including crystalline amino acids (AA). Sows were fed individually according to Danish recommendations, except for the recommended content of dietary CP. On d 2 postpartum, litters were equalized to 14 piglets and weighed on d 2, 10, and 17 to calculate milk production. Sows were fitted with urinary catheters on d 3, 10, and 17, and urine was collected three times during a 6-h period each week to estimate the daily urine production and N excretion. Additionally, milk samples were collected on d 3, 10, and 17 to estimate the daily secretion of N in milk. Fixed effects of week, treatment, and interaction were tested using a mixed

model. Overall, there was no effect of treatment on N content in urine ($P > 0.10$) or the amount of urine ($P > 0.10$). However, excretion of urinary N tended ($P < 0.10$) to be lowest for sows fed 164 g CP/kg DM (20.5 g N) and highest (1.5- to 1.8-fold higher) for sows fed 193 and 208 g CP/kg DM, respectively. The urinary N excretion averaged 28 g/d and did not change as lactation progressed ($P > 0.10$). Milk protein content increased with increasing dietary CP content, from 4.8 to 5.4% ($P < 0.05$). Milk production was comparable among treatments ($P = 0.09$) and ranged from 10.7 to 12.7 kg/d. The milk N secretion increased from 76 g/d on d 3 to 109 g/d on d 17, but it was not affected by dietary treatment ($P > 0.10$). In conclusion, the highest milk protein content was observed at 208 g CP/kg DM, whereas the lowest urinary N excretion was observed at 164 g CP/kg DM.

Key Words: milk protein, nitrogen loss, nutrition.

0867 Intramammary prednisolone affects the permeability of the blood-milk barrier during LPS and LTA induced mastitis in dairy cows.

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Mastitis can induce pathogen dependent changes in the permeability of the blood-milk barrier and therefore the paracellular transfer of blood and milk components. Glucocorticoids are known to increase the integrity of this barrier. The objective of this study was to examine the effect of intramammary prednisolone (PRED) on the blood-milk barrier in cows during mastitis induced by lipopolysaccharide (LPS) from *Escherichia coli* or by lipoteichoic acid (LTA) from *Staphylococcus aureus*. Thirty-one dairy cows, divided into 6 groups, were intramammarily challenged in one quarter with LPS, LTA, LPS and PRED, LTA and PRED, saline (control), or PRED. Quarters had a somatic cell count (SCC) of 60 ± 10 × 10^3 cells/mL before the experiment. The chosen doses of LPS and LTA induced a similar increase of SCC to 1420 ± 360 × 10^3 cells/mL at 4 h after challenge. Milk and blood samples were collected hourly from 0 to 8 h after challenge. Milk was analyzed for SCC, immunoglobulin (Ig) G, serum albumin (SA), and lactate dehydrogenase (LDH). Plasma was tested for the milk protein α-lactalbumin (ALA). Differences between treatments were tested by analysis of variance using a MIXED procedure and were considered significant if $P < 0.05$. The SCC in milk of control quarters and quarters treated only with PRED did not change throughout the experiment. In LTA challenged quarters with additional PRED administration, there was a reduction in SCC to control quarter level, whereas in LPS treated quarters, additional PRED administration had no effect on SCC. LDH activity did not significantly increase in LTA treated quarters, but increased in LPS quarters from 27 ± 7 U/L before challenge to 404 ± 115 U/L at 6 h after challenge, and decreased to control quarter levels with additional PRED administration. For SA and IgG, only LPS quarters showed an elevation from 0.25 ± 0.07 and 0.32 ± 0.04 mg/mL to 1.34 ± 0.57 and 1.16 ± 0.52 mg/mL, respectively, at 4 h after challenge. The PRED treatment reduced both concentrations to control quarter levels. There were no differences in plasma ALA concentrations in PRED-treated cows compared to cows that received only LPS or LTA. In conclusion, the pathogen specific appearance of blood constituents in milk during mastitis demonstrates a differential activation of the blood-milk barrier. These differential effects can be influenced by intramammary administration of glucocorticoids in a pathogen specific manner.

Key Words: blood-milk barrier, endotoxin, glucocorticoid, mastitis

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0868 Regulation of sterol regulatory element binding protein-1 in bovine mammary epithelial cells.

L. Chen* and B. A. Corl, *Virginia Tech, Blacksburg*.

The objective of this study was to investigate the molecular mechanisms by which nutrients regulate sterol regulatory element binding protein-1 (SREBP1) in bovine mammary epithelial cells (Mac-T). Three models were tested. First, the relationship between SREBP1 and the mechanistic target of rapamycin (mTOR) signaling was tested through mTOR activation/inhibition as well as SREBP1 knockdown by siRNA. Second, the relationship between AMPK and SREBP1 was tested in t10,c12-CLA-treated Mac-T cells. Third, the activation of SREBP1 was tested by glucose supplementation. Results showed that mTOR activation increased SREBP1 protein as well as the lipogenic gene expression by over 50%. While inhibition on mTOR failed to increase SREBP1, siRNA-directed SREBP1 knockdown confirmed that insulin enhanced lipogenic gene transcription through SREBP1. Further examination found that mTOR signaling regulates SREBP1 by preventing its proteosomal degradation. t10,c12-CLA decreased SREBP1 protein and lipogenic gene expression through phosphorylation of AMPK, while inhibition of AMPK phosphorylation partially rescued the SREBP1 reduction. Lastly, low glucose (1 mmol/L) was able to increase mature SREBP1 level by 2.2-fold. Increasing glucose concentration increased SREBP-cleavage activating protein, a key regulator of SREBP1 activation, in a dosage- and time-dependent manner. In conclusion, these results showed that major cellular metabolic regulators play roles in SREBP1 activation and degradation thus regulating lipogenesis in response to the nutrients provided.

Key Words: AMPK, glucose, mTOR, SREBP1, t10,c12-CLA

0869 Efficacy of dual X-ray absorptiometry as a means to measure mammary gland development in dairy heifer calves. A. J. Geiger*, C. L. M. Parsons, and R. M. Akers, *Virginia Tech, Blacksburg.*

A non-invasive means to assess mammary gland growth in dairy heifers is highly desirable from a research and animal welfare standpoint. We evaluated dual X-ray absorptiometry (DXA) as such a tool. Thirty-six Holstein heifer calves were reared on: 1) a control milk replacer (MR) fed at 454 g powder/d (CTL; 20% crude protein [CP], 20% fat), or 2) an enhanced MR fed at 1135 g powder/d (E; 28% CP, 25% fat). The MR was fed for 8 full weeks with weaning (half milk intake) occurring during the last week. Starter feed was offered after week 4 but was balanced between treatments. At weaning, a subset of calves were sacrificed ($n = 6$/diet). Remaining calves received estradiol (E_2) implants and were sacrificed at week 10. The 4 treatments were: 1) CTL, 2) CTL + E_2 (CTL-E2), 3) E, and 4) E + E_2(E-E2). After sacrifice, udders were removed and half-udders were snap-frozen. Frozen mammary glands were scanned and lipid and lean tissue contents were determined with and without the skin intact. Correlations were calculated between mammary gland lipid content via DXA, and biochemical extraction using PROC CORR function in SAS. Correlations were also calculated between mammary gland DXA lean tissue values and mammary parenchyma weight and DNA content. Correlations with skin removed were slightly higher. Overall, lipid content of the mammary gland as determined by DXA was highly correlated with lipid content determined biochemically, regardless of skin presence ($r = 0.92$; $P < 0.01$ for skin intact; $r = 0.94$; $P < 0.01$ for skin removed). With one exception, correlations were similar within treatments ($r = 0.59$, 0.91, 0.94, 0.91, and 0.96, 0.93, 0.97, 0.92 for treatments CTL, CTL-E2, E, and E-E2 with and without skin, respectively; $P < 0.01$ for all except for CTL with skin intact [$P = 0.16$]). Correlations between mammary gland lean tissue content determined by DXA and dissected parenchyma weight ($r = -0.01$; $P = 0.94$) or parenchyma DNA content ($r = 0.22$; $P = 0.21$) were low and nonsignificant. Results indicate that DXA analysis can be used to evaluate fat content of the mammary gland in young heifers but not the mass of mammary parenchymal tissue. It remains to be determined if this technology can be used in intact animals.

Key Words: calf, dual X-ray absorptiometry, mammary gland

0870 Percentages of milk fat, lactose, and protein are affected by diurnal variations in dairy goats. F. Rosa*[1], J. S. Osorio[1], J. Lohakare[1], M. Moridi[2], A. Ferrari[3], E. Trevisi[3], and M. Bionaz[1], *[1]Department of Animal and Rangeland Sciences, Oregon State University, Corvallis, [2]University of Guilan, Rasht, Islamic Republic of Iran, [3]Universita Cattolica del Sacro Cuore, Piacenza, Italy*.

Diurnal variations in milk synthesis in dairy goats are not known but can have important implications for nutrigenomic interventions to improve milk synthesis. The diurnal variation in milk synthesis was evaluated in 12 *Saanen* multiparous goats in early to mid-lactation. Six goats were treated with an intrajugular injection of 2,4-thiazolidinedione (TZD) at 1000 h, and 6 control goats received saline. Goats received an NRC-compliant diet at 0800 h. All goats received an intramammary infusion with *Streptococcus uberis* 10 d before the onset of treatment to induce sub-clinical mastitis in the right half of the udder, the left half being used as control. Goats were milked every 2 h from 0700 h to 1900 h. Besides milk yield, milk samples were collected for components analysis, and jugular blood samples were collected for analysis of NEFA, triacylglycerol (TAG), urea (BUN), and glucose. Data were analyzed using a GLIMMIX procedure of SAS with time, treatment, and treatment × time as fixed effects for blood variables, with the addition of udder halves and relative interactions as fixed effects for milk variables. Goat was used as random effect. Mean separation was done using Tukey's test. The TZD injection did not affect any of the measured milk variables. SCC was not affected by time but was greater in the right vs. left udder half in both treatment groups ($P < 0.05$). Percent milk fat peaked at 0900 h (4.9%) and decreased afterward. The percentages of milk protein and milk urea (MUN) peaked at 1100 h (2.6% and 28.2 mg/dL, respectively) and the percentages of lactose (4.4%) and solid nonfat (SNF; 7.8%) peaked between 1300 h and 1500 h. None of the single blood metabolites were affected by treatment or treatment × time interaction but all were greatly affected by time ($P < 0.05$). Glucose consistently increased until 1300 h, urea reached a peak at 1100 h, NEFA decreased until 1300 h and increased afterward, and TAG consistently decreased throughout the day. The sum of TAG and NEFA, an index of available fatty acids, was affected by treatment ($P < 0.05$), with values being greater in TZD compared with the control. Significant ($P < 0.01$) positive correlations were observed between blood glucose and percent milk lactose, NEFA and SNF, TAG and SCC, and between BUN and milk fat and MUN. Negative correlations ($P < 0.05$) were observed between glucose and percent milk fat, and between TAG and SNF. This data highlights the diurnal variations occurring in milk synthesis in goats, suggesting that synthesis of milk fat is not exclusively driven by the availability of fatty acids.

Key Words: diurnal variations, goat, milk synthesis

0871 Comparative effect of two commercial preparations of bovine somatotropin on milk yield and overall performance in Chilean dairy cows. M. A. Barrios[1], P. Melendez[*2], and M. Duchens[1], [1]*University of Chile, Santiago, Chile,* [2]*University of Missouri, Columbia*.

To compare the effect of two commercial preparations of bSTr available in Chile on milk production and overall performance of dairy cattle, 348 confined Holstein cows from a high-producing farm located in Casablanca, Valparaíso Region (33.31 S, 71.40 W) were used. Cows were randomly assigned from 70–76 DIM to one of two treatment groups. Group 1 (n = 161) was Boostin® (LG LifeSciences, South Korea) and Group 2 (n = 187) was Lactotropin® (Elanco, USA). In both groups, the hormone was administered every 14 d to about 30 d before dry off. Information was obtained from computerized systems and collected until the end of the eighth cycle of treatment (approximately 180 DIM). Milk data was processed through a repeated measures ANOVA. Fertility was analyzed by logistic regression to evaluate the risk of pregnancy at first insemination. Days open were analyzed with Kaplan-Meier survival analysis to compare days at pregnancy. Frequencies of clinical mastitis were analyzed by logistic regression. Monthly SCC linear scores were analyzed using repeated measures ANOVA. Finally, culling rate was assessed by a Kaplan-Meier survival analysis. No significant differences in the interaction of time by treatment were observed for milk yield (P = 0.07), averaging 42.3 L/d for Lactotropin®, and 42.8 L/day for Boostin®. No significant differences on calving-to-conception interval were recorded during the first 180 d of lactation (P = 0.19), showing a median of 101 d in Lactotropin® group and 90 d in cows treated with Boostin®. Conception rate at first insemination was 40% in cows treated with Boostin® and 32.8% in cows treated with Lactotropin® (P = 0.16). Cows treated with Lactotropin® have a higher incidence of clinical mastitis (33.5%) compared to Boostin® cows (21.1%) (P < 0.01). However, no significant differences were observed in SCC between groups. Finally, treatment has no effect on culling rate (P = 0.78). In conclusion, there are no substantial differences between hormone preparations regarding milk production, udder health, and fertility in high-producing Holstein cows.

Key Words: bST, fertility, mastitis, milk yield

LIVESTOCK WATER SYMPOSIUM

0872 Understanding blue and green water for feed production in animal agriculture. J. G. Warren*, *Oklahoma State University, Stillwater*.

Increasing demand for animal protein combined with concern about water scarcity demands thoughtful considerations of the water footprint of animal agriculture. This water footprint can be discussed in the context of green water, which is rainfall that does not become runoff, and blue water, which is surface or groundwater that is consumed as a result of the animal production system. Much of the green and blue water utilized by animal agriculture provides for the production of grain and forages. As such, the type of feed utilized by specific animal production systems can dramatically influence the water footprint of the system. Grazing systems will generally result in larger water footprints than grain-based production systems because the higher quality grain-based systems provide for more gain per unit of water used. However, this reduced water footprint comes with increased environmental impacts such as erosion and offsite nutrient losses from the grain production systems. Furthermore, pasture-based systems overwhelmingly utilize green water, which would likely be consumed at similar rates if the pasture was used for meat production or wildlife habitat. Lastly, regional differences in soil type, rainfall distribution, and atmospheric water demand (evapotranspiration) also influence the water footprint of animal agriculture by impacting crop water use efficiency.

Key Words: life cycle analysis, groundwater, feed production

0873 Mineral balances including TMR, drinking water and assay minerals in the milk. A. R. Castillo*, *UC Cooperative Extension, Merced, CA*.

Drinking water for dairy animals or manure for soil applications can be both a source of mineral nutrients and toxic substances. Commercial dairy production systems (grazing or indoors) are evolving to a larger scale, with more cows per farm and milk production per cow. Including assayed concentrations of minerals in the diet, drinking water and milk could improve the accuracy of calculations of herd or pen mineral balances. The aim of this presentation is to discuss mineral contents in TMR, water, and milk on mineral balances and excretion in lactating dairy cows. A mineral balance study in California on 40 dairies with low total salts (TS) drinking water for lactating dairy animals (0.2 to 1.5 g TS/L) was performed to compare TMR mineral content with the NRC requirement, with and without including minerals in drinking water, and the average NRC values for milk mineral concentrations to assayed minerals in the bulk tank milk. Most TMR minerals were in excess of NRC requirements. When including minerals in drinking water, Mg, Na, Cl, S, and Cu increased TMR median mineral contents by about 5% (ranging from 3.6% for S to 7% for Na). The assayed values of minerals in milk were lower than NRC averages (i.e., Mg, 49%; Na, 58%; Cu, 295%; and Fe, 525%). Estimated excretions of minerals via manure varied substantially across farms. Farms in the 10th percentile had estimated mineral excretions via manure 2 to 3 times less than those in the 90th. For example, daily K median excretion was 321 g/cow, from 240 (10th) to 425 g/cow (90th

percentile), daily Na excretion varied from 69 (10th) to 168 g/cow (90th percentile) with a median of almost 100 g. Median Cu and Zn excretions were 417 and 1700 mg/cow per day, but Cu excretion increased more than 3 times and Zn more than 2.5 times from the 10th to 90th percentiles. Estimates of dairy farm mineral balances should be based on assayed mineral concentrations in dietary ingredients, drinking water, and milk. Accurate estimates of mineral balance can then be used to manage excess minerals (diet and manure) and improve animal mineral nutrition, nutrient management plans, and soil mineral nutrition.

Key Words: dairy sustainability, dairy cows, drinking water, mineral balances

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0874 Water: The frequently neglected nutrient in growing and finishing diets. J. J. Wagner* and T. E. Engle, *Colorado State University, Fort Collins*.

The objective of this presentation is to describe water requirements of feedlot cattle and to discuss the effects of water sulfate concentration on water intake (WI). The Recommended Nutrient Allowances for Beef Cattle report was published by the National Research Council (NRC) in 1945 and was revised in 1950, 1958, 1963, 1976, 1984, and 1996 (update 2000). Water requirements were first described in the 1976 NRC and warranted a separate chapter in 1984. However, in the much aligned 1996 (update 2000) NRC report, the discussion of water was relegated to a section in the vitamin chapter. The findings of Winchester and Morris (1956), describing WI as a function of BW, DMI, and ambient temperature, were used as the basis of the water discussion in the 1976, 1984, and 1996 (update 2000) NRC publications. Also included in the 1996 (update 2000) revision was discussion of an equation predicting WI by feedlot cattle based on maximum daily temperature (Tmax), DMI, precipitation, and dietary salt concentration (Hicks et al., 1988). Arias and Mader (2011) developed models predicting WI from several environmental measurements. Solar radiation (SR, W/m^2) and thermal heat index (THI; Thom, 1959; NOAA, 1976) were the most important factors predicting WI during summer; however, Tmax and THI were the best predictors of WI during winter. Sexson et al. (2012), using a univariate analysis, found that WI from April through October was positively related to all measures of temperature, negatively related to all measures of relative humidity, positively related to wind velocity, negatively related to sea level barometric pressure, positively related to DMI, and negatively related to BW. A multivariate model predicting WI accounted for 32% of the variation in WI. Loneragan et al. (2001) and Sexson et al. (2010) demonstrated reduced WI for steers consuming water with >1000 mg/L sulfate as compared to steers consuming water with <1000 mg/L sulfate. The observed reduction in WI associated with increased sulfate concentration was greater during summer months as compared with spring or fall. Water is described in a separate chapter in the recently released Nutrient Requirements of Beef Cattle, Eighth Revised Edition (National Academies of Sciences, Engineering, and Medicine, 2016). Equations predicting WI in the eighth revised edition were developed using surface regression of the tabular values published by Winchester and Morris (1956) and include current effective temperature index, as computed from temperature, relative humidity, wind speed, and hours of daylight.

Key Words: water intake, water sulfate concentration, feedlot cattle

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0875 Simultaneous monitoring of water consumption in eight double pens as a tool for improving welfare and predicting diseases and unwanted behavioral changes in finisher pigs. K. N. Dominiak*[1], L. J. Pedersen[2], and A. R. Kristensen[1], [1]*University of Copenhagen, Department of Large Animal Sciences, Frederiksberg, Denmark,* [2]*Aarhus University, Department of Animal Science Behavior and Stress Biology, Aarhus, Denmark*.

Increasing animal welfare and heightening the level of management by sensor-based monitoring of water consumption in finisher pigs are the overall objectives of this study. It has previously been shown that water monitoring can be used to predict outbreaks of diarrhea in weaner pigs at the section level, and diarrhea or unwanted behavioral changes in finisher pigs at the double-pen level. A double pen is defined as two neighboring pens getting their water supply from the same pipe on which the sensor is placed. In this study the hourly water consumption was measured in a commercial farm by water flow sensors in eight double pens each containing 36 finisher pigs and distributed with two in each of four sections. The eight individual time series are modeled simultaneously in one dynamic linear model (DLM), and variance components are estimated by an EM-algorithm. Insertion dates are not synchronized but follow the production cycle, demanding the DLM to handle a varying number of time series at any given time. The diurnal drinking pattern is described by a combination of three harmonic waves (24 h, 12 h, and 8 h wavelength) as well as underlying levels and trends for herd, sections, and double pens. Preliminary results indicate a strong correlation between double pens in the same section as well as some pen-specific effects. In this study simultaneous monitoring is used to detect diseases (diarrhea, influenza, and respiratory diseases), as well as the unwanted behavioral changes preceding outbreaks of tail bite and fouling. Early warnings can be generated either independently at the double-pen level or merged at the section level or herd level. This quality can be used as a prioritizing tool minimizing the occurrence of false positive alarms if the warning pattern is highly different from what can be expected based on knowledge of the specific disease or behavioral change. This study is a part of an ongoing project aiming to improve the welfare and productivity of

growing pigs using advanced ICT methods.

Key Words: sensor-based, early warning, dynamic linear model

0876 Growth and health performance of dairy calves drinking reverse osmosis water compared to municipal water. N. D. Senevirathne*, J. L. Anderson, and M. Rovai, *Dairy Science Department, South Dakota State University, Brookings*.

Our objective was to determine effects of drinking reverse osmosis (RO) water versus municipal city (MC) water on growth and health performance of calves. Twenty-four Holstein calves (12 females, 12 males; 2 d old, 44.6 ± 6.10 kg BW), housed in individual hutches, were used in a 10-wk randomized complete block design study. Calves were blocked by birthdate and sex. Treatments were RO water (Culligan Water Filtration System, Brookings, SD) versus MC water (Brookings Municipal Utilities, Brookings, SD) which contained 13 and 387 mg/L total dissolved solids, respectively. Milk replacer (28% CP; 18% Fat) was fed twice daily during wk 1 through 5 and then once daily during wk 6. At each feeding, 0.45 kg of dry milk replacer was mixed with 2.8 L of respective water type, according to treatment. Calves were fed water and starter pellets ad libitum throughout the study. All intakes were recorded daily. Daily total respiratory scores (healthy ≤ 3, sick ≥ 5) were calculated from the sum of scores for rectal temperature, cough, ocular, and nasal discharge. Fecal consistency scores (0 = firm, 3 = watery) were also recorded daily. Body weights (BW) and frame growth were measured 2 d every 2 wk and jugular blood samples were collected 1 d every 2 wk at 3 h after morning feeding. Fecal grab samples were collected 5×/d for 3 d during wk 10 for analysis of total tract digestibility (TTD) of nutrients. Results were analyzed using MIXED procedures with repeated measures and Tukey's test for means comparison in SAS 9.4. Significant differences were declared at $P < 0.05$ and tendencies were declared at $0.05 \leq P < 0.10$. Total DMI and G:F increased more over time for RO than MC. Water intake was less in RO than MC, indicating more efficient water use by calves. Frame growth, BW, ADG, serum glucose, plasma urea nitrogen (PUN), β-hydroxyl butyrate (βHB), TTD of DM and CP were similar. Fecal scores tended to be less (firmer) in calves on RO, with an interaction by time. Respiratory scores had a tendency to decrease more over time when calves drank RO. Results demonstrated calves drinking RO had similar growth with improved G:F and health scores over time compared to MC.

Key Words: reverse osmosis water, growth performance, dairy calf

Table 0876.

Item	Treatment		SEM	*P*-values		
	RO	MC		Treatment	wk	Treatment × wk
DMI, g/d	1,508	1,502	83.2	0.72	<0.01	<0.01
Water intake, kg/d	3.66	3.85	0.36	<0.01	<0.01	0.27
BW, kg	70.2	70.2	1.79	0.99	<0.01	0.84
ADG, kg/d	0.72	0.69	0.04	0.69	<0.01	0.12
G:F	0.54	0.52	0.02	0.22	<0.01	<0.01
Glucose, mg/dL	111.2	105.9	3.04	0.12	<0.01	0.76
βHB, mg/dL	32.8	33.1	1.05	0.80	<0.01	0.83
PUN, mg/dL	16.3	15.8	0.62	0.45	<0.01	0.46
DM TTD, %	92.9	92.0	0.75	0.43	-	-
CP TTD, %	76.9	73.1	2.59	0.34	-	-
Fecal score	0.60	0.69	0.03	0.09	<0.01	<0.01
Respiratory score	1.95	2.03	0.05	0.32	<0.01	0.02

0877 Effect of protein supplementation on low-quality forage utilization and nitrogen balance by lambs drinking saline water. J. I. Arroquy*[1], A. Lopez[2], and A. Juarez Sequeira[3], *[1]INTACONICET–UNSE, Santiago del Estero, Argentina, [2]INTA EEA Santiago del Estero, Santiago del Estero, Argentina, [3]CONICET-FAyA UNSE, Santiago del Estero, Argentina.*

The aim of this study was to access the effect of protein supplementation on intake, digestion, and N utilization in lambs fed a low-quality hay (*Panicum maximum;* 6.4% CP, 79.5% NDF, 54.3% ADF) and drinking high-salt water. Twenty Hampshire lambs ($n = 4$; 31 ± 4 kg BW) allocated to in individual cages in a ten treatments by two period (10 × 2) trial. Treatments consisted (2 × 5 factorial) of two water qualities (WQ; low salt, LS; 442 mg/L of total dissolved solids (TDS) and 108 mg/L sulfate; and high salt, HS; 8358 mg/L TDS and 6363 mg/L sulfate) and five soybean meal levels (SBM; 0, 0.25, 0.50, 0.75, and 1.00% BW/d). Supplemental SBM × WQ interactions were significant for forage OM intake (FOMI; $P = 0.04$), total OM intake (TOMI; $P = 0.04$), whereas there was only a tendency for total tract digestibility OM intake (TTDOMI; $P = 0.07$). On average, HS had lower FOMI ($P < 0.01$; 33.0 vs. 26.1 g/kg $BW^{0.75}$), TOMI ($P < 0.01$; 42.2 vs. 35.3 g/kg $BW^{0.75}$), and TTDOMI ($P = 0.01$; 23.6 vs. 21.3 g/kg $BW^{0.75}$) than LS, while SBM levels did not significantly affect FOMI ($P = 0.86$) and TOMI ($P = 0.25$). In contrast, TTDOMI linearly increased in response to SBM ($P < 0.01$). There was no SBM × WQ interaction for water intake ($P = 0.60$), which tended to respond to SBM levels ($P = 0.07$) in linear fashion

($P < 0.01$), but was not affected by WQ ($P = 0.39$). There was no SBM × WQ interaction for total tract OM digestibility (TTOMD; $P = 0.69$). SBM linearly increased TTOMD ($P < 0.01$), and LS had lower TTOMD than HS ($P < 0.01$; 55.4 vs. 59.3% for LS and HS, respectively). Nitrogen balance was not affected by SBM × WQ interaction ($P > 0.12$), but N utilization (N-retained/N-intake ratio; $P < 0.01$) was. Regardless of WQ, we observed that SBM exerted a quadratic and linear response for N utilization ($P = 0.01$) and balance ($P < 0.01$). In LS, N balance and N utilization became positive at 0.25% of SBM, but in HS were positive only at the two greatest level of SBM (0.75 and 1.00%). In conclusion, according to our results lambs fed low-quality forage require greater levels of protein supplementation to maximize total digestible OM intake, N balance, and N utilization when they drink high-salt water compared to those drinking low-salt water.

Key Words: nitrogen balance, supplementation, saline water

MEAT SCIENCE AND MUSCLE BIOLOGY

0878 Chemical composition and expression of genes involved in lipid metabolism in the muscle of Nellore and Angus young bulls fed whole shelled corn diet.

M. M. Ladeira*[1], P. D. Teixeira[1], M. P. Gionbelli[1], M. L. Chizzotti[2], J. R. R. Carvalho[1], D. M. Oliveira[1], and T. C. Coelho[1], [1]*Universidade Federal de Lavras, Lavras, Brazil,* [2]*Universidade Federal de Viçosa, Viçosa, Brazil*.

The objective was to evaluate expression of genes involved in lipid metabolism and chemical composition of *longissimus dorsi* (LD) muscle of Nellore and Angus bulls fed whole shelled corn (WSC) or a ground corn (GC) diet. Twenty-eight bulls with average initial body weight of 378 ± 8.7 kg were used in a completely randomized design and arranged as a 2 × 2 factorial (2 breeds and 2 diets). The GC diet had 30% corn silage and 70% of a concentrate based on corn and soybean meal. The WSC diet had 85% whole shelled corn and 15% of a pellet based on soybean meal and minerals. After being harvested, samples were taken from the LD muscle between the 12th and 13th ribs for centesimal composition analyses and gene expression, which was analyzed by RT-qPCR. The model included the fixed effects of breed, diet, and their interaction. Expression of *PPARA* was greater in the LD of Nellore bulls (Table 1; $P < 0.01$) and also when bulls were fed the WSC diet ($P = 0.04$). Opposite results were found for *SREBF1* expression, which was less when bulls were fed the WSC diet ($P < 0.01$) and less in Nellore bulls ($P = 0.03$). *PPARG* and carnitine palmitoyl transferase 2 (*CPT2*) expression was downregulated in the LD muscle of Nellore bulls fed WSC and upregulated in the LD of Angus fed the same diet. Expression of lipoprotein lipase (*LPL*), fatty acid binding protein 4 (*FABP4*), acetyl CoA carboxylase (*ACACA*), and stearoyl-CoA desaturase (*SCD1*) was greater ($P < 0.05$) in the LD of Nellore bulls fed the GC diet. However, diets did not affect the expression of these genes in the LD muscle of Angus bulls. Fatty acid synthase (*FASN*) expression was greater in the LD of Nellore bulls ($P < 0.01$) and when animals were fed WSC ($P < 0.01$). Expression of acyl-coenzyme A oxidase 1 (*ACOX*) was greater for Angus fed WSC ($P = 0.04$). Meat from Angus bulls had greater intramuscular fat than meat from Nellore bulls (4.95 and 4.30; $P = 0.05$). However, there was no effect ($P > 0.05$) of diet on intramuscular fat. Moisture and protein were not affected ($P > 0.05$) by diet and breed. In conclusion, expression of *PPARA* and *SREBF1* have opposite regulation mechanisms in bovine muscle, regardless of the subspecies. Diets affected the expression of some genes involved in lipid metabolism differently in Nellore and Angus bulls.

Key Words: lipogenesis, marbling, *PPAR*, *SREBF1*, transcription factor

Table 0878.

Table 1. Expression of genes involved in lipid metabolism in the *longissimus dorsi* muscle of Nellore and Angus young bulls fed whole shelled corn (WSC) and ground corn (GC) diet.

	Nellore		Angus			*P*		
Genes	GC[1]	WSC[2]	GC	WSC	SEM	Breed	Diet	B*D
PPARA	3.78	4.72	1.00	2.83	0.32	<0.01	0.04	0.22
PPARG	2.61 b	1.00 c	2.8 b	5.67 a	0.33	<0.01	0.86	<0.01
SREBF1	5.25	1.00	5.71	2.61	0.28	0.03	<0.01	0.10
LPL	3.78 a	1.00 c	1.77 b	1.36 bc	0.29	0.04	<0.01	0.01
FABP4	13.47 a	1.00 c	8.93 b	10.16 b	0.86	0.34	<0.01	<0.01
ACACA	7.16 a	1.00 c	3.37 b	1.84 b	0.45	1.00	<0.01	<0.01
FASN	3.87	4.34	1.00	1.83	0.22	<0.01	0.01	0.16
SCD1	3.18 a	1.00 c	1.95 b	1.67 b	0.21	0.91	<0.01	0.02
CPT2	7.2 a	1.00 d	2.02 c	2.87 b	0.27	0.92	<0.01	<0.01
ACOX	1.33 c	1.00 c	2.67 b	5.29 a	0.38	<0.01	0.52	0.04

[1]GC: Diet containing 30% roughage and 70% concentrate
[2] WSC: Diet with 85% whole shell corn and 15% of a *pellet* based on soybean meal and minerals

0879 Effects of arachidonic acid and prostaglandins on proliferation, differentiation, and fusion of bovine myoblasts. X. Leng* and H. Jiang, *Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg*.

Arachidonic acid (AA) is a major lipid component of the plasma membrane and the precursor of prostaglandins (PG) in skeletal muscle. The objective of this study was to determine the effects of AA and its major PG derivatives PGE_2, $PGF_{2\alpha}$, and PGI_2 on the proliferation, differentiation, and fusion of bovine myoblasts. Satellite cells were isolated from 6 Angus or Angus crossbred steers (experimental unit) and were expanded as myoblasts in growth medium for a week before being used in the following tests. In the proliferation test, myoblasts were cultured in growth medium with 10 μM AA, 1 μM PGE_2, 1 μM $PGF_{2\alpha}$, 1 μM PGI_2, or vehicle control for 24 h. Proliferating cells were identified by EdU labeling. This test revealed that AA, PGE_2, $PGF_{2\alpha}$, and PGI_2 each increased the number of proliferating myoblasts by 13%, 24%, 16%, and 16%, respectively, compared to the control ($P < 0.05$). In the differentiation and fusion test, myoblasts were induced to differentiate and fuse into myotubes in the presence of the aforementioned treatments or control, for 24, 48, and 72 h. The differentiation status of myoblasts was assessed by reverse transcription-quantitative PCR of myogenin (*MYOG*), myosin heavy chain 3 (*MYH3*), and muscle creatine kinase (*CKM*) mRNAs, which are markers of differentiated myoblasts. The fusion level of myoblasts was estimated by calculating the percentage of nuclei located in myotubes, i.e., fusion index. Compared to the control, AA increased *MYOG* mRNA expression at 24 and 48 h, *MYH3* mRNA expression at 24 and 48 h, and *CKM* mRNA expression at 24, 48, and 72 h of differentiation ($P < 0.05$); PGE_2 increased *MYOG* mRNA expression at 24 and 72 h, and *MYH3* mRNA expression at 72 h of differentiation ($P < 0.05$); $PGF_{2\alpha}$ increased *CKM* mRNA expression at 72 h of differentiation ($P < 0.05$); and PGI_2 had no effect on mRNA expression of any of the three markers at any of the three times of differentiation. Compared to the control, PGE_2 increased the fusion index by 14% ($P < 0.05$) but the remaining treatments had no effect on this index. In conclusion, this study demonstrates that AA, PGE_2, $PGF_{2\alpha}$, and PGI_2 stimulate the proliferation, that AA and PGE_2 stimulate the differentiation, and that PGE_2 stimulates the fusion of bovine myoblasts in vitro.

Key Words: cattle, myoblasts, prostaglandins

0880 Influence of zinc amino acid complex and ractopamine hydrochloride supplementation on the sarcoplasmic protein profile of finishing steers. O. N. Genther-Schroeder*[1], E. Huff-Lonergan[1], M. E. Branine[2], and S. L. Hansen[1], [1]*Iowa State University, Ames,* [2]*Zinpro Corporation, Eden Prairie, MN*.

The objective of this study was to determine if Zn amino acid complex (ZnAA) and ractopamine hydrochloride (RH) supplementation affect the protein profile of the *longissimus dorsi* muscle of finishing steers. Twenty-four steers (477 ± 5.3 kg; SD) were fed a corn-based finishing diet in pens equipped with GrowSafe bunks to measure individual intake, as a part of a 2 × 2 factorial of ZnAA and RAC supplementation. All steers were supplemented with 60 mg Zn/kg diet DM as $ZnSO_4$ and were assigned to receive either 0 (CON) or 60 mg supplemental Zn/kg DM from ZnAA (ZN; $n = 12$ steers per treatment) for 56 d. On d 56 steers were equally assigned within treatments to receive RH at 300 mg·steer^{-1}·d^{-1} for 0 (NoRAC) or 28 d (RAC) before harvest ($n = 6$ steers per treatment). Muscle biopsies were collected from steers after 14 d of RAC supplementation. Four steers per treatment were selected to have sarcoplasmic extracts from muscle biopsy samples analyzed using 2D Difference-in-Gel Electrophoresis (2D-DIGE). Separate 2D-DIGE experiments were performed for the individual comparisons of CON+NoRAC vs. ZN+RAC (Exp. 1; $n = 4$ per treatment) to evaluate the effect of both RAC and ZnAA supplementation and CON+RAC vs. ZN+RAC (Exp. 2; $n = 4$ per treatment) to evaluate the effect of ZnAA supplementation within RH-fed steers. Proteins were selected based on relative abundance and were identified using mass spectrometry. In Exp. 1, abundance of isoforms of pyruvate kinase was decreased 20–25% ($P \leq 0.04$) in ZN+RAC, relative to CON+NoRAC steers. Phosphoglucomutase-1 abundance was decreased by 63% ($P < 0.0001$), phosphoglycerate mutase-2 was decreased by 21% ($P = 0.02$), and glyceraldehyde 3-phosphate dehydrogenase tended to be increased by 71% ($P = 0.06$) in ZN+RAC steers, relative to CON+NoRAC. In Exp. 2, phosphoglucomutase-1 abundance tended to be decreased by 60% ($P = 0.09$) and phosphoglycerate mutase-2 tended to be decreased 21% ($P = 0.06$) in ZN+RAC steers relative to CON+RAC steers. Decreases in phosphoglucomutase-1 and phosphoglycerate mutase-2 abundance in both experiments suggest these may be effects elicited by ZnAA supplementation. Changes in abundance of pyruvate kinase and glyceraldehyde 3-phosphate dehydrogenase were found only in the CON+NoRAC vs. ZN+RAC comparison and might be elicited by RH supplementation. These differences indicate that ZnAA and RH supplementation alter the protein abundance of enzymes involved in carbohydrate metabolism in skeletal muscle.

Key Words: ractopamine hydrochloride, zinc, 2D-DIGE

0881 Survey of attitudes for millennials who do not consume lamb. K. R. Wall[*1] and C. R. Kerth[2], *[1]Texas A&M University, College Station, [2]Texas A&M University Animal Science Department, College Station.*

Lamb consumption consists of the smallest percentage of red meat consumption in America. Our objective was to estimate how many Americans do not consume lamb and describe attitudes as to why not. The online survey consisted of demographic information and lamb consumption patterns and experiences. Participants were invited to complete the survey if they were within the millennial population (ages 18–34) and residing in the U.S. Participants (n = 2473) were 34.5% male, 65.5% female; 15.9% were ages 18–24, 83.2% were 25–34, and 0.9% were 35; 85.0% were Caucasian (non -Hispanic), 8.8% Latino or Hispanic, 3.0% Asian or Pacific Islander, 1.3% African American, and 1.8% other. Household income was 7.4% $24,999 or less, 17.9% $25,000–49,999, 20.8% $50,000–74,999, 19.5% $75,000–99,999, and 36.4% made $100,000 or more; 10.3% were not employed, 9.6% were employed part-time, and 80.0% were full-time. Participants reported consumption of the following protein sources either away from or at home: 92.3% chicken, 88.8% beef, 79.0% pork, 79.8% fish, 11% lamb, 92.6% eggs, and 25.8% soy-based products. 70.8% of the participants claimed to have eaten lamb before, and of these participants (n = 1719), 70.8% selected having a positive eating experience with lamb. Although 47.2% of the participants were uncertain how the lamb was prepared, braising (19.1%), grilling outside (12.5%), and panfrying (8.6%) were the most common methods of preparation. 65.1% of the participants would be willing to try lamb again, 23.2% selected maybe, and 11.6% would not be willing to try lamb again. Of the participants who had not tried lamb before (n = 716), 60.8% would be willing to try lamb. If lamb flavor were to be improved, 22.4% of the participants would definitely and 47.1% might consume more lamb. If lamb tenderness were to be improved, 23.7% of the participants would definitely and 44.8% might consume more lamb. If the eating quality of lamb were to be more consistent, 24.8% of the participants would definitely and 43.8% might consume more lamb. If lamb were to be implemented into the fast-food industry, 22.1% of the participants would definitely and only 22.8% might consume more lamb. While 72.8% of the participants selected they had never looked to buy lamb at their local grocery store, 14.4% selected lamb is hard to find and 5.1% selected finding lamb was hit or miss. Opportunities exist to increase the consumption of lamb by converting the millennial non-consumers of lamb.

Key Words: lamb, millennial, consumer

0882 Survey of attitudes for millennial lamb consumers. K. R. Wall[*1] and C. R. Kerth[2], *[1]Texas A&M University, College Station, [2]Texas A&M University Animal Science Department, College Station*.

As the interest in experiencing different foods increases among the millennial population, lamb consumption may be becoming more prominent. Our objective was to determine the attitudes of millennial consumers of lamb products by conducting an online survey. Participants were selected within the millennial population (ages 18–34) and residing in the U.S. Participants (n = 3292) reported consumption of the following protein sources either away from or at home: 99.4% chicken, 97.3% beef, 90.9% pork, 93.0% fish, 77.9% lamb, 96.9% eggs, and 35.5% soy-based products. 15.0% of participants eat lamb frequently (at least once every 2 wk), 24.1% eat lamb once a year, 30.0% eat lamb once every 6 mo, 31.0% eat lamb once every 3 mo. Participants reported eating lamb most frequently in the winter (December–February) at 35.0%, and 22.0% consume the most lamb in the month of December. When asked where consumers consume the most lamb, 66.0% responded away from home, and 23.0% responded at home. On a 5-point scale, 90.0% selected their experience consuming lamb has been "excellent" or "good," and 92.0% answered being satisfied with the eating quality of lamb at least 3 out 5 times. Only 34.0% of the consumers reported growing up eating lamb, and 94.0% selected having a positive first experience consuming lamb. Consumers declared choosing lamb over other protein sources 63.0% of the time due to flavor. When asked what origin of lamb consumers preferred, 78.0% selected no preference and only 11.0% selected American lamb. Consumers were prompted to distinguish between lamb and mutton, and 56.0% were "uncertain, they never tried both," whereas 33.0% selected that there are distinct differences. If lamb flavor were to be improved, 34.0% of the participants would definitely and 48.0% might consume more lamb. If lamb tenderness were to be improved, 35.0% of the participants would definitely and 46.0% might consume more lamb. If the eating quality of lamb were to be more consistent, 39.0% of the participants would definitely and 42.0% might consume more lamb. If lamb were to be implemented into the fast-food industry, 36.0% of the participants would definitely and 32.0% might consume more lamb. While 56.0% of the participants selected they had never looked to buy lamb at their local grocery store, 44.0% selected lamb is hard to find or that it was hit or miss. These data can be used to increase consumption among the millennial population.

Key Words: lamb

0883 A histologic and ultrastructural study of Wooden Breast Disease in modern broiler chickens.

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Wooden Breast Disease (WBD) is a novel muscle disorder in the poultry industry observed to frequently affect the breast muscles of high-yielding modern broilers. Characterized by extreme stiffening of the breast muscles on palpation of the pectoral region, WBD is known to result in significant economic loss in the poultry industry and may potentially cause behavioral alterations and reduced welfare in birds. To examine tissue changes associated with onset and pathogenesis of this disorder, a time-series experiment was conducted using chickens from a high-breast-muscle-yield, purebred commercial broiler line. Birds were raised for a period of 6 wk, and breast muscles sampled on a weekly basis from selected birds and processed for light and transmission electron microscopy. Histologic presentation indicated presence of focal single-myofiber degeneration and hyalinization in the second week, preceding inflammatory reaction that started in the third week. Lesions in the fourth week were generally characterized by multifocal to diffuse muscle fiber degeneration and necrosis accompanied by increased inflammatory cell infiltration. Lesions in the fifth and sixth week were characterized by diffuse muscle fiber damage, fibrosis, fatty infiltration including granulomatous tissue encompassing lipid droplets, and irregular myofiber regeneration. Ultrastructural examination showed fibrosis with dense regular collagen fibers, irregular Z-discs, myofibril splitting, displacement, and degeneration, including mitochondrial degeneration. This study therefore demonstrates that WBD exhibits an early onset in modern broilers and appears to assume a progressive course with acute inflammatory phase occurring in the earlier stages and chronic inflammation and fibrosis in the later stages of the disease course.

Key Words: broiler chickens, Wooden Breast Disease, transmission electron microscopy

0884 High-energy forage and feedlot finishing impact on beef consumer acceptability and sensory characteristics in the upper Midwest.

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The objective of this study was to determine consumer acceptability and sensory attributes of beef longissimus thoracis steaks from finishing steers grazing high-energy forages vs. fed a conventional feedlot diet. Steaks were from 32 steers fed 1 of 4 treatment diets including: mixed pasture (MIX); simple cereal grain/brassica mixture (SIMP); complex cereal grain/brassica mixture; and conventional feedlot ration (FLOT). All steers grazed a perennial mixed pasture diet before being assigned a treatment. Steers (n = 8) were fed FLOT diet for 92 d. Steers in the MIX (n = 8), SIMP (n = 8), and COMP (n = 8) grazed respective pastures for 76 d. Steers from all treatments were slaughtered on the same day. Carcasses were aged 7 d before fabricating 2.54-cm thick steaks. Vacuum packaged steaks were aged for an additional 7 d and frozen (−20°C) until evaluation for marbling score, instrumental color, pH, and Warner Bratzler shear force. Consumer panelists (n = 106) evaluated fresh steaks aged 15 d for flavor, texture and firmness, juiciness, and overall acceptability using a 9 point hedonic scale (1 = dislike extremely, 9 = like extremely). Data were analyzed with Proc Mixed and Proc ANOVA (SAS 9.4) for sensory characteristics and consumer acceptability, respectively. Marbling scores of steaks from FLOT steers (524.58) were greater ($P < 0.01$) compared to MIX (447.50), SIMP (437.50), and COMP (427.50) steers. There were no treatment differences ($P > 0.05$) for instrumental color, pH, and Warner Bratzler shear force. There were no correlations ($P > 0.05$) between marbling and Warner Bratzler shear force. Consumer panel results indicated that steaks from steers fed the FLOT diet had more preferable ($P < 0.05$) texture and firmness as well as overall acceptability (7.00 and 6.61) when compared to MIX (6.30 and 6.08) but were not different from COMP (6.63 and 6.21) and SIMP (6.69 and 6.51). Panelists detected no treatment differences ($P > 0.05$) in the hedonic ratings of flavor or juiciness. Results indicate that steaks from steers finished on high-energy forages are comparable to those finished on a conventional feedlot diet. Additionally, the brassica-rich forage diets did not impart any noticeable off-flavors in the steaks when compared to steaks from diets without brassicas.

Key Words: sensory, forage-finished, consumer panel

0885 Effect of growth-promoting technologies on the proteome of bovine *Longissimus lumborum*.

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The objective of this study was to identify the extent to which the protein profile of bovine *Longissimus lumborum* (LL) muscle in beef cattle is influenced by growth-promoting technologies (GP) during the finishing period. Crossbred heifers (n = 66) from two harvest groups were fed a conventional feedlot diet, blocked by BW, and randomly assigned to 1 of 3 treatments: no GP (CON, n = 22); implant, no ractopamine hydrochloride (IMP, n = 22); and implant and ractopamine hydrochloride (COMBO, n = 22). Heifers assigned to the IMP treatment were administered an implant containing 200 mg trenbolone acetate and 20 mg estradiol on d 0 of the study, and

the COMBO group received the same implant protocol as the IMP group, in addition to being fed 400 mg·d^{-1}·heifer $^{-1}$ of ractopamine hydrochloride for the final 28 d before harvest. Heifers were harvested on d 90 of feeding, and a section of the LL was removed (n = 66) 1 h post mortem, placed on dry ice, and stored at −80°C. A subset (n = 6) from each treatment from the first harvest group was randomly selected for proteome analysis by two-dimensional difference in-gel electrophoresis (2D DIGE) coupled with mass spectrometry (MS) to identify proteins of interest. Peptide identifications with > 95% probability with at least 2 identified unique peptides were accepted. Twenty-five spots selected in the sarcoplasmic fraction corresponding to 21 proteins differed in relative abundance among growth promoting programs. Nine spots from the myofibrillar fraction corresponding to 6 proteins were also identified to be different among treatment groups. Increased abundance (P < 0.05) of identified proteins in sarcoplasmic and myofibrillar fractions of the LL muscle from heifers subjected to the COMBO treatment when compared with the LL from CON included metabolic enzymes (creatine kinase M-type, triosephosphate isomerase, β-enolase), oxidative resistant proteins (peroxiredoxin-6, peroxiredoxin-2, protein deglycase DJ-1), muscle recovery proteins (myosin binding protein H, eukaryotic translation initiation factor 5A-1), and chaperone proteins (heat shock 70 kDa protein 1A). The results demonstrate that growth promoting technologies alter the protein profile of bovine muscle and suggest several metabolic pathways that are influenced by management practices that use these technologies. These pathways include metabolic processes, oxidative stress, and apoptosis cascades that can have an impact on growth efficiencies and meat quality in beef cattle.

Key Words: bovine, muscle, proteome

0886 Effects of post-weaning exposure to a high-concentrate diet vs. pasture on live performance, carcass characteristics, and meat quality of early harvested steers.

B. M. Koch*[1], L. E. Bowen[1], J. T. Milopoulos[1], G. Volpi Lagreca[2], and S. K. Duckett[1], [1]*Clemson University, Clemson, SC,* [2]*INTA, Anguil, Argentina*.

Twenty Angus steers (261 ± 21.5 kg) were used to evaluate the effect of post-weaning feeding strategy on live performance, carcass characteristics, and meat quality. Steers were randomly assigned to one of two feeding treatments: high-concentrate based diet (cracked corn, corn silage, and soybean meal [F]) or high-quality pasture (winter annuals, alfalfa, and non-toxic fescue [P]) for 127 d. At slaughter, subcutaneous adipose tissue samples were collected from each steer and flash frozen for later analysis. The 6–12 rib section of each carcass was collected for further analysis on Day 2 post-harvest. Steers consuming a high-concentrate based diet had a greater overall ADG than P ones (1.36 vs. 0.68 kg/d; P < 0.0001) resulting in heavier final BW and HCW, and greater dressing percentage (P < 0.001). Steers consuming grain had larger ribeye area (P = 0.0006) and more fat at the 12th rib (P < 0.0001) than steers on forages, whereas there were no differences for KPH and calculated yield grade (P = 0.22). The high-concentrate based diet resulted in much greater marbling scores than grazing high-quality forages (P < 0.0001; 448 vs. 240). Despite the increased marbling, there was no difference in longissimus muscle (LM) b* (P = 0.956), whereas LM from F were brighter and more red (greater a*; P < 0.003). Both subcutaneous L* and b* were not different between treatments (P = 0.20), whereas subcutaneous a* was greater for F than P (P = 0.0018). Fat cell sizes of subcutaneous tissue were larger in perimeter and area for F (P < 0.0001) whereas P had a greater fat cell number (P < 0.0001). Steers on F had greater LM total lipid (P < 0.0001), whereas P resulted in greater moisture, nitrogen, and ash (P < 0.0001). There were no differences in SFA or PUFA n-6 in LM (P = 0.49) whereas F had greater MUFA (P = 0.0037) and P had greater PUFA and PUFA n-3 percentages (P < 0.01) resulting in a more desirable PUFA n-6/PUFA n-3 ratio (P = 0.0003; 1.46 vs. 7.35 for P and F, respectively). This suggests that exposure to high-concentrate based diets early in the finishing process results in increased performance and carcass quality, along with deposition of intramuscular adipose tissue.

Key Words: grain, pasture, meat quality

0887 Effects of post-weaning exposure to a high-concentrate diet vs. pasture on carcass ultrasound, plasma insulin and glucose, and gene expression of lipogenic enzymes of early harvested steers.

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Twenty Angus steers (261 ± 21.5 kg) were used to evaluate the effect of post-weaning feeding strategy on plasma insulin and glucose levels and gene expression of lipogenic genes. Steers were randomly assigned to one of two feeding treatments: high-concentrate based diet (cracked corn, corn silage, and soybean meal [F]) or high-quality pasture (winter annuals, alfalfa, and non-toxic fescue [P]) for 127 d. Blood samples were collected at 21-d intervals. At slaughter, s.c. adipose tissue samples were collected from each steer and flash frozen in optimal cutting temperature compound for later histology. Steers consuming a high-concentrate based diet had a greater overall ADG (1.36 vs. 0.68 kg/d for F and P, respectively; P < 0.0001) resulting in heavier final BW and HCW (P < 0.001). There was an interaction of treatment and time for ultrasound ribeye area (REA) and 12th-rib fat thickness (P < 0.014) as F resulted in increased REA and fat deposition over time whereas P did not differ over time. Similarly, there was a treatment by time interaction for plasma insulin with insulin levels of steers consuming a high-concentrate based diet increasing over time while steers grazing forages did not. There was no interaction of treatment and time on glucose (P

= 0.469) whereas steers on F had greater plasma glucose than those on P ($P < 0.0001$). RefFinder was used to evaluate reference gene candidates. Thy1 was selected as the most stable reference gene. There was no difference in the expression of acetyl CoA carboxylase, elongase-6, leptin, or glucose transporter type 4 ($P > 0.14$). Fatty acid synthase and stearoyl CoA desaturase-9 were upregulated by 16- and 81-fold, respectively for steers on F when compared to P ($P < 0.002$). Additionally, steers receiving a high-concentrate based diet had a 42-fold increase in mRNA of elongase-5 compared to steers grazing high-quality forages ($P = 0.0006$) and threefold more expression of lipoprotein lipase ($P = 0.011$). Early exposure of steers post-weaning to high concentrate diets increased the ratio of insulin to glucose and marbling deposition with greater expression of lipogenic genes.

Key Words: gene expression, insulin, glucose

0888 Effects of dietary coated cysteamine hydrochloride on meat quality in finishing pigs. H. Liu[*1], M. Bai[1,2], K. Xu[1], B. Zou[3], R. Yu[3], Q. Xi[2], and Y. Yin[1,2], *[1]Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China, [2]College of Animal Science, South China Agricultural University, Guangzhou, China, [3]King Techina Group, Hangzhou, China*.

Cysteamine is used as a feed supplement in animal production to promote growth rate and improve feed efficiency. Coated cysteamine hydrochloride (CC) target releases cysteamine in small intestine and protects gastrointestinal mucosa from oxidative damage. However, little information is known regarding the effects of CC supplementation in carcass characteristics and meat quality. The aim of present study was to investigate potential effects of cysteamine supplementation on growth performance, carcass characteristics, and meat quality in finishing pigs. A total of 144 crossbred finishing pigs (87.60 ± 0.20 kg) were assigned randomly to one of the two dietary groups, with eight pens/group (nine pigs/pen). Pigs were fed with a basal diet containing 0 (control) and 70 mg/kg CC for 29 d. The CC was supplied by King Techina Group (Hangzhou, China), containing 27% cysteamine hydrochloride. One pig from each pen was selected randomly to be killed by exsanguination after electrical stunning. A longissimus dorsi sample was collected and stored at 4°C for meat quality measurement. Muscle pH was determined by the electrometric method using a Testo 205 thermometer (Testo, Germany) at 1 h, 24 h and 48 h postmortem Meanwhile, meat color (L* = lightness, a* = redness, b* = yellowness) was measured by a chromameter at 24 h and 48 h after slaughter. The meat tenderness of the longissimus dorsi was measured with a tenderometer, and longissimus dorsi heme pigment estimation (myoglobin, oxygen-myoglobin, and metmyoglobin) was conducted based on Krzywick's method (1982). MDA was determined by commercial reagents (Nanjing Jiancheng Bioengineering Institute, Nanjing, China) according to the manufacturer's instructions. We find that dietary CC has tended to increase average daily gain and decrease feed conversion rate ($0.05 < P < 0.1$). Compared with the control diet, supplementation of CC increased carcass weight, lean rate, and eye muscle area of finishing pigs by 8.9%, 15.9%, and 11.9%, respectively. Dietary CC increased the tenderness of the longissimus dorsi significantly ($P < 0.05$). There were no significant differences in the meat color lightness and yellowness, content of oxygen-myoglobin, metmyoglobin, and MDA between groups. But the redness of meat color and the relative contents of myoglobin increased with CC supplementation ($P < 0.05$). Collectively, 70 mg/kg coated cysteamine hydrochloride diet shows a positive effect on growth performance, tenderness, and meat quality in finishing pigs; in particular, coated cysteamine hydrochloride improves the meat color by regulating the content of myoglobin in the longissimus dorsi.

Key Words: cysteamine, finishing pigs, meat quality

0889 Meat quality of lambs fed diets containing different levels of residual frying oil. M. Capelari[*1], E. L. T. Peixoto[2], E. S. Moura[3], E. L. A. Ribeiro[3], and I. Y. Mizubuti[3], *[1]Michigan State University, East Lansing, [2]Universidade Federal do Sul e Sudeste do Pará, Maraba, Brazil, [3]Universidade Estadual de Londrina, Londrina, Brazil*.

The objective of this study was to evaluate the effect of feeding different levels of residual frying oil (RFO) on meat quality traits of confined lambs. Forty growing male lambs (21.0 ± 3.4 kg initial BW) were randomly allocated to 5 pens, each representing an experimental treatments (0, 20, 40, 60, and 80 g of RFO/kg of diet DM; 8 replications per treatment) in a completely randomized block design. Animals were fed ad libitum, twice daily, a 60:40 forage-to-concentrate basal diet consisting of sorghum silage, ground corn, soybean meal, and mineral and vitamin premix and formulated to be isonitrogenous and isocaloric among treatments. After 70 d, animals reached average BW of 35 kg and were transported to a slaughterhouse. Total *Longissimus dorsi* samples were taken from all animals, subdivided into 6 equal parts and transported to the meat science laboratory of Universidade Estadual de Londrina, where they were submitted to analysis of shear force, coloration and pH, marbling, water loss by pressure, sensory analysis, and lipid oxidation. Data was tested for normal distribution and submitted to analysis of variance and regression analysis with 5% significance level. There was a linear effect of RFO inclusion on shear force (2.72 vs. 3.84 kgf for 0 and 80 g RFO/kg DM, respectively; $P < 0.01$). However, even with the increase effect on shear force with higher inclusions of RFO, in the sensory test, samples were classified as high tenderness. Lipid oxidation, color parameters and pH, chemical composition, and

sensory attributes did not differ among levels of RFO inclusion in the diet. The inclusion of RFO in lamb diets up to 80 g/Kg DM did not affect meat quality.

Key Words: shear force, *Longissimus dorsi*, lipid oxidation

0890 Sensory properties of meat of Nellore cattle fed different levels of lipid-based diets.

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Use of agroindustrial by-products in the feed of animals should be analyzed for better understanding of their impacts on cattle meat quality. The objective of this study was to determine the effect of the dietary inclusion of lipid-based diets on the sensory properties. The study was performed on a farm in Aguaí, SP, Brazil. A group of 39 uncastrated Nellore cattle was enclosed in individual pens. The animals were 36 mo old, and the initial mean live weight was 494.1 ± 10.1 kg. Animals were randomly assigned to one of three treatments, based on dry matter: feed with control diet 2.50% cottonseed (CD), feed with 11.50% cottonseed (CS), and feed with 3.13% cottonseed added of 1.77% protected lipid (PL). After 63 d mean final live weight was 577.01 ± 11.34 kg. Then, part of the *M. longissimus thoracis* of each animal was removed between the 12th and 13th rib of the left half carcass. The samples steaks were 2.5 cm thick and were stored frozen in a freezer at −18°C. Sensory analysis was performed after samples were thawed in the refrigerator (± 20 h at 2.5 ± 0.5°C) and heated on automatic superposed grills. At an internal temperature of 71°C, the steak was removed from the grill and heated in a microwave oven for 30 s until the temperature reached 50°C. Immediately after, they were randomly distributed to the panelists in sterile Petri dishes codified with four-digit numbers. Sensory evaluations were conducted using 11 trained panelists. Sensory tests used a 9-point scale: aroma intensity (ranging from absent to extremely intense), strange aroma (ranging from absent, 1, to extremely strong, 9), flavor (ranging from extremely bad to extremely good), strange flavor (ranging from absent, 1, to extremely intense, 9), tenderness (ranging from extremely tender, 1, to extremely hard, 9), juiciness (ranging from extremely dry, 1, to extremely juicy, 9), color (ranging from bright cherry red to dark red), and overall appearance (ranging from very bad to very good). The intensity of the aroma (mean 5.66), strange aroma (mean 2.27), flavor (mean 6.09), strange flavor (mean 1.85), juiciness (mean 5.36), color (mean 5.60), and overall appearance (mean 6.48) were similar between treatments, except for tenderness ($P <$ 0.05) while for CD and CS mean 5.16 versus 6.36 for PL. The addition of PL in the diets of finishing cattle led to less tender meat. Acknowledgments for financial support in Brazil: IFGOIANO, FAPEG, and CNPq.

Key Words: beef quality, protected fat, whole cottonseed

0891 Genome-wide efficient mixed-model study for meat quality in Nellore cattle.

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The quality of meat, which includes several traits such as tenderness, juiciness, and fat thickness, is essential for the beef industry. Previous genome-wide association studies (GWAS) using Bayesian methods have shown that Brazilian Nellore cattle have enough genetic variation for improvement of these traits. Thus, the aim of this study was to further identify quantitative trait loci (QTL) associated with meat-quality-related traits in Nellore beef cattle by using the univariate linear mixed model (LMM) approach implemented in the GEMMA software and compare it with our previous GWA studies performed using Bayesian approaches. A total of 387 Nelore steers comprising 34 half-sib families were genotyped using the IlluminaBovineHDBeadChip. We analyzed the association between markers and Warner-Bratzler shear force, backfat thickness, ribeye muscle area, scanning parameters lightness (L*), redness (a*), and yellowness (b*) to ascertain color characteristics of the meat, water-holding capacity, cooking loss, muscle pH, myofibrillar fragmentation index, saturated fat sum, omega-6 fatty acids sum, omega-3 fatty acids sum, and ethereal extract. These phenotypes were measured in the Longissimus dorsi muscle between the 11th and 13th ribs collected at slaughter. We identified fifty-three genomic regions that each contained at least one single nucleotide polymorphism (SNP) that showed a significant association with meat quality traits (1-Mb SNP windows). Highlighted, we found regions associated with three genes—neuronal growth regulator 1 (NEGR1, chr03: 70884613–71949611), dynamin 3, and phosphatidylinositol glycan anchor biosynthesis class C (DNM3/PIGC, chr16: 37340706–38007593)—related to lipid metabolism and obesity. Our results provide a better understanding of QTL regions associated with meat quality unexplored in our previous Bayesian approach.

Key Words: GWAS, Nellore, meat quality

0892 Comparison of carcass and sensory traits and contents of fatty acids and volatile compounds in Longissimus dorsi of three cattle breeds.

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This study was performed to compare carcass and sensory traits, physicochemical composition, fatty acid (FA) contents, and volatile compounds in Longissimus dorsi (LD) of Korean cattle, Holstein, and American Angus. A total of 36 steer LD samples were obtained from Korean cattle (n = 12), Holstein (n = 12), and American Angus (n = 12) with quality grade (QG) 1+, QG 2, and Choice grade, respectively. Korean cattle had the highest ($P < 0.05$) contents of intramuscular fat and reducing sugar but the lowest ($P < 0.05$) shear force values. Korean cattle revealed the highest ($P < 0.05$) sensory traits (flavor, tenderness, juiciness, and overall acceptance), and these traits were positively correlated with fat ($0.95 \leq r \leq 0.99$; $P < 0.001$) and reducing sugar contents ($0.55 \leq r \leq 0.63$; $P < 0.001$). Korean cattle had the highest ($P < 0.05$) contents (g/100 g LD) of most of the FAs, including palmitic acid, stearic acid, oleic acid, saturated fatty acids, monounsaturated fatty acids, and unsaturated fatty acids, and these FA contents were positively correlated ($0.65 \leq r \leq 0.78$; $P < 0.001$) with all sensory traits. Korean cattle had the highest ($P < 0.05$) concentrations of several volatile compounds, including acetaldehyde, 2-methyl butanal, 3-methyl butanal, 2,3-butanedione, and 3-hydroxy-2-butanone, and these compounds were positively correlated ($0.56 \leq r \leq 0.81$; $P < 0.001$) with all sensory traits, whereas Angus had the highest ($P < 0.05$) concentrations of pentanal, hexanal, and n-pentane. In conclusion, the LD contents of fat, reducing sugar, and FAs, the concentrations of LD volatile compounds, and sensory traits varied among breeds of cattle. Sensory traits had positive correlations with contents of fat, reducing sugars, and most of the FAs, and these showed positive or negative correlations with several volatile compounds.

Key Words: cattle breed, reducing sugar, volatile compound

0893 Label-free MS^E proteomic analysis of the bovine skeletal muscle: New approach for meat tenderness evaluation.

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Meat tenderness is an important trait for beef consumer satisfaction and presents a large individual variation among animals. Meat from Nellore cattle is less tender, resulting in lower economic value. Although many biochemical factors associated with meat tenderness have been studied, the alterations in the muscle proteome profile that reflect the biological complexity of the tenderness process remain unclear. The aim of this study was to investigate pathways and biological mechanisms associated with meat tenderness in one Nellore steer population using label-free proteomic approach by high definition mass spectrometry with HDMS^E acquisition. We evaluated differential protein expression in the *Longissimus dorsi* muscle, collected at 20 min. postmortem, from 10 animals with lower and 10 with higher values of shear force at the seventh day postmortem. The proteome analysis was performed using the nanoACQUITY UPLC Synapt HDMS G2-S system (Waters, Manchester, UK), and the data were processed using Waters Progenesis QI for proteomics software. A Nellore transcriptome database build from RNaseq data from the *Longissimus dorsi* muscle was used to identify the proteins. A total of 5016 proteins were identified, of which 3311 were quantified and 1816 were present in at least 8 out of 10 biological replicates. Among these, 125 proteins were differentially expressed (DE, $P < 0.05$), 66 proteins presented as downregulated, and 59 as upregulated in the group of animals with lower values of shear force. Functional annotation analysis of the list of DE proteins using DAVID identified two pathways (KEGG): pyruvate metabolism and viral myocarditis; catabolic processes, such as glucose, hexose, carbohydrate, and monosaccharide; and molecular functions, such as actin binding, cytoskeletal protein binding, and calcium ion binding. These results provide a comprehensive protein profile of the skeletal muscle and indicate that changes in energy metabolism and cytoskeletal structure of muscle could influence meat tenderness.

Key Words: beef cattle, mass spectrometry, proteome

0894 Carcass grading effects on the fatty acid and amino acid composition of pork loin from Duroc pigs. J. Álvarez-Rodriguez[1], R. Ros-Freixedes[1], S. Gol[1], E. Henríquez-Rodríguez[1], R. N. Pena[1], L. Bosch[2], J. Estany[1], F. Vilaró[3], and M. Tor*[1], *[1]University of Lleida, Agrotecnio Center, Lleida, Spain, [2]Universitat de Girona, Girona, Spain, [3]University of Lleida, Lleida, Spain.*

Eighty purebred Duroc pigs slaughtered at 210 d of age were used to evaluate the effect of carcass grading according to lean content (R, 45–50%, n = 18; O, 40–45%, n = 28; P, < 40%, n = 34) on the fatty acid and amino acid composition of fresh pork loins. The crude protein content of loin was higher while the intramuscular fat content was lower in R carcasses than in the rest ($P < 0.05$). Carcass group had a major effect on fatty acid composition, with R carcasses showing lower MUFA and greater PUFA content than the rest of groups ($P < 0.05$) and with similar SFA content across groups ($P > 0.05$). Amino acid composition was not affected by carcass grading except for a tendency for isoleucine and glycine to have lower levels in P and R carcasses, respectively ($P < 0.1$). The balance of amino acids in the pork loin was compared with the recommended balance of indispensable amino acids for adults (WHO/FAO/UNU) by expressing the relevant amino acids relative to lysine and then calculating the proportion of the recommended amount of each amino acid that was provided by a sample containing the recommended amount of lysine. The balance of indispensable amino acids was less than ideal, with valine being the limiting amino acid by about 30–35%,

Table 0894.

Chemical composition of fresh loins (24 h post-mortem) from Duroc barrows according to carcass commercial grading

	R (45-50% lean)	O (40-45% lean)	P (<40% lean)	P-value
Dry matter, g/kg	282.7±2.7	287.2±2.2	286.5±2.0	0.40
Crude protein, g/kg	217.0±2.0a	214.3±1.6b	210.9±1.5b	0.05
Intramuscular fat, g/kg	31.8±2.5b	40.7±2.0a	43.2±1.9a	0.002
∑MUFA, g/kg fatty acids	492.0±4.0a	501.7±3.2ab	508.8±3.0b	0.006
∑SFA, g/kg fatty acids	391.4±4.5	403.2±3.6	402.1±3.4	0.10
∑PUFA, g/ kg fatty acids	116.5±3.6b	95.1±2.9a	89.1±2.7a	<0.0001
Amino acids, g/16 g N				
Lysine	8.48±0.29	8.43±0.23	8.62±0.22	0.83
Methionine	1.95±0.08	2.06±0.07	2.08±0.06	0.46
Threonine	4.68±1.00	4.80±0.08	4.85±0.07	0.45
Valine	4.96±0.11	5.09±0.09	4.94±0.08	0.45
Isoleucine	4.54±0.09	4.56±0.07	4.34±0.07	0.09
Leucine	9.29±0.13	9.42±0.11	9.20±0.10	0.34
Histidine	5.16±0.17	5.16±0.14	5.15±0.13	0.99
Phenylalanine	3.82±0.04	3.89±0.04	3.83±0.03	0.39
∑EAA	42.9±0.7	43.4±0.6	43.0±0.5	0.80
Cistine	0.97±0.04	0.97±0.03	0.96±0.03	0.99
Hydroxyproline	0.27±0.02	0.28±0.01	0.26±0.01	0.63
Proline	3.76±0.06	3.84±0.05	3.80±0.04	0.53
Alanine	5.21±0.10	5.27±0.08	5.14±0.08	0.52
Arginine	5.97±0.07	6.01±0.06	5.90±0.05	0.35
Aspartic acid	10.34±0.26	10.79±0.21	10.73±0.20	0.37
Glutamic acid	15.47±0.30	15.89±0.25	15.48±0.23	0.42
Glycine	3.92±0.08	4.15±0.06	4.03±0.06	0.06
Serine	4.13±0.08	4.28±0.06	4.28±0.06	0.26
Tyrosine	3.34±0.10	3.22±0.08	3.33±0.08	0.53
∑NEAA	53.4±0.6	54.7±0.5	53.9±0.5	0.27
Total	96.25±1.22	98.09±0.99	96.90±0.92	0.47

MUFA= monounsaturated fatty acids (C16:1n-7; C17:1n-7; C18:1n-9; and C20:1n-9); SFA= saturated fatty acids (C10:0; C12:0; C14:0; C16:0; C17:0; C18:0; and C20:0); PUFA=polyunsaturated fatty acids (C18:2n-6; C18:3n-3; C20:2n-6; C20:3n-6; C20:4n-6; C20:4n-6 and C22:6n-3). EAA= essential amino acids (Lysine, Methionine, Threonine, Isoleucine, Valine, Phenylalanine, Leucine and Histidine); NEAA= non-essential amino acids (Cistine, Arginine, Hydroxyproline, Tyrosine, Alanine, Glycine, Glutamic acid, Serine, Proline, and Aspartic acid). Within each row, different letter denotes statistical differences among carcass grading categories (P<0.05).

indicating that consumption of 144–151 g of pork loin would be needed to match 100 g of a sample with the recommended balance of the indispensable amino acids. The amount of Duroc pork meat that would need to be consumed to get a satisfactory balance of amino acids was highest in the P (< 40% lean) carcass grade group. In conclusion, in the Duroc swine breed, carcass adiposity modifies the fatty acid profile of meat but hardly affects the amino acid balance of raw loin.

Key Words: swine, intramuscular fat, amino acid.

0895 The longissimus thoracis muscle proteome in Alentejana bulls as affected by growth pattern.

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Beef production is an important economic activity worldwide. In southern Europe there are two major types of beef production systems based on the growth pattern the animals are subjected to: continuous versus discontinuous growth (CG vs. DG). The first can be characterized as more intensive with the animals being finished on concentrate and imported feedstuffs, while the second? The objective of this work is to conduct a comparison between the protein expression profiles of the longissimus thoracis (LT) muscle in CG and DG animals using label-free quantitative proteomics. Forty purebred *Alentejana* male calves (9 mo old, 239 kg live weight) were randomly allocated to two distinct feeding regimens: CG and DG. CG animals were fed ad libitum on concentrates plus grass hay throughout the trial and slaughtered at 18 mo of age. DG animals were only fed ad libitum on hay from 9 to 15 mo of age and then fed the same diet provided to the CG group (concentrates plus hay) until 24 mo of age. Animals were slaughtered and the LT muscle sampled. Samples (100 μg) were added to 500 μL of ammonium bicarbonate 50 mM, urea 8M, thiourea 2M buffer and homogenized and centrifuged and the supernatant recovered. Proteins were trypsin digested (FASP protocol) and desalted, and peptides were loaded onto reverse-phase C18 columns and analyzed on an LTQ-Orbitrap Velos mass spectrometer. Protein identification and label-free quantification were performed using Mascot (Matrixscience) and Progenesis (Nonlinear Dynamics). The study identified a total of 531 different proteins in the bovine LT muscle, with 26 showing differential expression, of which 25 were overexpressed in the CG group. Several of these proteins (e.g., myozenin-2, myosin regulatory light chain 2, glyoclythic pathway enzymes, and 14-3-3 protein zeta/delta) could be proposed as markers of a more intensive growth pattern that slaughters cattle at a younger age. The myosin binding protein H was the only protein having the higher expression in the DG group, suggesting that this protein may be putatively used as a marker of quality associated to discontinuous growth.

Key Words: growth pattern, longissimus thoracis muscle, proteome

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0896 Ferulic acid in diets of heifers and its effect on the oxidative stability of meat stored in refrigeration.

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Ferulic acid (FA) is a naturally occurring compound with important antioxidant activity. Therefore, it could be an interesting alternative to improve the shelf life of meat. The aim of this study was evaluate the oxidative stability in meat from commercial heifers supplemented with 5 or 10 ppm of FA by 30 d. Two hundred seventy heifers (480 ± 10 kg) in the finishing phase were fed with a basal diet (20:80 forage : concentrate ratio). Treatments were Control (without additive), 5 ppm of ferulic acid (FA5), and 10 ppm of FA (FA10) per kg of body weight, assigned randomized to 90 animals per treatment by 30 d. Finishing the feeding phase, animals were slaughtered and a section of the *Longissimus thoracis* muscle (LT) was collected between 4th and 12th rib (n = 9 per treatment). The LT muscle was sliced (1-inch thickness) for oxidative stability analysis for 0, 7, 10, and 14 d of storage. Objective color variables and pH were evaluated with a Minolta colormeter and Hanna pH meter, respectively; thiobarbituric acid-reactive substances (TBARS) and metmyoglobin were evaluated by spectrophotometry. A descriptive sensory test was done according to the guidelines of AMSA, and attributes, such as loss of fresh flavor, loss of fresh odor in cooked meat, and color and discoloration in raw meat, were evaluated. All data were analyzed by GLM-ANOVA with a 3 × 4 factorial arrangement considering as fixed effects the treatments and storage time using the statistical package NCSS 2007. There were no effects of FA supplementation or interaction to a*, b*, hue angle, and pH ($P > 0.05$), where the values were normal for fresh beef. L* values were higher in FA5 (40.48) and FA10 (41.03) compared with Control (38.91) ($P < 0.05$). On overall storage time, FA10 caused an increase in lipid oxidation of beef (TBARS values) compared with Control and FA5 ($P < 0.05$); while metmyoglobin values were lower in FA10 than FA5 and Control ($P < 0.05$). No differences were detected between treatments for sensory attributes ($P > 0.05$), which were qualified with high values. Results indicated that the doses of FA used in finished diets for heifers had no antioxidant effect.

Key Words: ferulic acid, shelf life, meat oxidation

0897 Label-free quantification of myosin isoforms in porcine skeletal muscles. J. Y. Jeong*[1], H. S. Yang[2], J. K. Seo[2], H. W. Yum[2], and G. D. Kim[1,3], [1]*Institute of Agriculture & Life Science, Gyeongsang National University, Jinju, The Republic of Korea,* [2]*Division of Applied Life Science (BK21 plus), Gyeongsang National University, Jinju, The Republic of Korea,* [3]*Department of Animal Sciences, University of Illinois Urbana-Champaign, Urbana*.

Myosin isoform (myosin heavy chain, MHC) in skeletal muscles has been usually qualified and quantified by electrophoresis, immunoblotting, and immunohistochemistry. However, it was difficult to clearly analyze myosin isoforms due to high homology among myosin isoforms. In the present study, label-free quantification (LFQ) was studied to both identify and quantify porcine myosin isoforms. *Longissimus thoracis* (LT), *psoas major* (PM), and *semimembranosus* (SM) muscles were taken from three pigs (180 ± 1 days old, female, 109.2 ± 2.4 kg slaughter weight) at 24 h postmortem in a slaughter house. Myofibrillar protein, which was isolated with rigor buffer (75 mM KCl, 10 mM K_2HPO_4, 2 mM $MgCl_2$, 2 mM EGTA, pH 7.0), was loaded onto sodium dodecyl sulfate-polyacrylamide gel electrophoresis. MHC bands were cut and in-gel digested with trypsin. Spectra were obtained by analysis of liquid chromatography (LC)-mass spectrometry (MS). LFQ was performed using MaxQuant software (ver. 1.5.3.30, Max-Planck Ins., Germany). Four myosin isoforms—myosin-1 (MHC 2x), myosin-2 (MHC 2a), myosin-4 (MHC 2b), and mysoin-7 (MHC I/slow)—were identified, and their matched peptides were 193.3, 154.7, 201.2, and 77.1, respectively. Unique peptides among the matched peptides were selected for quantification of each myosin isoform. The spectral count and summed MS intensity of selected peptide were evaluated. Similar patterns were found in the relative spectral count and relative peak intensity regardless of muscle types. LT and SM muscles had a higher composition of myosin-4 than PM muscle ($P < 0.05$), whereas myosin-7 was higher in PM than the others ($P < 0.05$). Myosin-1 and myosin-2 were relatively lower than myosin-4 and myosin-7 ($P < 0.05$). These LFQ results showed a similar trend to previous reports, which observed the composition of myosin isoforms or myosin heavy chain-based fiber compositions in porcine skeletal muscles. Therefore, LFQ can be a useful approach to overcome the problem of myosin quantification caused by high homology among their isoforms.

Key Words: label-free quantification, myosin, pig

0898 Identification of novel genes and mechanisms involved in bovine myogenic differentiation. H. Jiang*[1], R. Settlage[2], X. Leng[1], and Y. Hou[1], [1]*Department of Animal and Poultry Sciences, Virginia Tech, Blacksburg,* [2]*Biocomplexity Institute, Virginia Tech, Blacksburg*.

Myogenic differentiation, whereby the mononuclear myoblasts differentiate into the multinucleate myotubes, is a critical step in the formation of skeletal muscle. The objective of this study was to identify genes and pathways that regulate myogenic differentiation in cattle. Satellite cells, the myogenic progenitor cells in adult skeletal muscle, were isolated from 4 Angus crossbred steers (experimental unit). The isolated satellite cells were first propagated as myoblasts in growth medium containing 10% fetal bovine serum and then induced to differentiate into myotubes in differentiation medium containing 2% horse serum. Transcriptomes in myoblasts immediately before and 48 h after induction of myogenic differentiation were analyzed by RNA sequencing (RNA-seq). The RNA-seq analysis identified a total of 5538 transcripts that were differentially expressed (counts > 20; the false discovery rate-adjusted $P < 0.05$) between the two conditions. Of these transcripts, 2937 were upregulated and 2601 downregulated in differentiated myoblasts compared to undifferentiated myoblasts. Expression patterns for 20 of these genes were verified by reverse transcription-quantitative PCR. The list of genes upregulated in differentiated myoblasts included myogenin and myogenic factor 6, which are known to stimulate myogenic differentiation, and sex determining region Y-box 6 (SOX6) and growth hormone releasing hormone (GHRH), whose roles in myogenic differentiation are unknown. The list of genes downregulated in differentiated myoblasts included myostatin and myogenic differentiation family inhibitor (MDFI), which are known inhibitors of myogenic differentiation, and ZNF469 and SOX9, which are not known to be involved in myogenic differentiation. Functional annotation clustering analysis (DAVID 6.7) of 1107 transcripts upregulated $\geq$ twofold in differentiated myoblasts revealed enrichment (false discovery rate < 0.05) in contractile fiber, sarcoplasmic reticulum, calcium signaling, muscle contraction, cell adhesion, and steroid biosynthesis. Functional annotation clustering analysis of 817 transcripts downregulated $\geq$ twofold in differentiated myoblasts revealed enrichment (false discovery rate < 0.05) in cell cycle, microtubule cytoskeleton, growth factor binding, and ATP binding. Overall, this study not only confirms known factors and pathways that control myogenic differentiation but also suggest novel genes and mechanisms that may contribute to myogenic differentiation in cattle.

Key Words: cattle, muscle, myogenic differentiation

0899 Omega-3 and omega-7 oil supplementation on tissue fatty acid accumulation. S. K. Duckett*, I. F. Furusho-Garcia, M. F. Miller Jr., B. M. Koch, and G. Volpi Lagreca, *Clemson University, Clemson, SC*.

Eighteen Southdown ewe lambs (42 + 5.6 kg BW) were used to assess the effects of n-3 and n-7 oil supplementation on tissue accumulation of these fatty acids. Lambs were blocked by weight and randomly assigned to one of three treatments: 1) control (CON), no oil supplement, 2) flaxseed oil (FLAX; 56% C18:3 n-3) supplementation at 0.1% of BW, or 3) Provinal® oil (PO; 56% C16:1 n-7) supplementation at 0.1% of BW. All lambs were fed ad libitum the same basal diet consisting of 75% soybean hull pellets and 15% alfalfa pellets. Lambs were fed the treatment diets for 60 d individually. Overall average daily gain was reduced by PO compared to FLAX ($P < 0.05$). Hot carcass weights were also reduced by 12% for PO vs. FLAX ($P < 0.05$). Lambs in the PO treatment had a lower ($P < 0.01$) dressing percentage than CON or FLAX. Total lipid content of the LM was highest ($P < 0.05$) for FLAX and lowest ($P < 0.05$) for PO. Supplementation with PO increased palmitoleic (C16:1 n-7), cis-11 vaccenic (C18:1 cis-11), eicosapentaenoic (C20:5; EPA, n-3), and docosahexaenoic (C22:6; DHA, n-3) acids compared to CON or FLAX ($P < 0.01$). Supplementation of FLAX increased linolenic (C18:3 n-3) acid compared to CON or PO ($P < 0.1$). These changes in individual fatty acid concentrations with oil supplementation resulted in increased ($P < 0.01$) omega-3 fatty acid concentrations (+69%) and a lower (*P*..?) ratio of n-6 to n-3 compared to CON (3.13 for FLAX and PO vs. 5.02 for CON). In conclusion, supplementation with PO increased palmitoleic acid (+95%), cis-11 vaccenic acid (+77%; a known elongation product of palmitoleic acid), EPA (+104%), and DHA (+150%) compared to CON or FLAX. Flaxseed oil supplementation increased linolenic acid (+113%) but did not further convert this n-3 fatty acid into EPA, DPA, or DHA.

Key Words: lamb, n-7 fatty acids, n-3 fatty acids, oil supplementation

0900 Supplementation of glycerol or fructose via drinking water of pasture-fed lambs. G. Volpi Lagreca, I. F. Furusho-Garcia, B. M. Koch, M. F. Miller Jr., and S. K. Duckett*, *Clemson University, Clemson, SC*.

Eighteen wether lambs (40.1 ± 7.4 kg BW, 4.9 mo.) were used to assess the impact of glycerol or fructose supplementation via drinking water on animal performance and tissue glycogen content. Lambs were blocked by BW and allocated to alfalfa paddocks (2 hd/paddock, 3 paddocks/treatment). Each paddock within block was assigned randomly to drinking water treatments for 30 d: 1) control (CON), 2) 120 g fructose/L (FRU), or 3) 120 g glycerol/L (GLY). Lambs grazed alfalfa for 28 d and then were fasted in pens for 2 d before slaughter with access to water treatments only. Glycogen content was measured in the *Longissimus* muscle (LM) and *Semitendinosus* muscle (ST) at 30 min, 1, 2, 3, 4, 5, 6, 12, and 24 h postmortem. Data were analyzed using PROC MIXED of SAS. Daily water intake (3.5 L/animal/day) did not differ between treatments ($P > 0.05$). During the 28-d grazing period, ADG was greater ($P < 0.05$) for GLY (0.200 kg/an/d) compared to CON (0.116 kg/an/d) or FRU (0.078 kg/an/d). During the 2-d fasting period, BW shrink was lower ($P < 0.05$) for GLY (−0.392 kg/an/d) compared to CON (−1.680 kg/an/d) or FRU (−1.340 kg/an/d). HCW was greater ($P < 0.05$) for GLY compared to FRU (22.7 vs. 17.6 kg) and tended to be greater ($P = 0.06$) for GLY compared to CON. There was a treatment x time interaction ($P = 0.003$) in the LM; glycogen content was greater ($P < 0.05$) for GLY at 2 and 3 h and for FRU at 1 h compared to CON. Glycogen content in ST did not differ between treatments ($P > 0.05$). Liver glycogen content at 30 min postmortem was greater ($P < 0.01$) for GLY (5.61%) compared to FRU (1.45%) or CON (0.32%). Liver free glucose was greater for GLY, intermediate for FRU, and lower for CON ($P < 0.01$). Overall, GLY supplementation increased ADG during grazing period, reduced BW shrink during fasting, increased HCW, and increased glycogen in liver and muscle, and free glucose content in liver.

Key Words: lamb, liver, glycerol, fructose, glycogen

0901 Comparison of meat quality and fatty acid composition of grain-fed calves to grass-fed steers as an alternative beef production system in Chilean Patagonia. F. Sales*[1], R. Morales[2], R. Lira[1], L. Bravo[3], and Q. Sciascia[4], *[1]Instituto de Investigaciones Agropecuarias, Punta Arenas, Chile, [2]Instituto de Investigaciones Agropecuarias, Osorno, Chile, [3]Universidad del País Vasco, Bizkaia, Spain, [4]Leibniz Institute, Dummerstorf, Germany.*

Steers finishing in Chilean Patagonia are based on grazing lands with low nutritive value, which may lengthen the fattening phase of steers, so grain-fed calves appear as an option to reduce the farming period. However, the effect of grain inclusion in the diet on meat quality or fatty acid composition under those conditions is not clear. The aim of this study was to compare the effects on meat quality and the fatty acid profile of beef from grass-fed steers or grain-fed calves in Patagonia. Forty Angus cross steers were raised on pasture (2.0 Mcal/kg DM ME, and 11% CP) and slaughtered at 18–20 mo of age (448 ± 31.7 kg BW). On the other hand, ten calves were weaned at 9 mo of age (303 ± 8.0 kg BW) and started receiving 2.5 kg corn (3.4 Mcal EM, 8.5% CP) and 1.0 kg Cosetán® (2.95 Mcal EM, 15% CP) daily during 47 d. Meanwhile they were maintained on pasture (2.0 Mcal/kg DM ME, and 5% CP) until they reached slaughter weight (316 ± 13.9 kg BW). Animals were slaughtered the same day,

Table 0901.

Table 1. Meat quality analysis obtained from *longissimus lumborum* (lean muscle) of steers and calves that were slaughtered in Chilean Patagonia.

	STEER	CALVES	*P*-value
Body Weight in ranch (kg)	440 ± 33.0	316 ± 13.8	0.000
Slaughter Body Weight (kg)	417 ± 30.7	326 ± 13.9	0.000
Intramuscular fat (%)	7.95 ± 2.61	4.56 ± 1.18	0.000
Shear force (kgf)	2.22 ± 0.251	1.97 ± 0.298	0.030
Meat Color			
*L**	39.6 ± 1.76	42.4 ± 1.64	0.000
*a**	25.5 ± 1.83	23.2 ± 1.39	0.000
*b**	12.7 ± 1.17	12.7 ± 0.679	0.954
Fat color			
*L**	67.0 ± 1.86	65.9 ± 1.49	0.061
*a**	13.2 ± 2.03	12.9 ± 1.54	0.649
*b**	17.2 ± 1.47	14.1 ± 0.824	0.000
Fatty acid composition			
SFA (%)	47.6 ± 2.45	45.8 ± 3.22	0.120
MUFA (%)	39.0 ± 2.09	34.3 ± 1.79	0.000
PUFA (%)	7.60 ± 2.27	11.9 ± 2.91	0.001
P/S	0.162 ± 0. 0577	0.265 ± 0.0896	0.005
n-6	4.80 ± 1.36	7.88 ± 2.10	0.001
n-3	2.80 ± 0.927	3.99 ± 0.839	0.001
n-6/n-3	1.74 ± 0.155	1.96 ± 0.19	0.005
Rumenic acid (%)	0.268 ± 0.0407	0.425 ± 0.0526	0.000

SFA, saturated fatty acid; MUFA, monounsatured fatty acid; PUFA, polyunsatured fatty acid; P/S, PUFA/SFA; n-6/n-3, ratio between n-6 and n-3 PUFA.
Rumenic acid (9*c*,11*t*-18:2), principal conjugated linoleic acid.
P-value indicate significantly differences when $P \leq 0.05$.

and *Longissimus lumborum* muscle was obtained to perform meat quality and fatty acid profile analyses. A T-student was used to compare the two finishing methods (calves/grain vs. steers/pasture). As was expected, calves show lighter hot carcass weight than steers (173.9 ± 7.2 vs. 223.7 ± 17.5 kg, $P \leq 0.001$). Regarding meat quality characteristics, the color of calves' muscle was lighter (with higher *L** and lower *a** values, $P \leq 0.001$) and more tender ($P \leq 0.05$) than meat from steers. Calves' meat had lower intramuscular fat content (4.56 ± 1.18 vs. 7.95 ± 2.61%, $P \leq 0.001$), possibly because they were slaughtered younger than steers. In general, the fatty acid composition of steers' and calves' meat show healthy profiles, although calves' meat was healthier because of its higher content of polyunsaturated fatty acid, (PUFA, 11.9 ± 2.91 vs. 7.60 ± 2.27%, $P \leq 0.01$) and rumenic acid (0.425 ± 0.053 vs. 0.268 ± 0.041%, $P \leq 0.01$). However, calves' meat has a lower content of monounsatured fatty acids (MUFAs, 34.3 ± 1.79 vs. 39.0 ± 2.09%, $P \leq 0.001$) and higher n-6/n-3 ratio (1.96 ± 0.19 vs. 1.74 ± 0.155%, $P \leq 0.01$) than steers' meat. Results suggest that Patagonian beef meat has interesting quality characteristics and differs depending on the finishing methods and the slaughter age. Intramuscular fat content and fatty acid profile gave calves' meat (with an extra energy intake by grain) a higher nutritional and healthy quality compared to steers produced on pasture, which could be demanded by consumers.

Key Words: meat quality, calves' meat, beef

0902 Influence of tannins extract supplementation on lipid oxidation of beef kept in refrigerated storage.

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Steak samples of longissimus dorsi obtained from sixteen fattened bullocks (*Bos taurus* × *Bos indicus*) with 505 ± 22.23 kg final weight were used to evaluate the effect of tannin extract fed-supplementation on lipid oxidation of beef kept in refrigerated storage. Treatments were: 1) diet with 13.3% CP and 2.0 Mcal NE_m/kg DM (CTRL) and 2) CTRL plus 0.3% (DM basis) of tannin extract (TE). The tannin extract was offered from Bypro (Indunor S.A., Buenos Aires, Argentina), which contains 70% tannins. Treatments were fed during 70 d before harvesting. Bullocks were harvested in a processing plant, and after 24 h chilling at 4°C, a cross cut was performed in the longissimus dorsi of carcass left side, between 12th and 13th ribs. Beef samples were kept frozen (−20°C) until used for lipid oxidation analyses. Lipid oxidation was estimated as thiobarbituric acid-reactive substances (TBARS) and was determined at 0, 3, 6, 9, and 12 display d at 4°C. Because TBARS data were not normal ($P < 0.05$), before analyses, they were

transformed to $\log_{10}$ (n * 1000) to be normalized ($P = 0.68$). The results were analyzed by ANOVA for a completely randomized design, with a 2 × 5 factorial arrangement (two levels of factor TE: 0 and 0.3% diet DM; and five levels of factor d: 0, 3, 6, 9, and 12). The steak sample from each bullock was the experimental unit. A tendency ($P = 0.10$) for interaction TE × d was observed, where meat lipid oxidation from d 0 to d 9 was similar ($P > 0.10$) between treatments; but at display d 12, beef from TE supplemented bullocks exhibited a lower ($P < 0.05$) TBARS value than CTRL (0.04 vs. 0.11 mgMDA/kg meat^{-1} wet basis). The results suggest that supplementation of a 0.3% tannin extract to feedlot cattle may help to increase shelf life of beef by decreasing lipid oxidation.

Key Words: bovines, meat lipid oxidation, tannin

0903 Differentially expressed genes in genetically divergent Nellore steers for calcium content in the Longissimus dorsi muscle.

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Calcium is an important mineral for mammals, because it is involved in muscle contraction and neuro impulse transmission and controls the flow of substances in the cellular environment. Calcium is the major part of the mammal skeleton; it is found in great amount in milk and can be found in beef. In addition, the calcium content in bovine muscle can influence meat quality traits, such as meat tenderness, due to its importance for calcium-dependent proteases. Although calcium functions in the organism have been extensively studied, a lack of knowledge of the mechanisms regulating calcium content is still observed. In this study, we identified differentially expressed (DE) genes in genetically divergent Nellore steers for calcium content in the *Longissimus dorsi* (LD) muscle using an RNA-seq approach. From an initial population of 120 animals presenting genomic breeding value (GEBV) estimates for calcium content, we chose 10 animals in two groups selected for their extremely low or high GEBV. The analysis of RNA-seq samples using the Tuxedo suit pipeline revealed 43 DE genes, 32 upregulated in the group with low calcium content. A functional gene enrichment analysis performed by DAVID software indicated 10 functional clusters involved in membrane and extracellular matrix proteins, cell and tissue adhesion, skeleton, neurological system and cartilage development, calcium, carbohydrate and metal binding, and sensorial and sound perception. Gene functions, such as cell and tissue adhesion, and calcium, carbohydrate, and metal binding are related to meat tenderness due to their role in the rigor mortis process and in muscle contraction through the interaction with troponin. Among the upregulated genes in the low calcium content group, we found the collagen genes *COL11A1* and *COL11A2* involved in skeletal morphogenesis and associated with several genetic syndromes related to abnormal calcium deposits in humans. *COL11A1* is downregulated in female Quinchuan cattle, which might explain part of the higher tenderness in this sex, since there is a negative correlation between this trait and collagen. In *Bos taurus coreanae* both genes are upregulated in intramuscular fat in comparison with subcutaneous fat, along with integrins, calcium dependent proteins that are related to cellular adhesion. These are intermediate results and further experiments will allow the exploration of the genetic findings influencing muscle calcium concentration in Nellore cattle. The results will provide a more comprehensive picture of gene expression associated with calcium content in bovine muscle.

Key Words: *Bos indicus*, calcium, RNA-Seq

0904 Fatty acid profile and gene expression of lipogenic transcription factors in the muscle of Nellore bulls fed processed soybean.

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The objective was to evaluate the fatty acid profile and gene expression of *PPARA*, *PPARG*, and *SREBF1* in the muscle of Nellore bulls fed ground or extruded soybean. Sixty crossbred Nellore young bulls, with initial average weight of 320 ± 8.12 kg, were distributed in a completely randomized design. The animals were placed in 12 pens, with 3 treatments, 5 animals per pen, and 4 replications, and therefore pens were the experimental units. The bulls were fed the following diets: diet without soybean inclusion (NSB), ground soybean diet (GSB), and extruded soybean diet (ESB). These diets containing corn silage as forage (40% DM), 14% CP, and 2.4, 6.1, and 6.3% of ether extract (EE), respectively. Soybean content was 20.4% in both ground and extruded soybean diets. Bulls were slaughtered at an average of 442 ± 10.4 kg. After being harvested, samples were taken from the *longissimus dorsi* (LD) muscle of 24 bulls randomly, 2 bulls from each pen, between the 12th and 13th ribs for fatty acid analyses, using gas chromatography, and gene expression, which was analyzed by RT-qPCR. The model included the fixed effect of diet and was analyzed using the GLM procedure in SAS 9.4. Muscle of bulls fed soybean diets, regardless of processing, had lower

concentrations ($P < 0.05$) of C12:0 and the CLA C18:2 c9, t11; and higher ($P < 0.05$) concentrations of C18:0. The C14:0 content was higher ($P < 0.05$) in the muscle of bulls fed NSB, compared to those receiving GSB. The concentration of C18:1 *trans* isomers were higher ($P < 0.05$) in the muscle of bulls fed GSB compared to those fed ESB and NSB. On the other hand, C18:1 c9 content in the muscle of bulls fed GSB was lower ($P < 0.05$) compared to the muscle of bulls fed the other diets. LD muscle of bulls fed soybean diets, regardless of processing, had greater concentrations of saturated fatty acids. Polyunsaturated fatty acid content was lower ($P < 0.05$) when bulls were fed ESB. Gene expression of *PPARA* and *PPARG* was not affected by diet ($P > 0.05$). However, expression of *SREBF1* was greater ($P < 0.05$) in the muscle of bulls fed ESB. In conclusion, extrusion of soybean contributes to the greater biohydrogenation of polyunsaturated fatty acids and consequently greater expression of the gene *SREBF1*. The use of ground or extruded soybean does not increase CLA C18:2 c9, t11 content in beef cattle muscle.

Key Words: CLA, extruded soybean, *PPAR*, *SREBF1*

0905 Heat shock protein expression differs in 14 d aged longissimus lumborum in agreement with Warner-Bratzler shear force values. N. E. Ineck*, R. G. Christensen, S. M. Quarnberg, J. McClellan, J. F. Legako, and K. J. Thornton, *Utah State University, Logan*.

Despite similar production practices, beef cattle exhibit undesirable variation in the rate and extent of postmortem proteolysis lending to inconsistencies in tenderness. The objective of this study was to determine whether heat shock proteins (HSP) play a role in postmortem proteolysis and thus, development of tenderness. To address this, HSP expression was determined in the longissimus lumborum after 14 d of aging. A total of 32 samples were placed into either a more tender (MT; $n = 16$) or less tender (LT; $n = 16$) group based on previous Warner-Bratzler shear force (WBSF) values. Western blot analyses were then completed to determine expression of two different HSP: HSPβ1 and HSP70. Statistics were completed using Proc MIXED in SAS to determine whether HSP expression varied between MT and LT samples; the model included tenderness as a fixed effect and gel and sample as random effects. Spearman-Pearson correlations were also completed in SAS to determine whether WBSF value and HSP expression were related. The two tenderness groups had different ($P < 0.001$) WBSF values; the MT group had an average WBSF value of 1.9 kg, while the less tender group had an average WBSF value of 5.5 kg. Less tender samples showed increases ($P = 0.03$) in HSPβ1 when compared to the MT samples. Furthermore, there was a correlation ($R = 0.5238$, $P = 0.008$) between WBSF value and HSPβ1 expression. No differences ($P = 0.49$) in HSP70 expression were observed between the MT and LT groups. There was no ($R = 0.031$, $P = 0.89$) correlation identified between WBSF values and HSP70 expression. These data demonstrate that HSPβ1 expression in meat samples from the longissimus lumborum after 14 d aging may play a role in postmortem proteolysis, and thus development of tenderness. Further research is needed to improve our understanding of how HSP are involved in the postmortem proteolysis process.

Key Words: heat shock proteins, tenderness, Warner-Bratzler shear force

MEAT SCIENCE AND MUSCLE BIOLOGY SYMPOSIUM: SCIENCE OF RED MEAT CONSUMPTION

0906 Beef's role in a healthy diet. J. N. Martin*, D. R. Woerner, R. Delmore, K. E. Belk, and J. D. Tatum, *Colorado State University, Fort Collins*.

Although red meat has long been established as a tremendous source of essential nutrients, its posed contributions to heart disease, obesity, and various cancers have resulted in growing criticism of its role in the diet. This widespread criticism and posited associations to negative health outcomes have fostered an overall decrease in the consumption of red meats in the U.S. over the past several decades. Although this decrease hasn't resulted in overt and direct improvements to human health, its absence has highlighted the vital nutritional role of lean, red meat in the diet. Concurrently, the entirety of the meat industry has steadfastly pursued investigating—and further, communicating—the nutritional profile and health value of red meats. A noteworthy example of efforts to demonstrate the nutritional advancement of red meats has been the remarkable progress on reducing the total available fat in consumed red meat products. Through targeted efforts in animal husbandry and processing innovation, the meat industry has reduced the total fat available from red meats by up to 70% in the past three decades. Furthermore, multiple industry efforts have addressed concerns regarding the fatty acid profile of red meats by demonstrating the relatively high proportion of unsaturated fatty acids and the cardiovascular neutrality of certain saturated fatty acids (i.e., stearic acid) in red meats. Likewise, although the value of red meat proteins has been long established, recent investigations of their role in weight loss and weight maintenance have highlighted their beneficial contributions to the diet and long-term health. Similarly, the exclusion of red meats in certain dietary patterns has been demonstrated to exacerbate iron deficiency and sarcopenia. Overall, the totality of data regarding the nutritional profile of red meat suggests that criticisms of its inclusion in dietary recommendations are unwarranted. Instead, the body of evidence suggests that negative health outcomes are complex, yet the inclusion of lean, red meats in a balanced diet can promote health and well-being.

Key Words: health, nutrition, red meat

0907 How certain can we be about the association of meat consumption and cancer? D. M. Klurfeld*, *USDA Agricultural Research Service, Beltsville, MD*.

The recent evaluation from the World Health Organization's International Agency for Research on Cancer (IARC) Working Group 114 concluded that processed meat consumption is a definite carcinogen in humans and red meat is probably carcinogenic. These were expert opinions of the majority of members of the group who evaluated the evidence they deemed most convincing. Most of the data that drove these two decisions were epidemiological studies, which are limited in their ability to distinguish causation from association. Animal studies do not support the conclusions and mechanistic studies are not convincing. Importantly, there are two large intervention studies in humans that were published but were not taken into consideration. These studies reduced meat intake significantly, as part of an overall dietary pattern, but that reduction had no effect at all on development of either colon polyps or cancer. Schemes for evaluating the totality of evidence to establish causality have been in the literature for 50 yr but were not used by IARC. In addition, no systematic review or meta-analysis was done, both of which have become the standard for such comparisons. Weaknesses inherent in evaluating long-term intake of any foods in observational studies should preclude using such data as the sole or primary determinant of causality in relation to health. It has been demonstrated conclusively that the food frequency questionnaire used to estimate meat intake in those studies is not able to quantify the amount of protein consumed. Statistical adjustment for confounders and covariates differed from study to study making combined analysis problematic. Finally, lack of registration of most observational studies without clear designation of the hypotheses to be studied and the numerous associations reported force the conclusion that any findings from them need to be accorded the higher statistical threshold that should be required of secondary results. A convincing argument can be easily defended that we do not have enough valid data to classify the carcinogenicity of red or processed meat for humans.

Key Words: red meat, processed meat, cancer, health, human nutrition

0908 The role of red and processed meat in colorectal cancer development: A perspective. S. De Smet*, *Ghent University, Melle, Belgium*.

Red and processed meat provide high biological value proteins and important micronutrients, but at the same time there is increasing epidemiologic evidence for an association between red and processed meat consumption and the risk to develop several chronic diseases. With respect to colorectal cancer, meta-analyses have reported a 15–20% increased risk of colorectal cancer per 100 g per day of red meat and per 50 g per day of processed meat consumption. A working group of IARC recently assessed the carcinogenicity of red and processed meat consumption through an elaborate evaluation of epidemiologic, animal, and mechanistic studies. Taking into account the amount of data, the nature and quality of the studies, and the extent to which chance, bias, and confounding from other dietary and lifestyle factors can be ruled out, it was concluded from the epidemiologic studies that there is sufficient evidence in human beings for the carcinogenicity of the consumption of processed meat, and limited evidence for red meat. Inadequate evidence was found in experimental animals, but the mechanistic evidence for carcinogenicity in the digestive tract was assessed as strong for red meat and moderate for processed meat. For genotoxicity and oxidative stress, evidence was considered moderate. Substantial supporting mechanistic evidence is available for multiple meat components (N-nitroso-compounds, haem iron, and heterocyclic aromatic amines). Taking this together, the IARC working group classified processed meat as "carcinogenic to humans" and red meat as "probably carcinogenic to humans.. This classification has unfortunately frequently been misinterpreted and has led to polarized and scientifically incorrect statements in the media. However, it should be realized that the IARC assessment was a hazard analysis according to established procedures and was not a full risk assessment, nor was it intended to make dietary recommendations. The question remains whether nutrition authorities will adapt their advice on the role of meat in a healthy diet based on this report. This is evidently a concern for the meat industry. On the other hand, insight into the mechanisms of the association between meat consumption and diseases offers opportunities for mitigation, as was already shown for the use of calcium. More research is needed on the mechanisms and on strategies to improve the composition, processing, and heating of meat, allowing for reduction of the harmful effects. Even more important, it is believed that the interaction of meat with non-meat food ingredients in dietary patterns should be investigated.

Key Words: colorectal cancer, processed meat, red meat

0909 Is there a role for meat in a plant-based diet? M. A. Binnie*, *Canadian Pork Council, London, ON, Canada*.

Many North Americans are overfed and undernourished, resulting in significant negative health consequences. Obesity is of global concern, with rates tripling in Canada in one generation. Dietary patterns have shifted away from fresh and minimally processed foods to include alarming amounts of added sugars and ultra-processed foods. In the U.S., added sugars in ultra-processed foods (21.1% of calories) was eightfold higher than in processed foods (2.4%) and fivefold higher than in unprocessed or minimally processed foods and processed culinary ingredients grouped together (3.7%). Similarly, 22% of calories in the average Canadian diet come from foods that provide little or no nutritional value. Foods not included in Canada's Food

Guide make up a greater percentage of the calories in the diet of Canadians than do foods from the Meat and Alternatives, Milk and Alternatives, or Vegetables and Fruits food groups. To counter the obesity epidemic, plant-based diets are often promoted as a solution. However, it is widely accepted that animal products supplement and complement a diet based on plant foods so that it is nutritionally adequate. Replacing some carbohydrate with high quality protein foods may have clinical benefits. The nutritional lens needs to be adjusted to focus on the dietary quality meat contributes to a plant-based diet.

Key Words: dietary patterns, dietary quality

MILK PROTEIN AND ENZYMES

0910 Intrinsic and extrinsic factors affecting milk yield and composition of camel milk in northern Eritrea. Y. N. Berhane*, *Uludag University, Bursa, Turkey.*

Although camel milk contributes rich dietary components to the people living in Eritrean lowlands, factors affecting its average daily yield and composition have not yet been studied. Hence, the objective of our study was to investigate effects of extrinsic factors (season) and intrinsic factors (stage of lactation and parity) on milk yield and its composition in camels kept under traditional management conditions in northern semiarid areas of Eritrea. We collected 300 random milk samples from January to October in 2013, 30 samples each month. The analysis of milk composition was done using the lacto scan milk analyzer, an automated milk analyzer system, and the obtained data were analyzed using the general linear model on SPSS 18 software. The average daily yield of milk and compositions of fats, protein, and lactose were 3.78 L, 2.43%, 2.71%, and 4.8%, respectively. Stage of lactation, parity, and season of the year significantly influenced ($P < 0.05$) daily milk yield and composition of fats and protein. The percentage composition of lactose remained unaffected by any variables considered. The highest average daily milk yield was recorded at the second month of lactation (4.04 ± 0.10 L), whereas the least was after 8 mo of lactation. The daily milk yield was significantly higher at the third month. The percentage composition of fat and protein were also at their peak during the first 3 mo of lactation period (3.21 ± 0.14 and 2.76 ± 0.11%, respectively). Similarly, the highest average daily milk yield and percentage composition of protein, fat, and dry matter were recorded from camels of 3rd parity (4.43 ± 0.2 L, 5.11 ± 0.51, and 3.19 ± 0.22%, respectively). This study revealed that camels are a reliable source of milk with persistent yield and composition throughout most of the period of lactation. Effective herd management, proper selection and culling, and provision of supplemental feed during the dry seasons may contribute to high quality camel milk in the region.

Key Words: camel, Eritrea, milk composition, milk yield, extrinsic and intrinsic factors

0911 Effect of lactoferrin hydrolysates on cytokine expression in Raw264.7 cells. Y. W. Park*[1], J. Y. Son[2], G. Renchinkhand[2], S. H. Paik[3], and M. S. Nam[2], *[1]Fort Valley State University, Fort Valley, GA, [2]Chungnam National University, Daejeon, The Republic of Korea, [3]Cheonan Yonam College, Cheonan, The Republic of Korea*.

Lactoferrin (LF) is an iron-binding glycoprotein which is present in colostrum, milk, and other body secretions. LF is associated with human infants' inflammatory and immune responses. The objective of this study was to determine the effects of alkaline protease generated lactoferrin hydrolysates (LH) on immunomodulatory activities of nitric oxide (NO) production and cytokines production, including anti-inflammatory cytokines [interleukin(IL)-4], pro-inflammatory cytokines (interleukin-6, tumor necrosis factor-α, interferon-γ), Th2 cytokines (interleukin-4 or interleukin-6), and Th1 cytokines [tumor necrosis factor (TNF)-α, interferon (IFN)-γ] in immune cells. The presence of LH was confirmed by SDS-PAGE and HPLC analyses. The LH above 10 kDa and below 10 kDa were isolated from the extracted LH using 10 kDa cut-off centricon. Raw264.7 cells were treated with 3 different LH concentrations (1, 50, 100 μg/ml) for three types of LH (whole, above and below 10 kDa) treatments at 37°C for 3 hr, and then the culture supernatants were quantified by TNF-α and IL-1β ELISA kit. Cytokine expression levels in Raw264.7 cells were analyzed by reverse transcription-polymerase chain reaction (RT-PCR). Results showed that 1 μg/ml of three types of LH treatments produced 1500–2,000 ng/ml TNF-α, whereas the positive LPS (lipopolysaccharide) and negative controls produced 2450 and 1000 ng/ml TNF-α, respectively. The 50 μg/ml treatments of the three types of LH produced about 20–28 ng/ml IL-1β at 3, 6, 9 h, while the negative control had 7 ng/ml. TNF-α expression was decreased dose-dependently by the 3 LH groups, while none of the LH treated groups affected IL-6. The mRNA expression of IL-13 appeared in all LH concentrations. In RAW264.7 cells treated with 1, 50, 100 μg/ml for 3 h, the mRNA expression induced a remarkable increase in nitric oxide synthesis (INOS) with dose dependent manner. NO was secreted dose-dependently from macrophages which were activated by all concentrations of the 3 LH treated groups. The results of RT-PCR revealed that LH caused INOS and inhibited the production of TNF-α in Raw264.7 cells. It was concluded that lactoferrin hydrolysates had immunomodulating effects on anti-, pro-inflammatory, and anti-allergic reactions.

Key Words: lactoferrin hydrolysates, cytokines, Raw264.7 cells

0912 Three new bovine α_s-CN phosphorylation isoforms reveal different phosphorylation pathways. Z. H. Fang[*1,2,3], M. H. P. W. Visker[3], G. Miranda[1,2], A. Delacroix-Buchet[1], H. Bovenhuis[3], and P. Martin[4], *[1]INRA, UMR1313 GABI, Jouy-en-Josas, France, [2]Agroparistech, UMR 1313, GABI, Jouy-en-Josas, France, [3]Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands, [4]UMR1313 Gabi, INRA, AgroParisTech, Université Paris-Saclay, Jouy-en-Josas, France*.

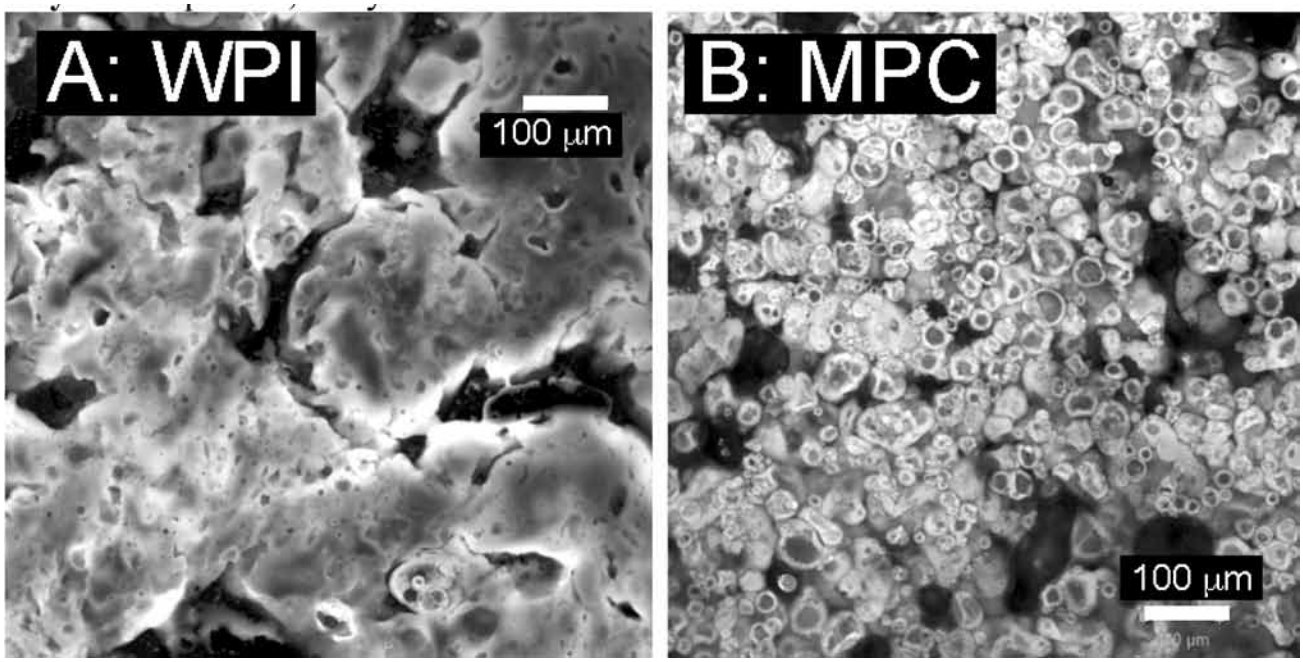
Casein (CN) phosphorylation is an important post-translational modification, and it is one of the key factors responsible for constructing and stabilizing casein micelles. Variation in phosphorylation degree of α_s-CN is of great interest because it is suggested to affect milk technological properties. Our objective was to investigate the variation in phosphorylation degree of α_s-CN among milk of individual cows and to explore relationships among different phosphorylation isoforms of α_s-CN. For this purpose, we analyzed morning milk samples from 529 French Montbéliarde cows using liquid chromatography coupled with electrospray ionization mass spectrometry (LC/ESI-MS). We detected three new phosphorylation isoforms: α_{s2}-CN-9P, -14P, and -15P in bovine milk, in addition to the known isoforms α_{s1}-CN-8P and -9P, and α_{s2}-CN-10P, -11P, -12P, and -13P. The relative concentrations of each α_s-CN phosphorylation isoform varied considerably among milk of individual cows (coefficient of variation $\geq$ 8). Furthermore, the phenotypic correlations and hierarchical clustering suggest two regulatory systems for the phosphorylation of α_s-CN: one responsible for isoforms with lower levels of phosphorylation (α_{s1}-CN-8P, α_{s2}-CN-10P and -11P), and the other responsible for isoforms with higher levels of phosphorylation (α_{s1}-CN-9P, α_{s2}-CN-12P, -13P and -14P). Identifying all phosphorylation sites of α_{s2}-CN and investigating the genetic background of different α_{s2}-CN phosphorylation isoforms may provide further insight into the phosphorylation mechanism of caseins.

Key Words: phosphorylation, casein, milk protein composition, LC/ESI-MS

0913 Hardening and microstructure of high protein nutrition bars made using whey protein isolate or milk protein concentrate. S. K. Hassan[1] and D. J. McMahon[*2], *[1]College of Education, Al-Qadisiya University, Al-Qadisiya- Diwaniya, Iraq, [2]Western Dairy Center, Utah State University, Logan*.

High-protein nutrition (HPN) bars (especially those containing > 30% protein) became hard during storage and have a limited shelf life, resulting in disappointment by consumers or loss of product as older products are discarded. The effect of different components on hardening of HPN bars was studied in bars containing 34% (wt/wt) whey protein isolate (WPI) or milk protein concentrate (MPC) powder, along with either sorbitol syrup or glycerol, and vegetable shortening or cocoa butter. The bars were stored at 20°C and 35°C and monitored for changes in hardness (measured using a penetration test), water activity, state of water and denaturation of whey proteins (measured using differential scanning calorimetry), and microstructure using confocal scanning laser microscopy. Substituting MPC for WPI made the bars brittle and crumbly. Using glycerol initially made bars softer but accelerated

Fig 0913.



hardening. Cocoa butter increased bar hardness because of its higher solid to liquid content. Most water (~99%) in HPN bars made using sorbitol syrup is present as bound water, with ~0.9% as intermediate water and ~0.1% as bulk water. During storage, bound water increased ~0.02 g/100 g of solids while intermediate water decreased, suggesting changes in state of water taking place at protein surfaces. During storage, there were changes in protein conformation indicated by an increase (~4°C) in heat denaturation temperature of β-lactoglobulin and α-lactalbumin and a 15 to 40% decrease in denaturation enthalpy. In bars made using WPI, the protein was present as a continuous network (see Figure A) while in bars made using MPC the protein remained in separate particles of protein powder dispersed throughout the sorbitol-water cosolvent mixture (see Figure B). It is proposed that hardening of HPN bars is a result of interactions between the cosolvents and the protein surface and not because of a phase separation between protein and cosolvents as was previously hypothesized.

Key Words: protein, whey microstructure

0914 Effect of casein non-phosphopeptides on the development of rat muscle analyzed using computed tomography (CT) scanning technology.

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About 2% of the population of age 50 suffers from sarcopenia, and the proportion is more than 50% after the age of 80. Sarcopenia may lead to physical weakness and reduced balance and mobility, which in turn have possible metabolic effects such as diabetes, arthritis, osteoporosis, and heart diseases. The leucine-rich whey protein α-lactalbumin has been found to counteract the muscle loss caused by sarcopenia. Casein non-phosphopeptide (CNPP) is a by-product from casein phosphopeptide production and is rich in leucine. The objective of this study was to investigate the effect of CNPP on the muscle development of healthy rats. Ten 32-wk-old male rats were fed one of the four dosage levels of CNPP or α-lactalbumin (high dose, 10 g/kg/d; moderate dose, 5 g/kg/d; low dose, 2.5 g/kg/d; and blank, 0 g/kg/d) for 50 d. Each feeding group was divided into two exercise groups: resistive exercise group (REG) and no exercise group (NEG). The resistive exercise consisted of three sets of 5 min of stair climbing with 1 min intervals daily. At 0, 15, 25, 35, and 50 d of feeding, rats were anesthetized and their cross-sectional body images were obtained using a transverse spiral CT scanner. Muscle groups were identified based on anatomical features. The areas of these muscle groups in the obtained images were determined using the CT software. The blood levels of growth hormone, insulin, and testosterone were determined using assay kits. Results were analyzed statistically using SPSS software. The results showed that the cross-sectional area of the trunk, back muscle group, and left upper limb muscle roots of the REG rats fed the moderate dose CNPP for 50 d increased significantly ($P < 0.05$). The cross-sectional area of the trunk and lumbar muscle group of the REG rats fed the high dose CNPP for 50 d also increased significantly ($P < 0.05$). Furthermore, the cross-sectional area of the trunk, β scapular muscles, and left upper limb muscle roots of the NEG rats fed the moderate dose CNPP for 50 d increased significantly ($P < 0.05$). In both CNPP-fed REG and NEG groups, the blood levels of growth hormone, insulin, and testosterone increased significantly after feeding for 50 d compared to those on Day 0 ($P < 0.05$). Our studies have demonstrated that the leucine-rich CNPP stimulates the synthesis of certain rat muscles and increases the blood levels of insulin, growth hormone, and testosterone.

Key Words: casein non-phosphopeptide, sarcopenia, CT scanning

Table 0914. Table 1 Increases in the cross-sectional area of different muscle groups in transverse spiral CT scanning images after 50 days of feeding.

		REG				NEG			
	Protein fed	Blank (cm^2)	Low dose (cm^2)	Moderate dose (cm^2)	High dose (cm^2)	Blank (cm^2)	Low dose (cm^2)	Moderate dose (cm^2)	High dose (cm^2)
Trunk	CNPP	6.87±0.65^a	7.97±0.56^b	6.20±0.48^a	8.58±0.88^c	7.01±0.60^a	7.47±0.42^a	8.37±0.76^b	7.31±0.78^a
Trunk	α-Lactalbumin	5.16±1.22^a	4.50±0.86^b	3.67±0.64^c	5.58±0.95^a	8.14±0.68^a	3.93±0.40^c	5.74±0.54^b	7.60±0.70^a
Lumbar muscles	CNPP	1.46±0.65^a	1.50±0.52^a	1.47±0.74^a	2.26±0.66^b	2.47±0.25^a	1.68±0.24^b	2.12±0.54^a	1.81±0.44^b
Lumbar muscles	α-Lactalbumin	0.26±0.18^a	0.73±0.09^b	0.28±0.14^a	1.47±0.21^c	1.20±0.20^a	0.84±0.22^b	0.68±0.42^c	0.66±0.32^c
Back muscles	CNPP	0.70±0.16^a	1.06±0.18^b	0.66±0.21^a	0.80±0.14^a	0.74±0.16^a	0.32±0.18^b	0.86±0.20^a	0.83±0.22^a
Back muscles	α-Lactalbumin	-0.28±0.12^a	0.50±0.15^b	-0.1±0.09^a	0.41±0.18^b	0.15±0.18^a	0.37±0.15^b	0.32±0.12^b	0.48±0.14^b
Beta scapular muscles	CNPP	0.87±0.11^a	0.88±0.15^a	1.05±0.10^b	0.77±0.07^a	1.06±0.42^a	1.22±0.28^{ab}	1.31±0.50^b	1.14±0.42^a
Beta scapular muscles	α-Lactalbumin	0.53±0.12^a	1.10±0.09^b	1.52±0.14^c	1.20±0.16^b	1.16±0.30^a	1.66±0.26^{bc}	1.42±0.18^b	1.72±0.16^c
Left upper limb muscle roots	CNPP	0.54±0.14^a	0.88±0.16^c	0.86±0.12^c	0.54±0.12^b	0.41±0.16^a	0.71±0.10^b	0.79±0.22^b	0.68±0.20^b
Left upper limb muscle roots	α-Lactalbumin	0.14±0.12^a	0.35±0.15^b	0.41±0.22^c	0.35±0.28^b	0.16±0.10^a	0.28±0.14^b	0.16±0.08^a	0.45±0.15^c

n=5, Different letters in each muscle group (a-c) indicate significant differences ($P < 0.05$).

0915 Physico-chemical properties and antioxidant efficacy of whey protein isolate and casein hydrolyzate stabilized nano-vesicular vehicle systems containing curcumin. Z. Z. Haque*and S. Mukherjee, *Food Science, Nutrition and Health Promotion, Mississippi State University, Mississippi State*.

Development of stable nano-emulsion systems, designed for efficient delivery of hyper-active natural antioxidants, nutraceuticals, and other bioactive compounds is crucial for effective enhancement of dairy product shelf-life as well as to alleviate the detrimental biological consequences caused by the reactive oxygen species. This study investigated the physicochemical and antioxidant properties of a nanoemulsion system, developed as nano-vesicular vehicles (NVVs) for efficient delivery of curcumin (CU), a highly potent, generally recognized as safe (GRAS) antioxidant. Coarse emulsions were first produced by dispersing whey protein isolate (WPI) (1% w/v, primary emulsifier), tween-20 (20% w/v of WPI, secondary emulsifier), chymotryptic hydrolyzate of casein (CH) (1:50 w/w of WPI), and CU (0.22% w/v) in 200 mM phosphate buffer with a pH of 8.0 (the continuous phase) for 3 h with gentle stirring at 22°C. The NVVs were generated by subjecting the coarse emulsion to single-pass ultra-high-pressure homogenization (UHPH) at 140 and 210 MPa. Physico-chemical and antioxidative properties of the CU-loaded-NVVs containing CH (CU+CH-NVVs) were analyzed and compared to the NVVs without CH (CU-NVVs) for 16 d of storage at 4°C. Increasing the trace amount of CH resulted in a significant enhancement ($P < 0.05$) of both short- and long-term antioxidative properties [antioxidant activity (AA) and persistence (AP), respectively], in all CU+CH-NVVs throughout the study compared to CU-NVVs. The CU+CH-NVVs generated using 210 MPa showed 497 and 567% enhancement of AA and AP, respectively, relative to the CU-NVVs on the 16th day of storage. The former also showed 6222 and 11278% enhancement of AA and AP compared to the control (buffer alone). The CU+CH-NVVs generated at 210 MPa exhibited a considerable (7.4%) reduction in mean globular particle diameter as well as a substantial increase (17%) in zeta potential compared to the CU-NVVs formulated using the same UHPH at the final day of storage, indicating the efficacy of even a minute quantity of CH to remarkably enhance the stability of NVVs.

Key Words: nanoemulsion, neutraceutical, free radical

MILK SYMPOSIUM: MARKETING MILK FOR ENTREPRENEURIAL AND BIG BUSINESS VALUE

0916 Get in the driver's seat: Marketing milk and dairy products to today's and tomorrow's consumers. D. M. Berry*, *Dairy & Food Communications, Inc., Chicago, IL*.

Who buys a head of iceberg lettuce anymore when pre-washed, trimmed lettuce blends are readily available? It's the same person who buys a gallon of the white stuff and a chunk of cheddar. It's not the consumer—today's consumer–who grew up with more than 87,000 possible Starbucks combinations to create a customized drink. Millennials and their offspring are today's and tomorrow's consumers, demographics with unprecedented expectations of the food supply chain. They want customization, simplicity, and transparency but at the same time demand convenience, deliciousness, and portability. According to the International Food Information Council Foundation's 2015 Food and Health Survey, compared to the general U.S. population, Millennials have differing opinions on traditional eating habits, usage of resources and information for staying healthy, and even on the value of some nutrients. Understanding these views is paramount for dairy brands to thrive. According to the International Dairy-Deli-Bakery Association, the food retail world is changing, and the products and the players must change in tandem. Traditional food retailers are the most challenged, with data suggesting they will experience a 9% drop in market share (from 71% to 62%) over the next 10 yr as non-traditional channels like fresh formats and online retailers gain 38% of the food market. Traditional supermarkets that want to survive are responding to the changing retail channel landscape by featuring full-service restaurants, smaller formats, and Millennial-focused products and services. In 2014, e-commerce sales for consumables were $24.4 billion, an increase of 13.5% from 2013. Online purchases of foods and beverages are projected to almost quadruple between 2015 and 2020, to $49 billion, representing 4.5% of all food retail sales. When it comes to dairy, deli, and bakery, as well as prepared foods, specialty cheese, and specialty meats, the six fresh parameter departments in the traditional supermarket, consumers continue to appreciate the in-person experience. It's no wonder that the greatest percentage of increase in store count has come from channels outside of traditional food, drug, and mass-merchandising formats, including convenience stores, warehouse clubs, and dollar stores. Stores that focus on fresh foods, in particular single-serve options and convenience, invite consumers inside. And once inside, they often buy more than they really intended. Dairy foods manufacturers must make sure they are competing in this space.

Key Words: Millennials, innovation, consumer

0917 Practices and programs to ensure the safety of artisan cheese. D. J. D'Amico*, *University of Connecticut, Storrs*.

Historically, milk processing and cheesemaking were conducted on farms. In the mid-1800s the factory system for cheesemaking was introduced in the United States and quickly came to dominate the industry. By the beginning of the 20th century, farmstead cheesemaking in the U.S. had all but disappeared. More recently, small-scale and on-farm processing of dairy products is experiencing a resurgence as producers are looking to add value to milk while consumers are increasingly looking for unique and locally produced products with minimal processing. This growth is particularly apparent in the artisan cheese sector that has seen the number of U.S. producers increase from ~75 in 1990 to ~1000 today. Increasing demand provides opportunities for selling and marketing unique dairy products in local, national, and international markets. From a food safety perspective, artisan and farmstead cheese producers face common as well as unique risks and challenges including those related to on-farm processing, the production of higher-risk cheese varieties, and the renewed interest in the use of unpasteurized milk. Many small and very small establishments may also lack the resources, capital, technical expertise, or training to implement robust food safety programs and related technology. With the changing food safety and regulatory landscape and the expansion of international trade, there is a need to preserve traditional practices and products while ensuring food safety. Using examples from various countries, including efforts in the U.S., this presentation addresses these food safety risks and challenges and discusses food safety programs and best practices.

Key Words: safety, small-scale, cheese

0918 Camel milk from commodity to added value product. The science behind the development of the camel dairy industry. P. Nagy*, *Emirates Industries for Camel Milk and Products, Dubai, United Arab Emirates*.

Until recently, camels were regarded mainly as packing or racing animals by many, including the general public, scientists, funding agencies, and policymakers, but the food production potential of the species has been neglected. Camel milk had been produced exclusively by hand milking in traditional farming systems for household consumption. Such production could not provide a constant quantity and acceptable quality of raw milk for urban markets. However, during the last 10 to 15 yr, intensive camel milk production has been going through a major development. Machine milking has been introduced in several traditional camel-keeping countries, like the United Arab Emirates, Saudi Arabia, and Tunisia. Small-scale farms in Australia, Europe, and the USA have also been reported to be using milking machines for dromedaries. The world's first large-scale camel dairy farm (EICMP, Dubai, UAE) with a processing facility and distribution was established during this period. In addition, several commercial and scientific projects have been started. The demand for camel milk triggered research and development on camel lactation physiology, behavior, nutrition, reproduction, husbandry, management, etc. In addition, camel milk microbiological quality and chemical composition have been defined; studies were conducted to improve product characteristics and new products were developed, such as probiotic fermented milk, laban, labneh, cheese, milk, and whey powder. The medicinal properties of camel milk has also received increased attention, and data have been published in peer-reviewed medical journals that support field observations and anecdotes from camel-keeping countries. Despite significant progress made in intensive dairy management, machine milking, composition, and product development, the task is far from completion. More basic and applied research is required in all of the above fields for better understanding and optimized production. Important areas for research could be (1) improvement of machine milking technologies, (2) neuro-endocrine control of lactation, (3) phenotypic and genetic variation of breeds/ecotypes, (4) role and application of environmental factors (like photoperiod, nutrition), (5) variation in milk quality and composition, and (6) chemistry of camel milk proteins. The aim of this presentation is to review the recent development of the camel dairy industry, summarize our present knowledge on camel milk production and processing, and highlight areas for future research.

Key Words: camel milk, intensive management, machine milking

0919 Terroir: Science based or marketing gimmick. L. Goddik*, *Oregon State University, Corvallis*.

The concept of terroir is rapidly gaining importance in the U.S. marketplace in alignment with the growth of the local food sector. Terroir for products such as coffee and wine are well recognized, but there is little science to support terroir for dairy products. Nevertheless, it's common to see promotions for regional cheeses such as Wisconsin cheese or New York Cheddar. This presentation will evaluate factors that influence farm and regional milk sources and their impact on cheese characteristics. Our current research has focused on the simple question: If all other factors are kept constant, will milk from different farms and regions produce cheeses that are different? Initial results have demonstrated that milk from farms, selected due to similar herd management principles, produce Cheddar cheeses that are different based on sensory and flavor chemistry profiles. Non-starter lactic acid bacteria (NSLAB) profiles

are unique to individual farms. The link to the individual farms (terroir effect) is more pronounced in 5 mo aged Cheddar than in 9 mo aged Cheddar. Milk from coastal regions appears to be particularly suited for cheese production, likely due to complex NSLAB profiles and flavor development.

Key Words: milk source, cheese, flavor

NONRUMINANT NUTRITION: ENZYMES

0920 The effect of increasing *Buttiauxella* phytase dose on performance in piglets: Meta-analysis from 5 trial studies. Y. Dersjant-Li, R. M. Bold, and W. Li*, *Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, United Kingdom*.

The effect of *Buttiauxella* phytase on the performance of piglets was evaluated combining the datasets of five trials. A total of 234 data points (364 piglets, average initial BW 10 kg) were used in the analysis. Treatments included a nutritionally adequate positive control diet (PC), a negative control diet (NC, with an average reduction of 0.15% calcium and 0.19% phosphorus compared to the PC), and NC supplemented with *Buttiauxella* sp. phytase at 500, 1000, or 2000 phytase units (FTU)/kg feed. One FTU was defined as the amount of enzyme required to release 1 μmol of iP per minute from sodium phytate at pH 5.5 at 37°C. Piglets received the test diets (based on corn/SBM, wheat/SBM or wheat/barley and SBM) for 14 d. No grain source × phytase dose interaction was found, thus data from the 5 trials were pooled for statistical analysis (JMP 11.0, SAS). Treatment means were separated using Tukey's HSD test, trial was used as a random factor. Linear or nonlinear response was tested with increasing phytase dose from 0 (NC) to 2000 FTU/kg. Phytase dose at 1000 and 2000 FTU/kg improved ADG by 12.3 and 19.3% respectively vs. NC ($P < 0.05$), and by 3 and 9.4% vs. PC ($P > 0.05$). No significant differences were seen in feed intake. FCR was improved with phytase at 1000 and 2000 FTU/kg by 8.8 and 10.2% vs. NC ($P < 0.05$), and by 5.5 and 6.3% vs. PC ($P > 0.05$). Increasing phytase dose from 0 (NC) to 2000 FTU/kg increased ($P < 0.05$) ADG linearly and reduced FCR in a nonlinear manner. The data demonstrated that phytase at 500 FTU/kg could replace 0.19% P and 0.15% Ca. Increasing phytase dose to 1000 or 2000 FTU/kg could further improve performance of piglets fed P and Ca deficient diets, most likely due to the extra-phosphoric effects of the phytase. Cost calculation (based on feed cost and 14-d performance data) showed a net value of $0.11, 0.35, and 0.62 per pig ($11.8, 39, and 65/ton of feed) with *Buttiauxella* phytase at 500, 1000, and 2000 FTU/kg respectively compared to PC. In conclusion, increasing *Buttiauxella* phytase dose up to 2000 FTU/kg may provide production benefits in piglets.

Key Words: piglets, meta-analysis, performance

0921 Effects of dietary β-mannanase supplementation with soybean meal in the performances in weanling pigs. B. Balasubramanian*, H. M. Yun, Y. M. Kim, J. K. Kim, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, South Korea*.

Soybean meal (SBM) is by far the most popular protein source used for feeding livestock. The objective of the present study was to test the efficacy of supplementation of β-mannanase in diets containing de-hulled or conventional hulled SBM (44% and 48%) as well as to evaluate the interactive effects of SBM and enzyme on growth performance, nutrient digestibility, fecal microflora, and noxious gas emission in weanling pigs. In total, 140 pigs [(Landrace × Yorkshire) ×Duroc] with a initial BW of 5.97 ± 1.01 kg were used in a 6-wk feeding trial, randomly allotted in a 2 × 2 factorial arrangement, with feed consisting of hulled or de-hulled SBM with or without β-mannanase [T1 (SBM 44%), T2 (SBM 44% + 0.05% β-mannanase), T3 (SBM 48%), and T4 (SBM 48% + 0.05% β-mannanase)]. Pigs were allocated randomly to 4 treatment groups consisting of 7 replicate pens per treatment with 5 pigs per pen. Pen was the experimental unit. In this study, pigs fed diets containing 0.05% β-mannanase had greater BW, ADG, G:F, and ADFI than pigs fed diets without β-mannanase, but the differences were not statistically significant; however, interactions of SBM diets showed significant differences for ADFI ($P = 0.0334$) at the second week and showed significant effects on DM ($P = 0.0077$), N ($P = 0.0082$), E ($P = 0.0362$), P ($P = 0.0472$) at the sixth week. Furthermore, when compared with SBM, β-mannanase had effects on DM ($P = 0.0105$), N ($P = 0.0416$), P ($P = 0.0591$), but not E and Ca. There were no significant differences for serum BUN, WBC, Lymphocytes, however observed significance on RBC ($P = 0.0130$), when compared with SBM diets at the sixth week. Effects on diarrhea score ($P = 0.0469$) at d 3 and noxious gas emission were not significantly different ($P > 0.05$). The significant effects of β-mannanase supplementation with SBM on fecal microflora (*E. coli* and *Lactobacillus*) showed a significant difference at sixth week ($P < 0.05$). In conclusion, β-mannanase supplementation in a SBM diet showed positive effects on nutrient digestibility (DM, N, E, P), on feed efficiency, and for reducing *E.coli* population in weanling pigs.

Key Words: β-mannanase, soybean meal, weanling pigs

0922 Effect of a multi-enzyme component on growth performance, nutrient digestibility, carcass quality, and gas emission in broilers.
D. H. Nguyen*, H. S. Kim, S. Kathannan, S. Shanmugam, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, South Korea*.

A total of 480 broiler chicks (BW = 42 ± 1 g) were used in a 5-wk feeding trial in which there were two phases, starter (1 to 18 d) and finisher (19 to 35 d), to investigate the effect of dietary supplementation with multi-enzymes in broiler chickens. The chicks were randomly divided into 4 treatments with 8 replications per treatment and 15 birds per pen. Experimental diets consisted of two different levels: high-energy diet (HE) and low-energy diet (LE). The LE diet had 12.34 (starter) and 13.08 MJ ME/kg (finisher); The HE diet had 12.66 (starter) and 13.39 MJ ME/kg (finisher). Dietary treatments included 1) LCON (low-energy diet); 2) LME (LCON + 375 g multi-enzyme/ton of feed); 3) HCON (high-energy diet); and 4) HME (HCON + 375 g multi-enzyme/ton of feed). The multi-enzyme component contained protease, amylase, xylanase, glucanase, pectinase, galactosidase, debranching enzymes, and phytase. The broilers were weighed by pen and feed intake (FI), and data was recorded on d 1, 18, and 35 for calculating body weight gain (BWG) and feed conversion ratio (FCR). Fresh excreta samples were collected from each pen for the measurement of nutrient digestibility according to the procedures of AOAC (2000). All data were subjected to the GLM procedures of SAS with a 2 × 2 factorial arrangement, and probability values of $P < 0.05$ were considered to be significant. During the starter phase and overall, the effect of multi-enzymes and HE were observed to increase BWG (overall, LME and HME vs. LCON and HCON were 1,581.8 and 1,607.8 vs. 1,534.8 and 1,582.5 g/d; $P < 0.05$). In addition, the FCR improved in broilers fed with HE during d 1 to 18 and overall ($P < 0.05$). The apparent total tract digestibility (ATTD) of DM and N was improved (DM: LME and HME vs. LCON and HCON were 76.8 and 77.9 vs. 75.3 and 76.0%; N: LME and HME vs. LCON and HCON were 73.4 and 74.0 vs. 71.9 and 72.2%; $P < 0.05$) by the multi-enzymes on d 35. An increase was observed in breast muscle on carcass quality when broilers fed with HE ($P < 0.05$). Furthermore, feeding chicks with multi-enzyme supplementation reduced fecal NH_3 and H_2S concentrations ($P < 0.05$). However, no other carcass characteristics were affected by the treatments. In conclusion, dietary supplementation with a multi-enzyme component improved BWG and nutrient digestibility and reduced excreta noxious gas emission in broilers. Breast muscle was improved when broilers were fed the HE diet.

Key Words: broilers, growth performance, multi-enzymes

0923 Efficacy of dietary supplementation of protease and xylanase in plant-based diets on growth performance and health of nursery pigs at 6 to 9 wk of age.
I. Park*, H. Chen, and S. W. Kim, *North Carolina State University, Raleigh*.

This experiment was conducted to determine the supplemental effects of protease and xylanase (BRI, Durham, NC) in plant-based diets on growth performance and health of nursery pigs at 6 wk of age. One hundred and twenty pigs (60 barrows and 60 gilts at 15.5 ± 3.0 kg BW) were randomly allotted to 4 treatments with 10 pens (3 pigs per pen) per treatment, and fed the experimental diets for 3 wk in a 2 × 2 factorial arrangement. Two factors were protease (0 or 15,000 unit/kg diet) and xylanase (0 or 1400 unit/kg diet), which were supplemented to the basal diet, which included yellow dent corn (50%), soybean meal (26%), and distillers dried grains with solubles (20%) as major feedstuffs. All diets contained essential nutrients meeting the NRC requirements. Feed intake and BW were recorded weekly. At the end of the study, a pig representing median BW of each pen was selected for blood collection from jugular vein. Blood was used to obtain plasma. Plasma samples were used to measure plasma urea nitrogen (BUN), tumor necrosis factor-α (TNF-α), and immunoglobulin G (IgG). Data were analyzed using the Mixed procedure in SAS with pen as the experimental unit with treatments and sex as fixed effects and initial BW as a random effect. Statistical differences among treatment means were considered significant with $P < 0.05$. Overall, supplementation of protease did not affect growth performance of nursery pigs. Supplementation of xylanase, however, increased ($P < 0.05$) ADG (1.62 to 1.83 kg/d) without affecting ADFI and tended to increase ($P = 0.061$) G:F (0.803 to 0.860). Combinational use of protease and xylanase on growth performance did not differ among treatments. Plasma BUN and IgG were not affected by both factors, whereas plasma TNF-α was decreased ($P < 0.05$, 40.2 to 25.2 pg/mL) by supplementation of xylanase. There were no interactions of the effects of protease and xylanase in any measurements. In conclusion, dietary supplemental xylanase improved growth performance by reducing systemic inflammatory response. However, a combinational use of xylanase with protease did not enhance the effects of a single use of xylanase in nursery pigs at 6 to 9 wk of age.

Key Words: growth performance, intestinal health, nursery pigs, protease, xylanase

0924 Effects of microbial phytase on the apparent and standardized total tract digestibility of calcium in milk co-products fed to growing pigs.
Y. She[*1], D. Li[2], and H. H. Stein[1], [1]*University of Illinois Urbana-Champaign, Urbana,* [2]*CAU, Beijing, China*.

The objective of the experiment was to determine effects of microbial phytase on the apparent total tract digestibility (ATTD)

and the standardized total tract digestibility (STTD) of Ca in milk co-products fed to growing pigs. Sixty-four growing barrows (average initial BW: 15.97 ± 3.11 kg) were allotted to a randomized complete block design with 8 diets, 2 blocks, and 4 pigs per treatment in each block. A basal diet based on corn, potato protein isolate, and soybean oil was formulated. Three additional diets were formulated by adding whey powder, whey permeate, or skim milk powder to the basal diet. All diets were formulated without or with 1000 units per kilogram of microbial phytase for a total of 8 diets. All diets were formulated to contain the same concentration of Ca and total P. The basal endogenous loss of Ca was assumed to be 0.123 g/kg DMI. Feces were collected quantitatively for 5 d based on the marker-to-marker approach after a 7-d adaptation period. Results indicated that the STTD of Ca in whey powder, whey permeate, and skim milk powder were 96.18, 52.52, and 95.94% without phytase, respectively, and 94.43, 73.12, and 98.90% with phytase, respectively. Regardless of inclusion of microbial phytase, the ATTD and STTD of Ca in whey powder and skim milk powder were greater ($P < 0.05$) than in whey permeate. Inclusion of microbial phytase increased ($P < 0.05$) the ATTD and STTD of Ca in the whey permeate diet. Microbial phytase also increased ($P < 0.05$) the ATTD of P in the whey powder diet from 79.31 to 81.29%, in the whey permeate diet from 64.17 to 73.05%, and in the skim milk powder diets from 80.15 to 86.40%. Regardless of inclusion of microbial phytase, the ATTD of P was greater ($P < 0.001$) in whey powder and skim milk powder diets than in whey permeate diets. In conclusion, skim milk powder and whey powder had greater ATTD and STTD of Ca than whey permeate, but microbial phytase increase digestibility of Ca in whey permeate. The ATTD of P was also greater in skim milk powder and whey powder diets than in the whey permeate diet.

Key Words: calcium, milk co-products, pigs

0925 Effect of different levels of zinc and phytase on growth performance in weanling pigs. L. Blavi*, D. Solà-Oriol, S. M. Martín-Orúe, and J. F. Pérez, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain*.

It is common to use 2500–3000 ppm Zn as ZnO to prevent post-weaning diarrhea. However, most of the dietary Zn supply is excreted, causing environmental accumulation, and recently antimicrobial resistance concerns have also increased. Phytate supplementation in most piglet diets may create insoluble salts with several divalent cations (Ca, P, Zn) inhibiting their absorption. Therefore, the objective of the present experiment was to observe the effect of the interaction between the use of therapeutic doses of Zn and phytase supplementation on growth performance in weanling piglets (0 to 35 d post-weaning). A total of 320 pigs were used in a 2 × 2 factorial arrangement, where the main factors were Zn inclusion (125 or 2500 ppm Zn) and phytase inclusion (0 and 1000 FTU). Piglets were reared in 32 pens (10 pigs/pen; 8 replicates per treatment). The pre-starter (0–14 d) and starter (14–35 d) diets contained 2520 and 2460 Kcal NE/kg, 19.65 and 19.00% CP, 1.25 and 1.23 digestible Lys, 0.35 and 0.77% Ca, and 0.33 and 0.25% P digestible, respectively. The pre-starter diet had low Ca levels (0.33%) without $CaCO_3$. Feed intake and individual BW were registered on d 0, 14, and 35 post-weaning. Performance parameters were analyzed with ANOVA by using the Mixed procedure of the statistical package SAS. There was an effect of Zn on BW at d 14 and 35 ($P < 0.05$); where pigs with no ZnO addition presented higher weights compared to pigs with ZnO (11.12 and 21.84 vs. 10.56 and 20.76 Kg, respectively). There was no phytase effect on BW, ADG, ADFI, and FCR. However, there were significant interactions on BW at d 35, ADFI 0–14 and ADG 0–35 ($P < 0.05$), where piglets without ZnO and 1000 FTU of phytase obtained better results (higher BW, ADG, and ADFI) compared to piglets with ZnO and 1000 FTU of phytase (22.2 vs. 20.19 Kg; 327.13 vs. 261.13 g/d; and 416.76 vs. 357.34 g/d, respectively), suggesting that phytase does not have the same benefits with high levels of Zn on the diet. There was also a statistical trend for the interactions on BW14 ($P = 0.08$), ADG 0–14 ($P = 0.07$), ADG 14–35 ($P = 0.06$), and ADFI 0–35 ($P = 0.06$), following the same pattern. It can be concluded that diets without therapeutic ZnO and low levels of Ca but 1000 FTU of phytase allow better growth than diets with high Zn levels.

Key Words: phytase, pigs, zinc

0926 New bacterial 6-phytase expressed in *Pseudomonas fluorescens* improved growth performance, bone parameters, and P digestibility in growing pigs. F. N. Almeida*, M. Vázquez-Añón, and J. Escobar, *Novus International, Inc., St. Charles, MO*.

A study was conducted to determine the effects of a new bacterial 6-phytase expressed in *Pseudomonas fluorescens* (CIBENZA® PHYTAVERSE®, Novus International, Inc., St Charles, MO) on growth performance, bone parameters, and P digestibility in growing pigs fed a diet deficient in standardized total tract digestible (STTD) P. A total of 144 pigs (initial BW = 44.27 ± 0.74 kg) were randomly allotted to 1 of 4 treatments with 18 replications and 2 pigs/pen. Treatments included 1) a positive control (POS) that met the requirements (NRC, 2012) for all nutrients, 2) a negative control (NEG) deficient only in STTD P (−0.10% vs. POS), 3) NEG supplemented with 250 FTU/kg phytase (NEG+250), and 4) NEG supplemented with 500 FTU/kg phytase (NEG+500). Data were analyzed using the Mixed Procedure (SAS® Institute, Cary, NC). The ADG and G:F was less ($P < 0.01$) for pigs consuming the NEG diet compared with POS (0.964 vs. 1.093 kg and 0.356 vs. 0.387, respectively). The ADG of pigs consuming NEG+250 or NEG+500 was not different ($P > 0.05$)

from that of pigs consuming POS (1.061 or 1.066 vs. 1.093, respectively). Phytase linearly ($P < 0.01$) improved the ADG of pigs fed the NEG diet. The G:F of pigs fed NEG+250 or NEG+500 was not different from pigs fed the POS. Phytase supplementation to the NEG diet tended ($P = 0.06$) to linearly improve the G:F of pigs. Bone ash weight and bone P weight were greater for pigs fed the POS diet than for pigs fed the NEG diet (6.42 vs. 4.70 g and 1.19 vs. 0.86 g, respectively). Supplementing pigs with either 250 or 500 FTU/kg, however, linearly improved ($P < 0.01$) bone ash weight compared with pigs fed NEG (4.70 vs. 5.63 or 5.99 g, respectively). Likewise, bone P weight was linearly increased ($P < 0.01$) in pigs fed NEG+250 (1.04 g) or NEG+500 (1.11 g) compared with pigs fed NEG (0.86 g). The STTD of P was greater ($P < 0.05$) for pigs fed NEG+500 (48.71%) that all other treatments, with the NEG being the least digestible (35.03%). In conclusion, this new phytase efficiently improved the growth performance, bone parameters, and STTD of P in grower pigs.

Key Words: bone, pigs, phytase

0927 Effect of timing of post-weaning supplementation of xylanase on growth performance, nutrient digestibility and fecal microbial composition in weanling pigs.

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The study was conducted to investigate the effect of timing of xylanase (Econase XT) supplementation to weanling pigs fed a corn-soybean meal based diet, and its effect on growth performance, nutrient digestibility, and gut microbial composition. A total of 128 weanling pigs ([Hampshire × Duroc] × [Yorkshire × Landrace]; barrows: gilts = 1:1; 6.2 ± 0.6 kg BW; weaning age: 21 d) were randomly assigned to 4 treatments, 8 replicate pens with 4 pigs per pen based on their BW at weaning. The 4 treatments were a combination of 2 dietary treatments (xylanase added at 0 or 16,000 BXU/kg) and 2 feeding time points [period 1 (d 0–14) and period 2 (d 14–42)]. Treatments were: xylanase-xylanase, xylanase-control, control-xylanase, and control-control. The study lasted 42 d with a 3-phase feeding program: d 0 to 14, d 14 to 28, and d 28 to 42. Chromic oxide marker was included in the diets at 0.5% from Day 28. BW and feed intake were recorded every 2 wk. On d 41, fecal samples were collected from each pig for determination of microflora diversity and apparent total tract nutrient digestibility (ATTD). Ileal digesta were also collected on d 42, for determination of apparent ileal nutrient digestibility (AID). From d 0–14, pigs had lower BW, ADG, and feed efficiency when xylanase was included in the diets. The final BW and overall ADG was higher ($P < 0.05$) when xylanase was supplied from d 14 compared with that from d 0. The AID and ATTD of DM, energy, N, and phosphorus was increased ($P < 0.05$) by xylanase and not impacted by timing of xylanase inclusion. The overall bacterial community structure was not influenced by different treatments. However, xylanase significantly decreased ($P < 0.05$) Veillonellaceae and tended to decrease ($P < 0.08$) *Megasphaera* abundance in period 2 compared to the control group. Therefore, timing of xylanase inclusion in weanling pig diets has an effect on performance in the nursery.

Key Words: weanling pigs, xylanase, digestibility, gut microbial profile

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0928 Effect of xylanase and live yeast supplementation on growth performance and gut microflora diversity of growing pigs.

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The objectives of current study were to determine the effect of xylanase and live yeast (LY) supplementation, and the timing of xylanase supplementation, on future growth performance and gut microflora diversity of pigs. In the study, 180 weanling pigs (21 ± 2 d, BW: 6.2 ± 0.16 kg) were assigned to 5 treatments in a randomized complete block design (6 replicate pens, 6 pigs per pen) from weaning to market. The 5 treatments were: control-control, control-xylanase, xylanase-xylanase, LY-xylanase, and xylanase+LY-xylanase, where the first diet was fed from weaning to 2 wk and thereafter 6 additional corn/soy/corn DDG based phases were fed until d 127. Xylanase (Econase XT) was added at 16,000 BXU/kg and LY (Vistacell) at 1 kg/t. On d 15, 2 pigs per pen were euthanized to obtain jejunal mucosa samples. Fecal samples from Days 0, 14, 43, and 127 were collected for volatile fatty acids (VFA) and microbial diversity analysis. Pigs fed with LY and LY+xylanase from d 0–15 had higher BW and ADG at d 15 compared with the control ($P < 0.05$). Overall, G:F was higher in the xylanase+LY-xylanase and control-xylanase groups ($P < 0.05$) on d 127. Additionally, glucose transporter 2 (GLUT2) mRNA expression was higher in the LY and LY+xylanase groups on d 15 compared with control ($P < 0.05$). Furthermore, intestinal alkaline phosphatase (IAP) mRNA expression was highest in the xylanase-xylanase group and lowest in the LY-xylanase group ($P < 0.05$). Fecal VFA concentration significantly increased with age ($P < 0.01$). LY supplementation significantly increased propionate acid, valeric acid, and isovaleric acid

concentrations on d 127 ($P < 0.05$). Age significantly affected microbial diversity structure ($P < 0.01$). In summary, LY supplementation with or without xylanase improved growth performance of weanling pigs in the first 2 wk after weaning. Fecal VFA concentrations and microbial community structure were significantly influenced by age, with xylanase and LY supplementation having only a minor effect.

Key Words: xylanase, live yeast, weanling pigs, growth, microbial profile

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0929 Effects of dietary supplementation of β-mannanase on digesta viscosity and intestinal health of nursery pigs. I. Park*, Y. I. Kim, and S. W. Kim, *North Carolina State University, Raleigh*.

This study was conducted to determine the effects of β-mannanase (CTC BIO Inc., Seoul, Korea) on digesta viscosity and intestinal health of nursey pigs. Pigs (36 barrows and 36 gilts at 15.5 ± 2.3 kg BW) at 45 d of age were housed individually and randomly allotted to 3 treatments (24 pens/treatment). Experimental diets had 3 levels of β-mannanase (0, 400, and 600 Unit/kg) and were fed to pigs for 10 d. Feed intake and BW were measured on d 7 and 10 to calculate growth performance. On d 10, all pigs were euthanized to obtain jejunal digesta to measure viscosity and mucosa from the duodenum and jejunum to measure tumor necrosis factor-α (TNF-α), immunoglobulin G (IgG), and malondialdehyde (MDA). Duodenal and jejunal tissues were used to measure morphology and proliferation of mucosa cells by Ki-67 immunohistochemistry. Tight junction proteins between jejunal mucosa cells were measured by the Western blot. Data were analyzed using polynomial contrasts in the Mixed procedure of SAS. Statistical differences among treatment means were considered significant with $P < 0.05$. Overall, viscosity of jejunal digesta was decreased ($P < 0.05$, 2.50 to 2.10 cP) as increasing β-mannanase from 0 to 600 Unit/kg diets. Increasing β-mannanase in the diets linearly decreased ($P < 0.05$) TNF-α (5.81 to 3.81 ng/g protein in the duodenum, 6.23 to 4.19 ng/g protein in the jejunum), IgG (1.44 to 1.07 mg/g protein in the duodenum, 1.20 to 0.80 mg/g protein in the jejunum), MDA (1.46 to 1.26 μmol/g protein in the duodenum, 1.06 to 0.69 μmol/g protein in the jejunum) and PC (7.11 to 4.22 μmol/g protein in the duodenum) of mucosa. Increasing β-mannanase in the diet linearly increased ($P < 0.05$) villus height (579 to 651 μm of duodenum, 426 to 516 μm of jejunum) and crypt depth (281 to 301 μm of duodenum, 175 to 246 μm of jejunum). Increasing β-mannanase in the diet linearly increased ($P < 0.05$) the number of proliferating cells (29.3 to 35.5%) and ZO-1 tight junction proteins (0.81 to 1.41) in the jejunum. Increasing β-mannanase in the diet, however, did not affect the growth performance of pigs during 45 to 55 d of age. In conclusion, dietary supplementation of β-mannanase (up to 600 Unit/kg diet) enhanced intestinal health by reducing the inflammatory response and oxidative stress which may be related to reduced viscosity of jejunal digesta. A 10-d feeding of β-mannanase, however, did not benefit the growth performance in nursery pigs.

Key Words: digesta viscosity, intestinal health, mannanase, nursery pig

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0930 Effects of dietary supplementation with xylanase on growth performance, ileal digesta viscosity, apparent ileal digestibility, and excreta noxious gas emission of broilers fed wheat-based diets. W. C. Liu*, J. H. Park, S. I. Lee, S. D. Upadhaya, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, South Korea*.

This study was conducted to evaluate the effects of dietary xylanase supplementation in wheat-based diets on growth performance, ileal digesta viscosity, apparent ileal digestibility, and excreta noxious gas emission of broilers. A total of 600 one-d-old male Ross 308 broilers were used in this 35-d growth trial. Birds with an initial average BW of 43 ± 0.6 g were randomly allotted into 4 treatments with 10 replicate pens per treatment and 15 broilers in each pen. Dietary treatments were as follows: (1) CON, basal diet; (2) T1, basal diet + 0.0125% xylanase (the concentration guaranteed 9000 U/g); (3) T2, basal diet + 0.025% xylanase; (4) T3, basal diet + 0.0375% xylanase. Broilers were weighed and feed consumption was recorded by pen on d 0, 18, and 35 to calculated BWG, ADFI, and FCR. From d 29 to 35, Cr_2O_3 was used as an indigestible marker and supplemented in the diets at a level of 2 g/kg. On d 35, 120 chicks (3 per pen and 30 per treatment) were slaughtered, and the ileal digesta was immediately collected for determining the ileal digesta viscosity and apparent ileal digestibility (AID) of nutrients. For analysis of excreta noxious gas emission, fresh excreta samples from each pen were collected in 2.6-L plastic boxes at the end of experiment. All data were analyzed by using the GLM procedure of SAS, orthogonal polynomial contrasts were used to test the linear and quadratic effects of the increasing levels of xylanase. Statements of statistical significance were based on $P < 0.05$. Dietary addition of xylanase improved (linear, $P < 0.05$) the BWG and decreased (linear, $P < 0.05$) the FCR during d 1–18 and d 0–35. Oral administration of xylanase led to a decrease (linear, $P < 0.01$) in ileal digesta viscosity. In addition, the AID of DM, CP, energy, and most amino acids, with the exception of Ile, Phe, Asp, Glu and Pro, were improved (linear, $P < 0.05$) by xylanase supplementation. Furthermore, xylanase supplementation reduced excreta NH_3 (linear, $P < 0.05$; quadratic, $P < 0.05$) and R.SH (linear, $P < 0.01$) emission. In conclusion, dietary xylanase supplementation in broilers' wheat-based diets could mitigate the detrimental effect of NSP from wheat, reduce the viscosity of gut contents, and improve nutrient digestibility, thus improving broilers' growth performance. Moreover, inclusion of xylanase not only led to more consistent and uniform performance, but it also reduced

the release of odor emissions from broiler houses.

Key Words: growth performance, ileal digesta viscosity, xylanase

0931 Effects of corn-expressed phytase on growth performance and gut health of nursery pigs. J. K. Lee*, H. Chen, I. Park, and S. W. Kim, *North Carolina State University, Raleigh*.

This study was conducted to determine the super-dosing effects of phytase from corn-expressed phytase (CEP, Agrivida, Inc., Medford, MA) on growth performance and gut health of nursery pigs. Pigs (16 barrows and 16 gilts; 21 d of age; 6.19 ± 0.71 kg BW) were individually housed and allotted to one of 4 dietary treatments based on a randomized complete block design with the initial BW and sex as blocks. Pigs were fed a basal diet supplemented with ground CEP to provide phytase activity at 0, 500, 1500, or 3000 FTU/kg during 2 phases (Phase 1: 10 d and Phase 2: 20 d) for a total period of 30 d. Dietary Ca and P were not reduced, with 0.83% Ca and 0.44% STTD P or 0.74% Ca and 0.36% STTD P during Phases 1 and 2, respectively. Feed intake and BW were recorded every 10 d. Plasma samples were collected on d 25 postweaning to measure cytokine tumor necrosis factor-α (TNF-α) and malondialdehyde (MDA). Pigs were euthanized on d 30 to collect tissues from the duodenum and jejunum for the evaluation of morphology, TNF- α, and MDA. Digesta were collected from the proximal jejunum to measure viscosity. Data were analyzed using polynomial contrasts in the MIXED procedure of SAS version 9.3 (SAS Inc., Cary, NC, USA). Increasing the levels of phytase increased (linear, $P < 0.05$) BW on d 20 (10.2 to 12.1 kg) and on d 30 (16.1 to 18.6 kg), increased (linear, $P < 0.05$) ADG from d 10 to 20 (0.32 to 0.49 kg/d), and tended to increase (linear, $P = 0.052$) overall ADG (0.33 to 0.41 kg/d). Increasing supplemental levels of phytase increased (linear, $P < 0.05$) villus height in the duodenum (420 to 559 μm) and jejunum (426 to 491 μm), and the villus height-crypt depth ratio (1.5 to 2.1) in the duodenum. Increasing levels of phytase tended to decrease (Con vs. $T_1 + T_2 + T_3$, $P = 0.089$) TNF- α (6.53 to 5.36 pg/mg) in the duodenum and tended to decrease (linear, $P = 0.080$) MDA (0.5 to 0.34 umol/g protein) in the jejunum. Viscosity of jejunal digesta tended to decrease (quadratic, $P = 0.078$) from 2.55 to 2.15 cP (at 1500 FTU/kg). In conclusion, super-dosing corn-expressed phytase up to 3000 FTU/kg enhanced the growth performance of nursery pigs with improved villus developments and reduced inflammatory cytokine levels and oxidative stress products.

Key Words: corn-expressed phytase, growth performance, gut health, nursery pigs

0932 Effects of xylanase and protease on gut health and growth performance of newly hatched broiler chickens. M. P. Herchler*, L. Zheng, and S. W. Kim, *North Carolina State University, Raleigh*.

This study was to investigate the effects of supplemental xylanase and protease (BRI, Durham, NC) on gut health and growth performance of broiler chickens (288-d-old, male) fed experimental diets for 28 d. Treatments were based on 2 × 2 factorial arrangement with xylanase (0 and 15,000 XU/kg) and protease (0 and 300 U/g) as 2 factors with 9 cages/treatment and 8 birds/cage. Birds and feeders were weighed weekly for calculation of ADG, ADFI, and feed:gain (F:G). On d 7 and 28, 2 birds per pen were randomly chosen to collect blood and gut tissues for immunoglobulin G (IgG), malondialdehyde (MDA), protein carbonyl, and morphology measurements. Ileal digesta were collected to determine viscosity and apparent ileal digestibility (AID). Digesta viscosity tended to decrease ($P = 0.059$) and decreased ($P < 0.05$) when both enzymes were used in wk 1 and 4, respectively, whereas it was not affected by using enzymes individually. Protease increased ($P < 0.05$) villus height (611 to 689 μm) in wk 4. Xylanase decreased ($P < 0.05$) concentrations of serum IgG (2.66 to 2.06 g/L) and ileal protein carbonyl (0.41 to 0.29 μmol/g protein) in wk 1. Protease tended to decrease ($P = 0.083$) serum protein carbonyl (0.78 to 0.66 μmol/L) in wk 1. Protease decreased ($P < 0.05$) ileal protein carbonyl (0.39 to 0.31 μmol/g protein) in wk 1, which was more effective ($P < 0.05$) with xylanase together. Protease decreased ($P < 0.05$) serum MDA (0.56 to 0.30 μmol/L) and ileal MDA (0.53 to 0.35 μmol/g protein) in wk 4. Xylanase did not affect AID, whereas protease tended to increase AID of DM ($P = 0.064$; 74.7 to 76.5%), which was more effective ($P < 0.05$) with xylanase together. In wk 1, xylanase decreased ($P < 0.05$) F:G (1.213 to 1.173) and tended ($P = 0.063$) to decrease ADFI (20.1 to 19.4 g/d), whereas protease reduced ($P < 0.05$) ADG (17.2 to 16.0 g/d) and ADFI (20.1 to 19.4 g/d). Overall, protease increased ($P < 0.05$) F:G (1.504 to 1.528) whereas tended ($P = 0.089$) to reduce ADG (51.3 to 50.2 g/d), which was more effective ($P < 0.05$) with xylanase together. Mortality was not affected ($P > 0.10$) by the treatments. In conclusion, xylanase and protease benefited gut health by decreasing digesta viscosity, enhancing gut morphology, decreasing gut oxidative stress, and increasing nutrient digestibility, whereas these benefits were not related to growth performance.

Key Words: broiler chickens, protease, xylanase

0933 Effect of supplemental enzyme on growth performance, digesta viscosity, apparent total tract digestibility of nutrients in nursery pigs. U. P. Tiwari*[1], H. Chen[2], S. W. Kim[2], and R. Jha[1], [1]*University of Hawaii at Manoa, Honolulu,* [2]*North Carolina State University, Raleigh*.

Arabinoxylans and mannans are present in high concentrations in coproducts like distillers dried grain with solubles (DDGS), which are not degraded by the endogenous enzymes of swine, increase the digesta viscosity, and subsequently reduce the digestibility of nutrients. Feed enzymes can mitigate the negative effect of fiber, thereby enhancing the utilization of relatively low-cost coproducts in swine feeding. Three enzymatic treatments (xylanase, mannanase, and xylanase + mannanase) were used in a 20-d feeding trial to evaluate the effect of supplemental enzymes on fiber degradation and nutrient digestibility in nursery pigs fed corn-soybean meal based diet with 15% DDGS. A total of 32 weaner pigs (PIC 337 × Camborough 22, initial BW 6.2 kg) were used in the study. Feed intake and BW were recorded weekly. On d 14, titanium dioxide was blended into experimental diet (0.3%) as an indigestible marker for calculation of digestibility. Fecal samples were collected over 3 consecutive days, from d 17 to 19. On d 19, pigs were fasted overnight, and exactly 4 h after refeeding on d 20 in the morning, pigs were euthanized by captive bolt followed by exsanguination. There was no significant effect of enzymes on the growth performance of pigs, as the 20-d period might not have been sufficient to show the change, as well as on the pH of jejunal, ileal, and colon digesta. Addition of xylanase reduced ($P < 0.05$) the viscosity of jejunal digesta (2.1 to 1.5 centipoise) and increased ($P < 0.05$) apparent total tract digestibility (ATTD) of acid detergent fiber (18.1 to 26.9%) and neutral detergent fiber (35.1 to 41.2%). Addition of mannanase tended to increase ($P = 0.060$) ATTD of neutral detergent fiber (35.1 to 41.4%). In conclusion, use of feed enzymes targeting fiber in coproducts degrades fiber, increases fiber digestibility, and decreases the viscosity of digesta, ultimately increasing the digestion and absorption of nutrients.

Key Words: coproducts, enzymes, fiber digestibility

0934 Effects of full fat or defatted rice bran and microbial xylanase on growth performance of weanling pigs. G. A. Casas*and H. H. Stein, *University of Illinois at Urbana-Champaign*.

The objective was to determine effects of increased concentrations of full fat rice bran (FFRB) or defatted rice bran (DFRB) in diets without or with supplementation of a microbial xylanase on growth performance and concentrations of tumor necrosis factor-α (TNF-α) and IgA in plasma of weaned pigs. A total of 532 pigs (initial BW: 9.3 ± 0.5 kg) were allotted to 14 diets in a randomized complete block design using 4 blocks and 2 replicate pens per diet in each block. A diet containing corn, soybean meal, and whey powder, and 6 diets containing corn, soybean meal, whey powder, and 10, 20, or 30% of either FFRB or DFRB were used. All diets were prepared without or with 16,000 units per kg of microbial xylanase (Econase XT-25, AB Vista, Marlborough, UK). All diets also contained 1500 units per kg of microbial phytase. On the last day of the 23-d experiment, blood samples were collected from one pig per pen to determine TNF-α and IgA. Results indicated that ADFI decreased linearly ($P < 0.05$) as inclusion of FFRB increased in diets, and that there was a tendency ($P = 0.08$) for reduced ADFI as DFRB increased in the diets. Pigs fed diets containing DFRB had greater ADFI ($P < 0.05$) than pigs fed diets containing FFRB, but ADG increased and then decreased (quadratic, $P < 0.05$) with increasing concentrations of FFRB or DFRB, in the diets. The G:F ratio was not affected by inclusion of DFRB in the diets but increased linearly and quadratically ($P < 0.05$) as the inclusion of FFRB increased, and G:F was greater ($P < 0.05$) in pigs fed diets containing FFRB than in pigs fed diets containing DFRB. There was a tendency for the concentration of TNF-α to decrease linearly ($P = 0.09$) as the inclusion of FFRB increased in the diet, but that was not the case when DFRB was added to the diets. Addition of xylanase had no effect on the variables evaluated. The concentration of IgA was not affected by inclusion of FFRB or DFRB in the diets. In conclusion, both FFRB and DFRB may be included in diets fed to weanling pigs from 2 wk post-weaning by at least 20% without compromising growth performance.

Key Words: pigs, rice bran, xylanase

935 Addition of optimal non-starch polysaccharide enzymes using in vitro method to a corn-soybean meal diet and a corn-miscellaneous meal diet for growing pigs. L. Gao, L. Chen, R. Zhong, L. Zhang, and H. Zhang*, *Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China*.

The objectives of the present study were to evaluate the effect of optimized non-starch polysaccharide (NSP) enzymes using an in vitro digestion method on the digestibility of energy and nutrients in a corn-soybean meal diet and a corn-miscellaneous meal diet (corn–soybean meal–rapeseed meal–cottonseed meal–sugar beet pulp meal diet) of pigs. In Exp. 1, the optimal NSP enzymes (cellulase, xylanase, β-glucanase, β-mannanase, α-galactosidase, and pectinase) of the two diets were screened using a quadratic regress-orthogonal rotary design. In Exp. 2, the effects of the optimal NSP enzymes on the digestibility of energy and nutrients in the 2 diets were determined. A total of 12 ileal-cannulated pigs (initial BW = 50.9 ± 4.9 kg) were allotted to 4 treatments in an incomplete block design (4´3), 4 diets (the 2 diets with or without the addition of optimum NSP enzymes) were fed to the growing pigs. The NSP enzymes had a quadratic effect on the in vitro

dry matter digestibility (IVDMD), and the optimal enzyme combination was 534 U/kg cellulase, 9984 U/kg xylanase, 1014 U/kg β-glucanase, 4081 U/kg β-mannanase, 252 U/kg α-galactosidase, and 107 U/kg pectinase in the corn-soybean meal diet (R^2 = 0.69, P = 0.04), and 960 U/kg cellulase, 17,178 U/kg xylanase, 406 U/kg β-glucanase, 19,023 U/kg β-mannanase, 307 U/kg α-galactosidase, and 97 U/kg pectinase in the corn-miscellaneous meal diet (R^2 = 0.72, P = 0.02), respectively. Pigs fed the corn-soybean meal diet with the addition of NSP enzymes had greater ($P < 0.05$) apparent ileal digestibility (AID) of DM, NDF, and insoluble NSP, and apparent total tract digestibility (ATTD) of soluble NSP and total NSP than those fed the diet without NSP enzymes. The AID of all nutrients, with the exception of the ether extract and the ATTD of GE, DM, CP, EE, and insoluble NSP, were greater in a corn-miscellaneous meal diet with the NSP enzymes than without the NSP enzymes ($P < 0.05$). The ATTD of total NSP content had a tendency (P = 0.05) to increase with the corn-miscellaneous meal diet having the addition of NSP enzymes. In conclusion, a corn-soybean meal diet and a corn-miscellaneous meal diet with the optimal NSP enzymes using in vitro digestion method can increase nutrient digestibility of diets fed to growing pigs.

Key Words: digestibility, energy, in vitro digestion method, non-starch polysaccharide enzyme, nutrient, pig

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0936 Growth performance, bone measurements, and P digestibility in nursery pigs fed diets supplemented with increasing levels of a new bacterial 6-phytase expressed in *Pseudomonas fluorescens*. F. N. Almeida*, M. Vázquez-Añón, and J. Escobar, *Novus International, Inc., St. Charles, MO*.

An experiment was conducted to determine the effects of a new bacterial 6-phytase expressed in *Pseudomonas fluorescens* (CIBENZA® PHYTAVERSE®, Novus International, Inc., St Charles, MO) on the growth performance, bone parameters, and P digestibility in nursery pigs. A total of 280 pigs (initial BW = 6.25 ± 1.03 kg) were randomly allotted to 1 of 5 treatments with 14 replications and 4 pigs/pen. Treatments included 1) a positive control (POS) that met requirements (NRC, 2012) for all nutrients, 2) a negative control (NEG) deficient only in standardized total tract digestible (STTD) P (−0.18% vs. POS), 3) NEG supplemented with 500 FTU/kg phytase (NEG+500), 4) NEG supplemented with 1000 FTU/kg phytase (NEG+1000), and 5) NEG supplemented with 2000 FTU/kg phytase (NEG+2000). Data were analyzed using the Mixed procedure (SAS® Institute, Cary, NC). Orthogonal polynomial contrasts were used to determine linear and quadratic effects of increasing levels of phytase. ADG, ADFI, and G:F were greater ($P < 0.01$) in POS fed pigs than in NEG fed pigs. The ADG was improved (linear and quadratic, $P < 0.01$) from 0.308 (NEG) to 0.475 (NEG+2000) kg as phytase supplementation level increased. Likewise, ADFI and G:F were also improved (linear and quadratic, $P < 0.01$) by increasing levels of phytase. Bone ash and bone P content were greater ($P < 0.01$) in pigs fed POS vs. pigs fed NEG (1.159 and 0.215 g vs. 0.557 and 0.101 g, respectively). As phytase supplementation increased, bone ash and P weight also increased (linear and quadratic, $P < 0.01$) compared with NEG fed pigs. Bone ash and P weight in pigs receiving NEG+2000 were not different ($P > 0.05$) from that of pigs receiving the POS diet (1.106 and 0.192 g vs. 1.159 and 0.215 g, respectively).Phytase supplementation improved (linear and quadratic, $P < 0.01$) the STTD of P from 17.31 (NEG) to 70.74% (NEG+2000). Results from this experiment demonstrate the efficacy of this new 6-bacterial phytase to improve growth performance, bone traits, and the STTD of P.

Key Words: bone, pig, phytase

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937 Nutritive value of cold-pressed soybean cake with or without extrusion or supplementation of multi-carbohydrase for pigs. T. A. Woyengo*[1], R. Patterson[2], and C. L. Levesque[1], [1]*South Dakota State University, Brookings,* [2]*Canadian Biosystems, Calgary, AB, Canada*.

The objectives were to determine the standardized ileal digestibility (SID) of AA and the NE value of cold-pressed soybean cake (CP-SBC), and the effect of extrusion or adding multi-carbohydrase to CP-SBC diet for growing pigs. Eight ileal-cannulated pigs (initial BW = 80 kg) were fed 4 diets in a replicated 4 × 4 Latin square design to give 8 replicates per diet. Diets included a cornstarch-based diet with CP-SBC, extruded CP-SBC, and SBC plus multi-carbohydrase (1200 U of xylanase, 150 U of glucanase, 500 U of cellulose, 60 U of mannanase, 700 U of invertase, 5000 U of protease, and 12,000 U of amylase/kilogram of diet; Superzyme CS, 1 g/kg); and a N-free diet. The CP-SBC was the sole source of protein in the CP-SBC-containing diets. The ratio of cornstarch to sugar and soybean oil in CP-SBC-containing diets was identical to the N-free diet to allow calculation of energy digestibility of CP-SBC by the difference method. The evaluated CP-SBC had been produced by heating the soybean seed at 105°C for 60 min followed by pressing the heated soybean seeds at less than 42°C (barrel temperature). On a DM basis, CP-SBC and extruded CP-SBC contained 47.8 and 47.1% CP, 15.6 and 10.5% ADF, 7.23 and 8.85% ether extract, 3.11 and 3.08% Lys, and 2.25 and 3.70 TIU/mg, respectively. Extrusion increased ($P < 0.001$) the SID of AA for the CP-SBC by an average of 12%. Also, extrusion increased ($P < 0.001$) the NE value of the CP-SBC from 2743 to 2853 kcal/kg of DM. Supplementation of CP-SBC diet with the multi-carbohydrase increased ($P < 0.05$) the SID of Arg and Pro and tended to increase ($P < 0.1$) the SID of Ile and Trp. However, the multi-carbohydrase supplementation did not affect the NE value of CP-SBC. In conclusion, the CP-SBC evaluated in the

present study could be an alternative source of AA and energy in swine diets, and its nutritive value can be increased by extrusion after the cold-pressing. However, there was little additional benefit in nutritional value of the CP-SBC gained with multi-carbohydrase supplementation.

Key Words: cold-pressed soybean cake, nutrient digestibility, pig

0938 Influence of *Acacia tortilis* leaf meal-based diets on growth performance of pigs. M. Khanyile, S. P. Ndou, and M. Chimonyo*, *University of KwaZulu-Natal, Pietermaritzburg, South Africa*.

The objectives of the study were to assess the nutritive value of *Acacia* leaf meals and to determine the optimum inclusion level of *Acacia tortilis* leaf meal in finishing pigs. Five dominant leguminous leaf meals namely, *Acacia tortilis*, *Acacia robusta*, *Acacia nilotica*, *Acacia nigrescens* and *Acacia xanthophloea*, were individually hand-harvested and analyzed for their chemical and physical properties. Although the crude protein content of *A. xanthophloea* and *A. tortilis* were similar, the latter was incorporated into the experimental diets as it had the lowest water-holding capacity and swelling capacity and moderate levels of condensed tannins. *A. tortilis* was also the most abundant in the locality. Thirty finishing male F_1 hybrid (Landrace × Large White) pigs with an initial weight of 60.6 (s.d. = 0.94) kg were randomly allotted to six diets containing 0, 50, 100, 150, 200, 250 g/kg DM inclusion levels of *A. tortilis* leaf meal. Each diet was offered ad libitum to five pigs in individual pens for 21 d. Average daily feed intake (ADFI), average daily gain (ADG), and gain:feed (*G*:*F*) ratio were measured every week. There was an increase in both ADFI and ADG ($P < 0.001$) as *A. tortilis* leaf meal increased, before they started to decrease. An increase in *A. tortilis* leaf meal levels in the diets caused a quadratic decrease ($P < 0.01$) in the *G*:*F* ratio. The change in ADFI, ADG, and *G*:*F* ratio during each week of successive feeding decreased ($P < 0.05$) with incremental levels of *A. tortilis* in the diets. Using piecewise regression (broken-stick analyses), it was observed that *A. tortilis* leaf meal can be included up to 129 g/kg DM in finishing pig feeds without negatively affecting the *G*:*F* ratio. The ability with which pigs utilize leaf meal-based diets improves with duration of exposure to such diets.

Key Words: *Acacia tortilis*, condensed tannins, feed intake, pig performance

0939 Different responses of Ross 308 and 708 broiler strains in growth performance and related properties to diet treatment with or without tributyrate glycerides. A. Bedford[1], H. Yu[1], M. Hernandez[1], J. Squires[2], S. Leeson[3], Y. Hou[4], and J. Gong[*1], *[1]Agriculture and Agri-Food Canada, Guelph, ON, Canada, [2]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [3]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [4]Wuhan Polytechnic University, Wuhan, China*.

Within genetically similar broiler strains, there can be significant performance differences, making strain selection an important decision for producers to meet their requirements. This study has investigated the differences in growth performance, including body composition, between Ross 308 and Ross 708 birds, and compared how each strain responds to the supplementation of tributyrin. Tributyrin is a butyric acid glyceride that has been shown to have multiple positive effects on broiler performance and can be a potential alternative to in-feed antibiotics. Two hundred and forty-day-old Ross 308 and 240-d-old Ross 708 birds were divided into treatment groups and fed either a basal diet or diets supplemented with low or high levels of tributyrin for 35 d. Neither the strain nor tributyrin supplementation had an effect on overall average daily gain or feed:gain ratios ($P > 0.05$). Ross 708 control birds had significantly decreased relative abdominal fat weight at 5 wk of age compared to Ross 308 control birds ($P < 0.05$), and tributyrin supplementation further decreased relative abdominal fat weight in Ross 708 birds ($P < 0.05$). Ross 708 control birds had significantly higher fat deposition in the breast muscle compared to Ross 308 controls ($P < 0.05$), and the addition of tributyrin lowered this deposition in both strains ($P < 0.05$). Breast muscle lipid profiles were significantly different between strains, with Ross 308 control birds having decreased saturated and monounsaturated fatty acids and increased polyunsaturated fatty acids compared to Ross 708 control birds ($P < 0.05$). Significant differences in the hepatic expression of genes associated with lipid metabolism (SREBP-1 and ATPCL) were observed both between strains and with tributyrin supplementation ($P < 0.05$). These results support the modulation of lipid metabolism by tributyrin and show that even genetically similar strains can perform significantly differently at the metabolic level and respond differently to dietary supplementation of tributyrin.

Key Words: broiler, tributyrin, growth performance

0940 Immunomodulatory effects of whole yeast cells and capsicum in weanling pigs challenged with pathogenic *Escherichia coli*. S. Wojnicki[*1], V. G. Perez[2], and R. N. Dilger[1], [1]*University of Illinois, Urbana,* [2]*ADM Animal Nutrition, Decatur, IL*.

Global concerns over antibiotic resistance triggered the development of nutritional technologies to support animal health. In weaned pigs, enterotoxigenic *Escherichia coli* infections are common. In this study, we sought to quantify the combined dietary effects of whole yeast cells (WYC) and capsicum (CAP) on performance and immune indices in weanling pigs experiencing an *E. coli* infection. Weanling pigs (32 barrows and 32 gilts, 21 d of age, 5.90 ± 1.03 kg BW) were allotted to experimental treatments in a randomized complete block design based on genetics, sex, and initial BW. Four pigs were individually housed within each containment chamber and assigned to 1 of 4 dietary treatments (n = 13), which included a control diet without or with 0.2% WYC (CitriStim, ADM, Decatur, IL) or 10 ppm of CAP, provided either alone or in combination. After receiving diets for 13 d, pigs were orally inoculated with F18$^+$ *E. coli* and maintained on the same diets for an additional 10 d; a separate cohort of pigs (n = 12) receiving the control diet was sham-inoculated using PBS. Body and feeder weights were recorded, and fecal swabs collected, on 0, 5, and 10 d post-inoculation (DPI), with blood sampled at 7 DPI for clinical outcomes. Data were analyzed as a 2-way ANOVA (infected pigs only), with a separate comparison between unchallenged and challenged control-fed pigs. While no interactive effects were observed for growth performance, main effects revealed that WYC increased (P < 0.05), and CAP decreased (P < 0.05), ADFI 0–10 DPI; reciprocal effects were observed for G:F due to a lack of differences in ADG. The challenge *E. coli* strain was undetectable in fecal swabs on 0 and 10 DPI but differed between unchallenged and challenged control-fed pigs at 5 DPI. Total bacterial counts were lower (P = 0.02) at 5 DPI in pigs fed CAP-containing diet, and the combination of additives elicited higher total bacteria counts compared with either additive alone (interaction, P = 0.03) at 10 DPI. Blood leukocyte counts were increased in infected pigs receiving the combination of additives compared with infected pigs on other dietary treatments (interaction, P = 0.04), and addition of WYC increased lymphocyte counts (main effect; P = 0.01) at 7 DPI. Overall, these data indicate that WYC and CAP have different effects on ADFI and individually or in combination may affect the immune response in weaned pigs experiencing an enterotoxigenic *E. coli* infection.

Key Words: *Escherichia coli*, yeast, essential oils

0941 Comparing the effects of zinc oxide, milk hydrolysate, yeast β glucan, and combination of milk hydrolysate/yeast β glucan on growth, gut microbiota, and cytokine gene expression in weaning piglets. *A*. Mukhopadhya[*1], J. V. O'Doherty[2], N. Noronha[3], M. T. Ryan[1], and T. Sweeney[1], [1]*School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland,* [2]*School of Agriculture and Food Science, University College Dublin, Dublin 4, Ireland,* [3]*Food for Health Ireland, University College Dublin, Dublin, Ireland*.

Concerns over the usage of prophylactic antibiotics and pharmacological doses of zinc (ZnO) are driving the need to develop natural sustainable alternatives to support gut health in the piglet during the post weaning period. Our hypothesis was that a diet consisting of a combination of yeast β-glucan (YBG) and sodium caseinate hydrolysate (NaCASH) will improve gut health in weaning piglets and replace the requirement for ZnO in the diet. Thus, the objective of this experiment was to compare the effects of supplementing the weaning piglet diet with ZnO, NaCASH, YBG, and a combination of NaCASH + YBG on piglet body weight (BW), gut microbiota, and gut cytokine gene expression. Forty 21-d-old piglets (7.3 ± 0.2 kg) were weaned and assigned to either 1) control diet, 2) control diet supplemented with 3.1 g/kg ZnO, 3) 0.25 g/kg NaCASH, 4) 0.25 g/kg YBG, or 5) 0.25 g/kg NaCASH + 0.25 g/kg YBG (combination) for 12 d (n = 8). Fecal scores per pen were recorded daily and BW recorded on Days 0, 6, and 12. Following sacrifice on Day 12, caecal and colonic digesta and colonic tissues were collected. Digesta samples were used to enumerate a selected panel of bacterial colonies by 16s rRNA QPCR, while tissue samples were used to evaluate a selected panel of cytokine gene expression by QPCR. Lower fecal scores were recorded in piglets from d 6–12 supplemented with either ZnO (P < 0.01) or the combination (P < 0.05) compared to control group. Similarly, overall ADG, FI, and gain to feed ratio were improved in ZnO and combination (P < 0.05) groups compared to the control group. However, only ZnO supplementation improved BW (P < 0.05) compared to control group. In caecal digesta, *Bacteroidetes* abundance was increased by ZnO and NaCASH supplementation (P < 0.05) compared to control group, whereas YBG group had higher enteropathogenic AEEC compared to control group (P < 0.05). In colonic tissues, while *IL-1α, IL-1β, IL-8*, and *IL-17* expression were downregulated in ZnO group, only *IL-1α* expression was downregulated in NaCASH and combination diet groups compared to control group (P < 0.05). Therefore, NaCASH or YBG individually did not improve weaning piglet growth or health, yet in combination they improved growth parameters similar to ZnO supplementation. Hence, these results substantiate our hypothesis that a YBG-NaCASH combination could be a suitable alternative to

zinc oxide during the weaning period.

Key Words: gastrointestinal tract, post-weaning nutrition, inflammation

0942 Effects of a standardized blend of carvacrol, cinnamaldehyde, and capsicum oleoresin on performance of growing finishing pigs using multiple trial analysis methodology.

C. Oguey*, *Pancosma, Geneva, Switzerland*.

The optimization of performance at limited expense in growing-finishing pigs is a constant concern of producers. Many phytomolecules have been reported to influence production efficiency of monogastric animals. The objective was to assess the effect of a standardized protected blend of cinnamaldehyde, carvacrol, and capsicum oleoresin (XT, XTRACT® 6930, Pancosma, Geneva, Switzerland) on performance and carcass quality of growing-finishing pigs. The database regrouped 14 trials organized in 7 studies (500 pigs; mean initial BW of 47.0 kg, mean duration of 69.0 d, mean XT dose of 83.5 g/t). All trials reported side-by-side comparisons of an unsupplemented control diet and the inclusion of XT in pigs. Outcomes selected were DMI, ADG, FCR, carcass yield, fat thickness in G2, and meat %. Data were analyzed using a mixed model with the TRIAL variable as a random effect and the TRT variable as a fixed effect. Mean values were calculated using the LSMEANS procedure of XLstat, weighting the data for the variance among trials. Results showed that XT increased ADG by 2.6% ($P < 0.05$) and reduced FI and FCR by. respectively. 1.1% ($P < 0.05$) and 3.8% ($P < 0.01$). For these outcomes, the lower limit of the 95% confidence interval was then used to assess the effect of XT supplementation on fattening duration or pig weight at slaughter. For a fixed slaughter weight of 120 kg, the effect of XT on performance resulted in a reduction of growing and fattening by 2.2 d. After 115 d of fattening, XT increased final BW by 1.7 kg. Finally, XT did not affect carcass yield and fat thickness G2 ($P > 0.50$) but increased meat percentage by 1.2% ($P = 0.06$). These findings suggest that the dietary supplementation of XT improves performance of growing-finishing pigs.

Key Words: multiple analysis, phytomolecules, pig performance

0943 Extracts of laminarin improve growth rate and small intestinal morphology in newborn chicks but do not influence *Campylobacter* colonization.

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Promoting growth performance while limiting the proliferation of bacteria such as *Campylobacter jejuni* is a key goal of the broiler industry. Therefore, the objective of this study was to evaluate the effects of supplementing the post-hatch diet with laminarin and fucoidan extracts on growth performance, small intestinal morphology, and *C. jejuni* colonization following an experimental challenge in 13 d old chicks. The experiment consisted of three diets: 1) basal diet, 2) basal diet + 200 ppm laminarin (LAM), and 3) basal diet + 200 ppm LAM and 160 ppm fucoidan (LAM/FUC). Day-old Ross chicks ($n = 135$) were housed in groups of three, with 15 replicates per treatment group. On Day 3, all chicks were orally gavaged with 0.1 ml × 10^6 colony forming units of *C. jejuni.* Following humane sacrifice on Day 13, caecal digesta samples were collected for enumeration of *C. jejuni* and *Lactobacillus*. Ileal tissue was also collected post-slaughter to examine small intestinal morphology. Chicks offered diets containing the seaweed extracts LAM or LAM/FUC had increased live weights (311 g, s.e. 4.14 and 302 g, s.e. 3.99, respectively, $P < 0.05$) compared to the basal diet (290 g, s.e 3.99) at the end of the experimental period (Day 13). The mean total intake for the chicks fed the LAM and LAM/FUC extracts at the end of the experiment (Day 13) were 373 g/d (s.e. 3.89), 411 g/d (s.e. 4.03), and 411 g/d (s.e 3.89), respectively, with chicks fed the basal diet having lower feed intake compared to both the LAM and LAM/FUC fed chicks ($P < 0.05$). Dietary inclusion of LAM/FUC combination increased the feed conversion ratio (FCR) (1.63 g/g vs. 1.69 g/g; s.e ± 0.02) compared to the basal diet ($P < 0.05$). Chicks offered the LAM diet had increased ileal villus height compared to chicks offered the basal diet (307 µm vs. 231 µm s.e ± 17.24, $P < 0.05$). There was no effect of LAM or LAM/FUC extracts on the proliferation of *C. jejuni* or on *Lactobacilli* numbers in the cecum. In conclusion, supplementation with LAM or LAM/FUC in the post-hatch period improved growth performance and positively modified small intestinal architecture but did not impact the extent of *C. jejuni* proliferation.

Key Words: broiler chicks, *Campylobacter jejuni*, performance, histology, seaweed

0944 Effects of defatted microalgae on nutrient digestibility and retention in broiler chicks.
T. Sun*, A. D. Magnuson, L. Tao, M. Burke, M. Barcus, and X. G. Lei, *Cornell University, Ithaca, NY*.

This experiment was to determine the impact of supplemental 10% defatted microalgae (*Nannochloropsis oceanica*, 45% CP and 3.8% ether extraction, EE) from biofuel production in a corn-soybean meal basal diet (BD) on nutrient digestibility and retention in broiler chicks. Day-old hatchling Cornish Giant cockerels were divided into two groups (5 cages/group, 4–5 chicks/cage) and fed the BD or the microalgae diet for 6 wk. Starting at wk 3, chicks were fed diets containing 0.2% chromic oxide as an indigestible marker. Total excreta of individual cages was collected daily for consecutive 5 and 3 d during wk 5 and 6, respectively. At the end of wk 6, chicks were euthanized to collect ileal digesta from 1 chick/cage. Concentration of DM, CP, EE, AA, and chromic oxide in digesta, excreta, and diets were assayed. Apparent nutrient retention was calculated based on total excreta collection and chromic oxide as an indigestible marker. The latter was also used to estimate apparent ileal digestibility of nutrients. Data were analyzed by Student *t* test. Chicks fed the two diets had similar ADFI and G:F ratio, although those fed the microalgae diet had 3–5% ($P < 0.05$) heavier BW than chicks fed the BD. Feeding the microalgae diet enhanced ($P < 0.05$) and decreased ($P < 0.05$) apparent retention and digestibility of DM by 3.3% and by 1.8%, respectively. Feeding the microalgae diet elevated (1.6 to 3.8%, $P < 0.05$) apparent retention of EE determined by the indirect method, but not by the direct method. Supplemental defatted microalgae did not affect apparent retention of CP determined by both methods at either time point except for a 17.8% decrease ($P < 0.01$) by the 5-d total collection. Feeding the microalgae diet decreased ($P < 0.05$) apparent ileal digestibilities of 8 essential AA and 6 nonessential AA, ranging from 32% for isoleucine to 7% for glutamic acid. Feeding that diet decreased ($P < 0.05$) apparent retention of 6 essential AA and 5 nonessential AA, ranging from 16% for threonine to 0.6% for leucine. In conclusion, supplementing 10% of defatted microalgae in the corn-soybean meal diet did not show consistent effect on apparent retention or ileal digestibility of DM, EE, or CP determined by the two methods at the two time-points, but the diet decreased apparent retention or ileal digestibility of a number of AA. (Supported by USDA/DOE Biomass R&D Initiative Grant and a Cornell Hatch Grant).

Key Words: algae, amino acid, broiler, digestibility, retention

0945 Defatted microalgae-mediated enrichment of n-3 polyunsaturated fatty acids in muscle of broiler chicks was not affected by supranutrition of vitamin E and(or) Se.
L. Tao, T. Sun, A. D. Magnuson, M. Burke, and X. G. Lei*, *Cornell University, Ithaca, NY*.

We previously demonstrated an enrichment of docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA) in breast and thigh muscles of broiler chicks fed defatted microalgae. This study was to determine if that enrichment affected the physical quality of the meat and was enhanced by feeding less corn oil and extra vitamin E/Se. Day-old hatchling Cornish Giant cockerels (total: 216) were divided to six groups (6 replicate cages/treatment and 6 chicks/cage). The treatments included Diet 1 (control) = corn-soybean meal based diet containing 4% corn oil, 25 IU vitamin E as dl-α-tocopherol/kg, and 0.2 mg Se as sodium selenite/kg; Diet 2 = Diet 1 + 10% defatted *Nannochloropsis oceanica* (45.1% CP, 3.8% EE); Diet 3 = Diet 2 − 2% corn oil; Diet 4 = Diet 3 + 75 IU vitamin E/kg; Diet 5 = Diet 3 + 0.3 mg Se/kg; and Diet 6 = Diet 3 + 75 IU vitamin E and 0.3 mg Se/kg. The experiment lasted for 6 wk. Data were analyzed by one-way ANOVA with Bonferroni's post-hoc comparisons tests or by Student's *t* test (GraphPad Prism 6.0). Diets produced no difference in growth performance of chicks. Feeding Diet 2 enhanced ($P < 0.05$) concentrations of breast CP (14%), glycine (60%), and serine (70%) at wk 6 compared with the control. Feeding Diet 2 elevated ($P < 0.05$) DHA and EPA concentrations of both breast and thigh muscles over the control, whereas feeding Diets 3–6 did not further enhance the enrichments. Both breast and thigh muscles were cooked (175°C oven for 30 min) for texture analysis. Springiness of the thigh muscles was elevated by 23% ($P < 0.05$) in chicks fed Diet 2 than in those fed Diet 1. Chewiness of the breast muscle was elevated by 41–83% ($P < 0.05$) in chicks fed Diet 5 than in those fed the other diets. Chewiness of the thigh muscles was elevated by 79% ($P < 0.05$) in chicks fed Diet 5 than in those fed Diet 1. In conclusion, supplementation of 10% defatted microalgae in the corn-soybean meal basal diet effectively enriched DHA and EPA in breast and thigh muscles, whereas inclusions of extra vitamin E and Se or less corn oil in the diets did not enhance the enrichments. The additional Se, however, improved chewiness of the muscles. (Supported in part by a USDA/DOE Biomass R&D Initiative Grant and a Cornell Hatch Grant).

Key Words: chicken quality, DHA, EPA, microalgae, selenium, vitamin E

0946 Effect of supplementing milk during first 4 d postweaning on growth performance, energy digestibility, gut morphology, and severity of diarrhea for nursery pigs in a commercial farm.
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The experiment was conducted to evaluate the effects of supplemental milk (6.5, 8.7, 10.9, and 10.9 g DM milk/pig/d; 10% of estimated feed intake) during the first 4 d postweaning on growth performance, energy digestibility, and severity of diarrhea of nursery pigs. A total of 644 crossbred pigs, weaned at 3 wk of age (6.4 ± 1.2 kg of BW), were randomly assigned to 2 dietary treatments (12 pens/treatment, 27 pigs/pen) in a randomized complete block design with sex and initial BW as blocks. Pigs were fed pellet feed either with or without milk supplementation from d 1 to 4 postweaning (4 times daily) in a T-shaped feeder that was placed in the pens for 2 h at each feeding. All pigs had free excess to another nursery feeder with the same pellet feed during the entire nursery period in 3 phases (phase I: 10 d; phase II: 14 d; and phase III: 25 d). Fecal score was evaluated daily according to the observation of fresh feces in pens from d 1 to 4 postweaning following a scale of 1 to 3 (3 = liquid diarrheal feces). Titanium dioxide (0.3%) was added in the phase I pellet feed as an indigestible marker to measure apparent ileal digestibility (AID) of DM and GE. Jejunal tissue and ileal digesta from 1 pig/pen were collected at d 4 and 10 postweaning. Data were analyzed using the Mixed procedure of SAS. Statistical differences among treatment means were considered significant with $P < 0.05$. The results showed that milk supplementation did not affect the ADG and ADFI during the entire nursery period. However, supplementing milk tended to increase ($P = 0.073$) the G:F ratio (0.708 to 0.748) during phases I and II. The AID of DM and GE at d 10 of postweaning did not differ between treatments. Supplemental lipid milk tended to enhance ($P = 0.062$) villus height:crypt depth (2.04 to 2.15) in the jejunum at d 10 postweaning. Supplemental milk tended to reduce ($P = 0.065$) the fecal score (2.04 to 1.84) and decreased ($P < 0.05$) mortality (4.35 to 1.55%) during the entire nursery period. Collectively, supplementing milk 4 times daily for the first 4 d postweaning helped nursery pigs by enhancing feed efficiency and gut morphology with decreased severity of diarrhea and mortality during phases I and II.

Key Words: growth performance, gut health, milk, nursery pigs

0947 Effects of dietary lysophospholipid complex on apparent ileal digestibility and growth performance in nursery pigs.
L. Zheng*, A. C. Weaver, and S. W. Kim, *North Carolina State University, Raleigh*.

Two experiments were conducted to evaluate the effect of dietary lysophospholipid complex (LPC; Lipidol, Easybio System, Korea) on apparent ileal digestibility (AID) and growth performance of nursery pigs. The LPC used in this study includes lysolecithin, lysophosphatidylinositol, lysophosphatidylethanolamine, and lysophosphatidic acid (5%) with calcium silicate as a carrier (95%). In Exp. 1, 24 newly weaned pigs (12 barrows and 12 gilts at 7.2 ± 0.1 kg BW) were randomly allotted to 2 treatments in a randomized complete block design. Sex and initial BW were used as blocks. Pigs were fed a basal diet supplemented with either 0 or 0.1% LPC in 2 phases (7 and 12 d, respectively). Titanium dioxide (0.5%) was added to the diets from d 14 as an indigestible external marker. Body weight and feed consumption were recorded on d 7, 14, and 19. On d 19, jejunal digesta were collected to measure viscosity, and ileal digesta were collected to measure AID of DM, GE, lipid, and CP. In Exp. 2, 150 pigs at 6 wk of age (75 barrows and 75 gilts, 14.2 ± 0.2 kg BW) were randomly allotted to 2 treatments in a randomized complete block design. Sex and initial BW were used as blocks. Pigs were fed a basal diet supplemented with either 0 or 0.1% LPC for 3 wk. Body weight and feed consumption were recorded weekly. Blood samples were collected at the end of the study to measure the concentrations of tumor necrosis factor-α and immunoglobulin G to observe general health status of the pigs. Data were analyzed using the Mixed Model procedure of SAS. In Exp. 1, AID of lipid tended to be increased (72.7 to 84.2%, $P = 0.086$) by LPC whereas AID of DM, GE, and CP were not affected. Viscosity of jejunal digesta were not affected by LPC. Dietary LPC increased ADG (681 to 774 g/d, $P < 0.05$) and ADFI (1000 to 1089 g/d, $P < 0.05$) of nursery pigs from d 14 to 19. In Exp. 2, dietary LPC tended to increase ($P = 0.072$) ADG (664 to 708 g/d) during the 3-wk period whereas ADFI and G:F were not affected by dietary LPC. Serum concentrations of tumor necrosis factor-α and immunoglobulin G were not affected by dietary LPC. In conclusion, dietary supplementation of LPC improved the growth of nursery pigs, potentially by enhancing lipid digestibility.

Key Words: apparent ileal digestibility, growth performance, lysophospholipid, nursery pigs

0948 Effects of dietary supplementation of phytobiotics on intestinal health and growth performance of nursery pigs. I. Park*, J. K. Lee, J. Wang, and S. W. Kim, *North Carolina State University, Raleigh*.

This study was to determine the effects of dietary supplementation of phytobiotics (By-O-reg, Advanced Ag Products, Hudson, SD) on growth efficiency and intestinal development of nursery pigs. Phytobiotics included encapsulated oregano essential oil. Forty pigs (20 barrows and 20 gilts at 6.4 ± 0.3 kg BW) were randomly allotted to 4 treatments (2 × 2 factorial arrangement) with 10 pens (1 pig per pen) per treatment based on a randomized complete block design, and fed the experimental diets for 3 wk. Two factors were antibiotic growth promoter (AGP; 0 or 0.5 g/kg) and phytobiotics (0 or 0.5 g/kg diet), respectively. All diets were formulated to meet or exceed the NRC nutrient requirements. Feed intake and body weight were measured weekly. Blood samples were taken on d 20 to measure tumor necrosis factor-α (TNF-α), immunoglobulin G (IgG), IgA, and protein carbonyl (PC). On d 21, all pigs were euthanized to obtain the duodenal and jejunal mucosa and tissue. The mucosa samples were used to measure TNF-α, IgG, IgA, and PC. The tissues were used to measure morphology. Data were analyzed using the Mixed procedure in SAS with factors, interaction between factors, and sex as fixed effects and initial BW as a random effect. Interaction between factors were again analyzed using PDIFF to evaluate a different effect of each treatment. Overall, there were AGP × phytobiotics interactions ($P < 0.05$) on ADG and G:F. Among these interactions, both dietary AGP ($P = 0.071$; 627 g/d) and phytobiotics ($P = 0.057$; 624 g/d) tended to increase ADG compared with the basal diet (543 g/d) at wk 3. Dietary phytobiotics increased ($P < 0.05$) jejunal villus height (443 to 471 μm). Dietary phytobiotics decreased ($P < 0.05$) the concentrations of TNF-α (4.41 to 3.82 ng/g protein) and IgG (1.42 to 1.19 μg/mg protein) in the jejunum and PC (4.2 to 2.9 nmol/mg protein) in the plasma. Dietary AGP tended to decrease ($P = 0.063$) jejunal IgA levels (1.60 to 1.14 μg/mg protein) in the jejunum. Collectively, both dietary AGP and phytobiotics enhanced ADG only when they were used independently. A combinational use of AGP and phytobiotics had negative effects on growth performance. Dietary phytobiotics improved jejunal development by reducing inflammatory and humoral immune reaction.

Key Words: antibiotic growth promotor, growth performance, intestinal health, nursery pigs, phytobiotics

0949 Growth performance and toxic response of broilers fed diets containing unfermented or fermented cottonseed meal. J. L. Xiong[1], L. Y. Wu*[1], H. L. Zhou[2], Z. J. Wang[1], F. T. Meng[1], and L. H. Miao[1], *[1]Hubei Key Laboratory of Animal Nutrition and Feed Science, Wuhan Polytechnic University, Wuhan, China, [2]Xiangyang Engineering Research Center of Animal Medicine, Xiangyang Vocational and Technical College, Xiangyang, China.*

Cottonseed meal (CSM) is produced locally in sizeable quantities in China, but the amount of CSM used in animal diets has been limited mainly by the presence of toxic gossypol. Microbial fermentation is now known as one of the most promising detoxification techniques of CSM. Therefore, reliable evaluation of fermented cottonseed meal (FCSM) can give guidance on its appropriate dose in animal diets to ensure animal health and welfare. The objective of this study was to verify the hypothesis that the reduced free gossypol content and the improved growth performance were not the only marker factors to evaluate FCSM using in broiler diets. A total of 150 1-d-old male Cobb 400 broilers were randomly assigned to 3 dietary treatments with 5 replications of 10 birds per treatment and were fed diets with 31.0% soybean meal (SBM) (control), 15.5% SBM and 15.5% CSM, 15.5% SBM and 15.5% FCSM until 21 d of age, respectively. Birds were weighted after 12 h feed withdrawal on the end day, and then were slaughtered for measure of organ weights. Blood samples were collected through a jugular vein for analysis of serum enzyme activities on the finishing day. All data were statistically analyzed by SAS software. The level of significance was based on probability of 0.05. Fermentation decreased free gossypol from 583.40 to 191.70 mg/kg CSM, and degraded total gossypol from 5830.19 to 3882.91 mg/kg CSM. Compared with the control, the diet with 15.5% FCSM did not affect ($P > 0.05$) average daily growth and feed conversion ratio, while the diet containing 15.5% CSM decreased ($P < 0.05$) these parameters. However, the diet with 15.5% FCSM, similar with the diet containing15.5% CSM, increased ($P < 0.05$) the relative weight of liver and the activity of serum alanine aminotransferase, and decreased ($P < 0.05$) the relative weight of thymus compared with the control. In conclusion, residual gossypol or/and degradation products of gossypol in FCSM may still be hepatotoxicity and immunotoxicity, even though free gossypol and total gossypol have been markedly reduced so as not to alter adversely growth performance of broilers fed the diet with 15.5% FCSM, as half replacement of the SBM in the control.

Key Words: cottonseed meal, gossypol, fermentation, broilers

0950 Protein value of eight triticale genotypes for pigs based on standardized ileal amino acid digestibility. E. J. P. Strang[*1], M. Eklund[1], P. Rosenfelder[1], J. K. Htoo[2], and R. Mosenthin[1], *[1]University of Hohenheim, Institute of Animal Science, Stuttgart, Germany, [2]Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany.*

The study was conducted to determine the chemical composition, physical characteristics and standardized ileal digestibility (SID) of CP and AA of 8 currently available genotypes of triticale fed to growing pigs. The experiment was conducted with 8 barrows (initial BW of 30 ± 2 kg) that were fitted with a simple T-cannula at the distal ileum. The pigs were randomly allotted to an 8 × 8 Latin square design. Diets were based on 1 of the 8 triticale genotypes each, with triticale as the sole source of CP and AA. An N-free diet was fed to determine basal ileal endogenous losses of CP and AA. Diets were supplemented with titanium dioxide as an indigestible marker, and fed at a daily intake level of 4% of pigs' average BW corresponding to about 3 times the pigs' energy requirement for maintenance (106 kcal of ME/kg of $BW^{0.75}$). Each experimental period consisted of 5 d for adaptation to the diets and 2 d for ileal digesta collection. Ileal digesta samples were collected consecutively for a total of 24 h. Data were analyzed by the Mixed Procedure of SAS with genotype and pig as fixed effects; period and period × pig were considered as random effects. The CP and non-starch polysaccharide (NSP) contents (as-fed basis) of the 8 triticale genotypes ranged from 10.5 to 11.8% and 8.5 to 10.0%, respectively. The greatest contents of NDF, ADF and ADL in the 8 genotypes amounted to 14.9, 2.9 and 0.6% (as-fed basis), respectively. Among the 8 genotypes, SID of CP, Lys, Met, Thr and Trp ranged from 81 to 85, 72 to 77, 84 to 87, 73 to 77 and 79 to 83%, respectively. The SID of CP and AA did not differ among the 8 triticale genotypes, except for SID of Arg, Glu and Gly ($P \leq 0.05$). The SID of CP and AA was not affected by NSP or NDF content due to the small variations of these fiber fractions among genotypes. Compared to SID values for triticale in current feed tables, the SID of CP, Lys, Met and Trp in the present 8 triticale genotypes was up to 4, 4, 4, and 1%-units lower, respectively, and up to 5%-units higher for Thr. These differences in SID of AA need to be accounted for in diet formulation for pigs when new genotypes of triticale are used.

Key Words: amino acid digestibility, growing pigs, triticale

0951 Effect of metabolizable energy and sulfur amino acid levels on productive performance and economic return of laying hens. C. Gallardo[*1] and E. Salvador[2], *[1]University of São Paulo, Pirassununga, Brazil, [2]National University of San Luis Gonzaga, Ica, Peru.*

One trial was conducted to evaluate the effect of metabolizable energy (ME) and sulfur amino acids (AAAS) on the productive performance and economic return of laying hens. A total of 405 ISA Brown laying hens (5 birds/pen) of 30 wk of age were distributed in a randomized experimental block design in a 3 × 3 factorial arrangement, composed of three levels of ME (2,646, 2,793 and 2,940 Mcal/Kg) and 3 levels of SAAs (0.67, 0.71 and 0.745%). Egg production, feed intake, feed conversion ratio, egg weight and egg mass, ME intake, SAAs intake, Haugh unit and feed cost (kg of egg mass), were evaluated. Significant interaction ($P < 0.05$) between ME × SAAs was observed on feed intake, feed conversion, ME intake and SAAs intake. 2,793 Mcal/kg of ME and 0.745% of SAAs propitiated higher ($P < 0.05$) feed intake, SAAs intake and better feed conversion ratio. Birds fed low-ME and SAAs diets showed low feed intake, egg production, feed conversion, egg mass, ME intake and SAAs intake. Diets providing 2,793 Mcal/kg of ME maximized ($P < 0.01$) egg production and egg mass. While Diets providing 0.745% of SAAs maximized ($P < 0.05$) egg weight and egg mass. The diet with 2,793 Mcal/kg of ME and 0.745% of SAAs had the lowest feed cost and the higher profit per kg of egg mass. Thus, the best productive performance and economic return of laying hens diet may be obtained with levels of 2,793 Mcal/kg of ME and 0.745% of SAAs.

Key Words: Egg production, intake, egg mass

0952 Intestinal microbiota, microbial metabolites and carcass traits are changed in a pig model fed a high-fat/low-fiber or a low-fat/high-fiber diet. S. N. Heinritz[*1], E. Weiss[1], M. Eklund[1], T. Aumiller[1], S. Messner[1], C. M. E. Heyer[1], S. Bischoff[2], and R. Mosenthin[1], *[1]University of Hohenheim, Institute of Animal Science, Stuttgart, Germany, [2]University of Hohenheim, Department of Nutritional Medicine, Stuttgart, Germany.*

For gastrointestinal functions and health, the intestinal microbiota and its metabolites appear to be an important factor. However, further elaboration of potential relationships between nutrition, gut microbiota, and host's health by means of a suitable animal model are required. The present study was designed to examine the impact of diets high in fat or fiber content, thus rather representing an "unhealthy" or "beneficial" diet, on gut microbiota composition, microbial activity, and carcass traits by using the pig as a model for humans. Eight pigs (initial BW 28 ± 2 kg) were allotted to 2 treatments,

either fed a low fat/high fiber (LF), or a high fat/low fiber (HF) diet for 7 wk. Then, pigs were slaughtered to determine carcass and intestinal weights, as well as backfat thickness. Digesta samples of cecum and colon were taken to measure short-chain fatty acid (SCFA) concentration and gene copy numbers of total eubacteria, *Lactobacillus* spp., *Enterobacteriaceae*, *Bifidobacterium* spp., and *Bacteroides-Prevotella-Porphyromonas* (*Bacteroides* group) by use of real-time qPCR. Body weight at slaughter was 72.5 kg for the HF treatment and 77.1 kg for the LF treatment ($P > 0.05$). Carcass weight was also similar for both treatments, whereas full stomach and colon as well as liver weights were higher for the LF when compared to the HF treatment ($P < 0.05$). Gene copy numbers of total bacteria in the cecum digesta were higher in the HF compared to the LF treatment ($P < 0.05$), yet abundance did not differ in colon digesta. *Bifidobacterium* spp. occurred in higher numbers in the LF treatment, both in cecum and colon digesta ($P < 0.05$). Higher numbers in HF than in LF pigs were found for the *Bacteroides* group ($P < 0.05$) and *Enterobacteriaceae* ($P < 0.001$) in cecum and colon digesta. Total SCFA, acetate and butyrate showed higher colonic concentrations in LF than in HF pigs ($P < 0.05$), while in cecal digesta of LF only acetate and butyrate concentrations were higher ($P < 0.05$). Results confirmed the trophic action of dietary fiber on epithelium of digestive organs and revealed that the low-fat/high-fiber diet stimulated beneficial bacteria and SCFA production, especially butyrate. On the other hand, the high-fat/low-fiber diet promoted potential pathogenic bacteria. These findings are comparable to those in humans and are in support of the potential of the pig to serve as model for assessing diet-gut-microbiota interactions.

Key Words: dietary fat/fiber content, intestinal microbiota, pig model

0953 Use of zinc oxide nanoparticles as growth promoter for weanling pigs. N. C. Milani*, N. Y. Ikeda, M. Sbardella, and V. S. Miyada, *Universidade de São Paulo, Piracicaba, Brazil.*

Pharmacological levels of zinc (as ZnO) have been used in weanling pig diets for diarrhea control and growth performance improvement. Due to its low absorption, Zn-excretion has motivated environmental concerns. Thus, ZnO nanoparticles (ZnO-N) appear to be an alternative to reduce zinc oxide (ZnO) use in diets, once this form has shown higher antimicrobial activity. The purpose of this study was to evaluate the effects of dietary ZnO-N on performance and diarrhea occurrence of weanling pigs. One hundred and ninety-two 21d-weaned pigs (5.90 ± 0.83 kg BW) were used in a randomized complete block design experiment with 6 treatments, 8 replications per treatment, and 4 animals per experimental unit (pen). The treatments were: negative control (NC): basal diet (based on corn, soybean meal, dried whey and dried plasma) with 100 mg Zn (as ZnO)/kg diet; positive control (PC): basal diet with 2400 mg Zn (as conventional ZnO, 150nm)/kg diet and basal diet with 12, 24, 48 or 96 mg Zn (as ZnO-N, 70nm)/kg diet. Pigs were fed dietary treatments from 1 to 21 d feeding period followed by a common diet (same diet for all treatments) from 22 to 35 d feeding period. ANOVA and polynomial regression analysis (for levels of Zn as ZnO-N) were performed. No effects of Zn levels (as ZnO-N) were observed on performance and diarrhea occurrence (Table 1). The PC had higher ADFI and lower diarrhea occurrence compared to NC and Zn (as ZnO-N) levels during the first 21 d post-weaning period ($P = 0.0001$), without affecting ADG, G:F and BW. No residual effects of treatments were observed during 22 to 35-d period, when all pigs were fed with same diet. Therefore, ZnO-N was not effective for post-weaning diarrhea control and growth rate improvement.

Key Words: nanoparticle, performance, pigs, zinc oxide

Table 0953.

Table 1. Effects of dietary zinc oxide on the performance and diarrhea occurrence of weanling pigs

Item	Treatments						SEM	P-Value
	2,400 mg Zn/kg	Zn (as ZnO-N) levels, mg/kg						
		0	12	24	48	96		
Initial BW, kg	5.89	5.90	5.89	5.89	5.90	5.88	0.28	0.7692
1 to 21d period								
BW, kg	13.24	12.16	12.83	12.38	12.46	12.27	0.52	0.1192
ADG, g/d	349.85	298.24	330.43	309.23	312.18	303.94	17.44	0.1149
ADFI, g/d	513.27	434.45*	464.46*	440.24*	446.26*	434.88*	18.69	0.0013
Diarrhea[1],%	3.86	24.60*	22.91*	25.14*	20.68*	19.34*	3.38	0.0001
22 to 35 d period								
BW, kg	19.76	18.97	19.68	19.49	19.41	19.01	0.81	0.8632
ADG, g/d	447.35	497.21	481.6	512.58	499.61	490.15	28.70	0.5716
ADFI, g/d	804.80	891.79	799.86	857.10	843.26	825.42	25.95	0.1258
Diarrhea[1], %	5.35	3.72	6.69	6.17	8.18	6.47	2.41	0.8493

*Different from positive control (2,400 mg Zn/kg as ZnO) by orthogonal contrast test (P<0.05)
[1]Diarrhea occurrence in each period (% of days)

0954 Effect of dietary flaxseed oil on growth performance, nutrient digestibility, blood profiles, and meat quality in pigs. P. Y. Zhao*, T. S. Li, S. Shanmugam, S. Kathannan, R. X. Lan, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, South Korea.*

Alpha-linolenic acid (ALA) is the parent compound of the omega-3 fatty acids, which have several specific metabolic and structural roles within the body. However, ALA can't be synthesized by mammals. As flaxseed oil is rich of ALA, 2 experiments were conducted to investigate the effect of dietary flaxseed oil in pigs. In Exp. 1, 135 weanling pigs (5.50 ± 0.42 kg) were used in a 4-wk trial and were allotted to 3 treatments: 1) CON, basal diet, 2) FO0.5, CON + 5 g/kg flaxseed oil, 3) FX1, CON + 10 g/kg flaxseed oil. There were 9 replications with 5 pigs per pen. In Exp. 2, 40 finishing pigs (89.90 ± 0.41 kg) were used in a 4-wk trial and allotted to 2 treatments: 1) CON, basal diet, 2) FO0.5, CON + 5 g/kg flaxseed oil. There were 5 replications with 4 pigs per pen. Individual pig BW and the feed consumption of each pen were monitored to calculate the ADG, ADFI, and G:F. Chromium oxide (2 g/kg) was added to the diets to determine the ATTD of DM, N, and GE. Blood profiles were analyzed by using an automatic biochemistry blood analyzer. All data were subjected to the GLM procedures of SAS as a randomized complete block design (SAS Inst. Inc., Cary, NC). Tukey's range test was used to compare the means of the treatments. A $P < 0.05$ was considered to be statistically significant. In Exp. 1, no difference ($P > 0.05$) was observed on growth performance and nutrient digestibility in weanling pigs, but total cholesterol (65.29 vs. 54.14 mg/dL) and triglycerides concentrations (30.43 vs. 24.71 mg/dL) were decreased ($P < 0.05$) by 5 g/kg flaxseed oil supplemention. In Exp. 2, flaxseed oil did not affect ($P > 0.05$) growth performance and nutrient digestibility. Total cholesterol (120.42 vs. 104.11 mg/dL), LDL-cholesterol (73.69 vs. 52.18 mg/dL) and triglyceride concentrations (55.02 vs. 48.87 mg/dL) were decreased ($P < 0.05$) by 5 g/kg flaxseed oil, however, HDL-cholesterol concentration (44.43 vs. 49.64 mg/dL) was increased ($P < 0.05$). Higher ($P < 0.05$) meat pH (5.77 vs. 5.59) was observed in pigs fed 5 g/kg flaxseed oil diet. There was no difference ($P > 0.05$) in meat quality and back fat thickness in finishing pigs. In conclusion, the inclusion of 5 g/kg flaxseed oil decreased total cholesterol, LDL-cholesterol, and triglyceride concentrations, increased HDL-cholesterol concentration without any negative effect on growth performance, nutrient digestibility, and meat quality of pigs.

Key Words: blood profile, flaxseed oil and pigs

0955 The effect of three levels of unmilled rice on growth performance and digestive tract development in broilers and ducks. C. P. Villemarette*, E. Lyons, B. Chung, E. Ferguson, and F. M. LeMieux, *McNeese State University, Lake Charles, LA.*

Three experiments Exp. 1 = 144 broilers; Exp. 2 = 118 mallard *Anas platyrhynchos* ducklings; and Exp. 3 = 75 mature mallard *Anas platyrhynchos* ducks were conducted to determine the effects of 3 levels of unmilled hybrid rice on growth performance, linear measurements and weights of organs, and gastrointestinal tract. Each experiment had 3 dietary treatments: (1) corn-soybean meal (basal), (2) basal + 5% hybrid rice, and (3) basal + 10% hybrid rice. All diets were formulated to meet or exceed dietary requirements for ducks and broilers from 0 to 9 wk of age. Treatments were replicated 8 times with 6 birds per pen (Exp. 1), eight times with 4 or 5 birds per pen (Exp. 2), and 3 replications with 8 or 9 birds per pen (Exp. 3). At Day 11 (Exp. 1), and Day 14 and 21 (Exp. 2) 1 bird from each pen ($n = 24$) was randomly selected to determine linear measurements and weights of organs and gastrointestinal tract. At experiment termination 28 d and 35 d experiment 2 and 3 respectively all remaining birds $n = 70$ (Exp. 2) and $n = 75$ (Exp. 3) were euthanized for internal tract measurements. Average initial weight of the chicks and ducks was 34.8 g, 31.8 g, and 821 g in Exp. 1, 2, and 3, respectively. Final BW of the chicks and ducks was 362.1 g, 446.6 g, and 1202.0 g in Exp. 1, 2, and 3, respectively. Data was analyzed by ANOVA procedures using the GLM procedure of SAS. Tukey's Honestly Significant Difference test was used to find difference among treatments and significance was considered at ($P < 0.05$). In Exp. 1 and 2, birds fed 10% rice grew slower ($P < 0.05$) than birds fed the basal diet. In Exp. 3 the addition of rice did not affect growth, feed intake or feed efficiency. Rice addition did not affect organ length or weight ($P > 0.1$) in Exp. 1. However in Exp. 2 birds fed 5% rice had increased ($P < 0.05$) pancreas, ileum, and jejunum weights and in Exp. 3, the addition of 10% rice increased ($P < 0.05$) liver weight. These results suggest the addition of 10% unmilled rice to broiler and duck diets may decrease growth performance.

Key Words: broilers, ducks, rice

0956 Influence of zinc-methionine complex supplementation on reproductive performance and immunity of gestating-lactating sows under hot weather condition. J. M. Romo[1], J. A. Romo[2], R. Barajas[*2], H. R. Güémez[1], I. Enriquez[2], and G. Silva[1], *[1]FMVZ-Universidad Autónoma de Sinaloa, Culiacán, Mexico, [2]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico.*

Thirty eight pregnant sows (Yorkshire × Landrace) were used to determine the influence of zinc-methionine complex supplementation on reproductive performance and immunity of gestating-lactating sows under hot weather condition. Thirty 5 d after be pregnant, sows were randomly assigned to treatments as follows: 1) Basal corn-soybean meal gestation diet (14.17% CP; 3.27 Mcal ME/kg) and lactation diet (17.95% CP; 3.35 Mcal ME/kg) that provided 60 mg of inorganic Zn/kg from $ZnSO_4$ (Control; CTR); and 2) Control plus 100 mg Zn/kg provided from Zn methionine complex (ZnM; ZINPRO 120, Zinpro Corp., Eden Prairie, MN). Treatments were offered since d 35 of gestation period, until Day 21 of lactation when piglets were weaned. Sows were placed in individual cages and fed ad libitum. Parametric data were analyzed by ANOVA for a completely randomized design, and percentage of piglet mortality was analyzed by Chi-square test using 2 × 2 tables. Each sow was the experimental unit. Across experiment weather means values were: air temperature 31.1 ± 1.2°C; relative humidity 68.24 ± 7.26%; and THI 82.57 ± 1.30, respectively. Sow back fat thickness (BFT) at d 35 of gestation was similar between treatments ($P = 0.93$), but in d-111 of gestation BFT was increased ($P = 0.05$) by ZnM (16.6 vs. 14.9 mm).The litter size (12.6 vs. 11.6 piglets), litter weight (12.6 vs. 12.3 kg), piglets born alive (10.4 vs. 9.4 piglets), and number of piglets weaned (7.7 vs. 8.3) were not affected by treatments ($P > 0.10$). Adjusted-21 d weaned litter weight was similar ($P = 0.32$) between treatments, with mean values of 42.3 and 45.6 kg for CTR and ZnM, respectively. Zinc methionine supplementation decreased ($P < 0.01$) piglets-mortality with mean values of 26% and 11% for CTR and ZnM, respectively. IgA in colostrums (1 682 ± 500 ng/mL) was no altered by treatments ($P > 0.10$). In piglet 14 d post weaned serum concentration of IgG (178 ± 144 ng/mL) and IgM (185 ± 101 ng/mL) were similar ($P > 0.10$) between treatments. Results suggest that ZnM supplementation to gestating-lactating sows under hot weather conditions could contribute to increase sow fat reserves and decrease mortality of piglets.

Key Words: reproductive performance, sows, zinc.

0957 Japanese quail (*Coturnix japonica*) responses to low protein diets supplemented with crystalline lysine, methionine, and threonine. C. R. Herrera Cortés[1], H. Bernal Barragán[*1], F. Sánchez Dávila[1], J. E. Hernández Quiroz[1], M. A. Montemayor Abundiz[1], and M. Cervantes Ramírez[2], *[1]Universidad Autónoma de Nuevo León, San Nicolás de los Garza, Mexico, [2]ICA- Universidad Autónoma de Baja California, Mexicali, Mexico.*

This study was conducted with the aim to determine the effect of dietary levels of lysine, methionine, and threonine on growth efficiency, environmental impact, and carcass quality of growing quails (*Coturnix japonica*). A sorghum-SBM basal diet with 21.1% crude protein, 1.08% lysine, 0.32% methionine, and 0.78% threonine (Diet 1) was formulated. Four additional diets (Diet 2 to 5) were supplemented with crystalline lysine, methionine, and threonine to contain 1.19, 1.30, 1.41, and 1.53% lysine; 0.46, 0.50, 0.54 and 0.59% methionine and 0.93, 1.02, 1.11, and 1.20% threonine, respectively. All diets were isoenergetic (2,958 kcal EM/kg feed). Ninety 14-days old quails were distributed in 30 cages, and randomly assigned to the five experimental diets ($n = 6$ replicates/treatment) during 28 d. Body weight, feed intake, average daily weight gain, and feed efficiency were monitored weekly. On the fourth week, excreta were collected during 48 h. Data were statistically analyzed with ANOVA. Final body weight, and average daily gain responded in a quadratic manner ($P < 0.05$) to incremental levels of crystalline amino acids. Birds fed Diet 5 had a body weight gain 12% higher ($P < 0.005$) than those fed the basal diet (3.26 g/d). Birds fed Diets 2 and 4 had 50 to 70% heavier thighs than birds in basal diet (16.9 vs. 9.7 g; $P < 0.05$), with no other carcass differences. On the other hand, birds receiving Diet 3 with 1.30% lysine, 0.50% methionine, and 1.02% threonine, reduced 23% ($P < 0.05$) the amount (1.17 g) of N excreted per unit of body weight gain of birds fed the basal diet. It was estimated that requirements of lysine, methionine, and threonine for growth traits of quails are 1.53%, 0.59%, and 1.20%, respectively. In conclusion, supplementing crystalline lysine, methionine, and threonine, improved growth efficiency, carcass quality, and protein utilization of growing Japanese quails fed a 21.1% CP sorghum-SBM based diet.

Key Words: Japanese quail, essential amino acids, growth efficiency

0958 Bioavailability of D-methionine relative to L-methionine for nursery pigs using slope-ratio assay. C. Kong*, J. Y. Ahn, and B. G. Kim, *Konkuk University, Seoul, The Republic of Korea.*

An experiment was conducted to determine the bioavailability of D–methionine (Met) relative to L–Met for nursery pigs using the slope-ratio assay. A total of 50 crossbred barrows with an initial BW of 13.5 kg (SD = 1.0) were used in an N balance study. A Met-deficient basal diet (BD) was formulated to contain adequate amount of all AA for 10 to 20 kg pigs except for Met. Two reference diets were prepared by supplementing the BD with 0.4 or 0.8 g L–Met/kg at the expense of corn starch, and the equivalent concentrations of D–Met were added to the BD for the 2 test diets. The pigs were adapted to the experimental diets for 5 d and then total but separated collection of feces and urine was conducted for 4 d according to the marker-to-marker procedure. Nitrogen intakes were similar across the treatments. Fecal N output was not affected by Met supplementation regardless of source, and apparent N digestibility did not change. Conversely, there was a linear response ($P < 0.01$) to Met supplementation from both Met isomers in urinary N output, which resulted in increased retained N (g/4 d) and N retention (% of intake). No quadratic response was observed in any of the N balance criteria. The estimated bioavailability of D–Met relative to L–Met from urinary N output (g/4 d) and N retention (% of intake) as dependent variables using supplemental Met intake (g/4 d) as an independent variable are 87.6 and 89.6%, respectively, but approximate 95% fiducial limits for the relative bioavailability estimates included 100%. In conclusion, with the absence of statistical significance, the present study indicated that the mean relative bioequivalence of D–Met to L–Met was 87.6% based on urinary N output and 89.6% based on N retention.

Key Words: methionine isomers, nitrogen balance, relative bioavailability, swine

0959 Energy value of bakery meal and peanut flour meal for broiler chickens determined using the regression method. F. Zhang*[1] and O. Adeola[2], *[1]Purdue University, West Lafayette, IN, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN.*

The energy value of bakery meal (BM) and peanut flour meal (PFM) for broiler chickens were determined in the current experiment with Ross 708 broiler chickens from d 21 to 28 post hatching. The birds were fed a standard broiler starter diet from d 0 to 21 post hatching. 320 birds were grouped by weight into 8 blocks of 5 cages with 8 birds per cage and assigned to 5 diets. Experiment used a corn-soybean meal reference diet (RD) and 4 test diets (TD) in which test ingredients partly replaced the energy sources in the RD. The TD consisted of 200 g BM, 400 g BM, 100 g PFM, or 200 g PFM/kg, respectively. The DM of BM and PFM were 878, and 964 g/kg, respectively and the respective gross energies were 4,060, and 5,783 kcal/kg DM. The result showed that an addition of either BM or PFM to the RD did not affect the growth performance of birds from d 21 to 28 post hatching. The ileal digestible energy (IDE), ME, and MEn of both ingredients were determined by the regression method. The determined IDE values were 3,412 kcal/kg DM for BM and 4,801 kcal/kg DM for PFM; ME values were 3,176 and 4,601 kcal/kg DM for BM and PFM, respectively. And the MEn values were 3,093 kcal/kg DM for BM and 4,112 kcal/kg DM for PFM. In conclusion, the current study provides energy values for BM, and PFM, and shows that adding up to 100 g BM or PFM/kg broilers diets from d 21 to 28 did not affect growth performance.

Key Words: bakery meal, metabolizable energy, peanut flour meal

0960 Kinetics of lipid peroxidation in fats and oils as affected by lipid source, heating temperature, and length of heating. S. C. Lindblom*[1], G. C. Shurson[2], J. Moser[3], and B. J. Kerr[4], *[1]Iowa State University, Ames, [2]Department of Animal Science, University of Minnesota, St. Paul, [3]USDA-ARS, Peoria, IL, [4]USDA- ARS, Ames, IA.*

Lipid peroxidation is a chain reaction of generation and degradation of peroxidation compounds including acids, aldehydes, ketones, and polymers. However, assays used in farm animal research commonly measure 1 or 2 compounds and do not assess the change in a lipid's peroxidation status over time. Consequently, a laboratory-study was conducted to evaluate the impact of heating temperature and length of heating on the generation of lipid peroxidation products in lipids varying in fatty acid composition. Six lipids were selected based on their divergent fatty acid composition and predicted peroxidizability index (Hammond, 1954). Lipids used in this study included tallow, palm oil, soybean oil, linseed oil, menhaden oil, and a manufactured oil were heated at 4 temperatures to reflect ambient, summertime feed temperature in a bulk bin, an elevated feed processing temperature, and a frying temperature (22.5°, 45°, 90°, and 180°C, respectively). Oils (2.5 L each) were placed in a 5 L round-bottom glass flask and heated with an electric heating mantle with power controller, with bubbling air at 3 L/min. Because tallow and palm oil were solids at room temperature, they were evenly spread into a 30.5 × 45.7 cm pan to allow for air reaction to the lipid. Samples were taken at equally distributed time points within a temperature (22.5°C for 0, 6, 12, 18, 24 d; 45°C for 0, 3, 6, 9, 12 d; 90°C for 0, 18, 36, 54, 72h; and 180°C for 0, 3, 6, 9, 12h). Lipid analysis for composition, quality, and peroxidation indicators were conducted. Depending on the lipid source, heating temperature, and sampling time, peroxide value increased from 11 to 1200 mEq/kg, *p*-anisidine value from 0 to 810, hexanal from 0 to 300 mg/kg, 2,4-decadienal from 0 to 690 mg/kg, polar

compounds from 5 to 60%, polymers from 0 to 30%, and OSI from 0 to 22 h at 110°C. The data show that the peroxidizability of lipids varies greatly depending on their fatty acid profile, the degree of heating and time of sampling. Because peroxidized lipids have been shown to impact animal performance, gastrointestinal integrity, gene expression, immune competence, and metabolic oxidative status, the understanding of how and when lipid peroxidation compounds are generated and degraded, and their concentration in a lipid at specific time point is important to their use in livestock feeding programs.

Key Words: kinetics, lipid peroxidation, lipid quality

0961 Effects of feeding dried cabbage leaf residues on broiler performance, ileal digestibility and total tract nutrient digestibility. A. Mustafa, V. Higginson*, and B. Baurhoo, *McGill University, Ste-Anne De Bellevue, QC, Canada.*

A study was conducted to determine the effects of feeding dried broccoli floret residues on growth performance, apparent ileal digestibility, apparent total tract nutrient digestibility and intestinal microbial populations in broiler chickens. One thousand two hundred 1-d-old male Ross 508 broilers were randomly allotted to 4 dietary treatments and were grown over a 35-d experimental period. Dietary treatments included 4 levels of dried broccoli floret residues: 0, 3, 6, and 9%. Results showed that inclusion of dried broccoli floret residues increased body weight gain (quadratic effect, $P = 0.004$) and feed conversion ratio (quadratic effect, $P = 0.002$) with no effect on feed intake. Apparent ileal crude protein (CP, quadratic effect, $P = 0.003$) and dry matter (DM, quadratic effect, $P = 0.002$) digestibility for younger birds (25 d of age) increased as the level of dried broccoli floret residues in the diet increased. However, apparent ileal CP (linear effect, $P = 0.022$), DM (linear effect, $P = < 0.001$) and gross energy (linear effect, $P = 0.001$) digestibility for older birds (35 d of age) decreased as a result of dried broccoli residue inclusion. Nitrogen correct apparent metabolizable energy decreased (linear effect, $P < 0.001$) as the level of dried broccoli floret residues in the diet increased. However, N retention was not influenced by dried broccoli floret residue inclusion. It was concluded that incorporation of dried broccoli floret residues in broiler diet at moderate levels (i.e., 3 to 6%) may improve the growth of broiler chickens with no detrimental effects on nutrient digestibility and retention. However, at high levels (i.e., 9%), dietary dried broccoli floret residues may compromise ileal and total tract nutrient digestibility.

Key Words: Broiler, dried boccoli residues, ileal digestibility, total tract digestbility

0962 Effect of type of fibrous sources in the phosphorus-free diet on the basal endogenous loss of phosphorus in growing pigs. A. R. Son[*1] and B. G. Kim[2], [1]*Konkuk University, Seoul, South Korea,* [2]*Konkuk University, Seoul, The Republic of Korea.*

The objective of this study was to investigate the influence of fiber sources in P-free diets on the basal endogenous loss (BEL) of P in growing pigs. Eight barrows with an initial BW of 37.4 ± 2.7 kg were individually housed in metabolism crates. The pigs were allotted to dietary treatments in a replicated 4 × 4 Latin square design with 4 diets, 8 pigs, and 4 periods. Four P-free diets were formulated based mainly on cornstarch, sucrose, and gelatin, and contained 10% of cellulose, pectin, silica sand, or sawdust as a fiber source in each P-free diet. Each period consisted of a 4-d adaptation period and a 4-d period of total collection of feces according to a marker-to-marker procedure. Chromic oxide was added at 0.5% to the morning meal as an indigestible marker on d 5 and 9 in each period. The feed intake of pigs fed the sawdust diet was less ($P < 0.05$) than that of pigs fed the silica sand diet. The total fecal output of pigs fed the cellulose and silica sand diets were greater ($P < 0.05$) than that of pigs fed the pectin diet. The P concentration in the feces was greater ($P < 0.05$) in the pigs fed the pectin diet compared with the pigs fed the cellulose and silica sand diets. The total P output was not affected by the fiber sources. The BEL of P was 206, 350, 252, and 431 mg/kg DMI in the cellulose, pectin, silica sand, and sawdust diets, respectively. The BEL of P of the pigs fed the sawdust diet was greater ($P < 0.05$) than that of the pigs fed the cellulose diet. There were differences ($P < 0.05$) in the apparent total tract digestibility of DM, OM, CP, ether extract, NDF, ADF, and Ca among the experimental diets. In conclusion, the fiber sources in the P-free diet may have different effects on the BEL of P estimate and the apparent total tract digestibility of nutrients.

Key Words: basal endogenous loss of P, fiber, P-free diet

0963 Effects of feeding dried cabbage residues on performance, ileal and total tract digestibility, and selected microbial population in broiler chickens. A. Mustafa, B. Baurhoo, and V. Higginson*, *McGill University, Ste-Anne De Bellevue, QC, Canada.*

A study was conducted to investigate the effects of partially replacing corn and soybean meal with dried cabbage leaf residues (DCR) on broiler growth performance, apparent ileal nutrient digestibility and apparent total tract nutrient utilization. Dietary treatments include 4 levels of DCR (0, 3, 6, and 9%). Two hundred and twenty four 1-d old male broilers were randomly assigned to 1 of 4 groups (8 cage replicates; 7 birds/cage) and grown over a 35-d experimental period. Results showed that feeding DCR had no effects on daily body weight gain (average 53.4 g/d), daily feed intake (average 94.9 g/d), and feed

conversion ratio (average 1.78 g of feed/g of gain). Inclusion of DCR reduced apparent ileal DM (quadratic effect, $P < 0.001$), OM (linear effect, $P = 0.012$), and CP (quadratic effect, $P = 0.001$) digestibility of younger birds (d 21) while incremental levels of DCR had no effect on apparent ileal nutrient digestibilities of older birds (d 35). Apparent total tract digestibility of DM, OM, and CP increased (linear effect, $P < 0.001$) as the level of DCR increased. It was concluded that the inclusion of DCR in broiler diets up to 9% had no negative impact on bird performance and apparent ileal digestibility of older birds and improved apparent total tract nutrient digestibility.

Key Words: broilers, dried cabbage residues, ileal digestbility, total tract digestibility

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0964 Effect of different levels of zinc and calcium on growth performance in weanling pigs. L. Blavi*, D. Solà-Oriol, S. M. Martín-Orúe, and J. F. Pérez, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra (08193), Spain.*

High Zn levels (2,500 to 3,000 mg/kg ZnO) are widely used to prevent diarrhea in piglets after weaning. The NRC recommendations of Ca levels after weaning are defined at 0.85 to 0.80% to piglets 5 to 11 kg. In a previous study we observed that piglets with low Ca in pre-starter diet (0.35% Ca) had higher BW than piglets with high levels (0.95%). Therefore, the objective of this trial was to observe the effect of Ca with addition of therapeutic ZnO or not on growth performance during pre-starter phase (0–14 d). A total of 320 pigs were used in a 2 × 2 factorial arrangement, where the main factors were: Zn levels (125 or 2,500 ppm Zn) and Ca levels (0.35% and 0.95%). Piglets were reared in 32 pens (10 pigs/pen; 8 replicates per treatment). From Day 14 onward, the Ca level was fixed at 0.77% for all diets. The pre-starter (0 to 14 d) and starter (14 to 35d) diets contained 2,520 and 2,460 Kcal NE/kg, 19.65 and 19.00% CP, 1.25 and 1.23 digestible Lys, and 0.33 and 0.25% P digestible, respectively. Feed intake and individual BW were registered on d 0, 14, and 35 post-weaning. Performance parameters were analyzed with ANOVA by using the mixed procedure of the statistical package SAS. There were a significant effect of the level of Ca and Zn on BW at d 14 and 35 ($P < 0.05$); where pigs with low Ca (0.35%) and also pigs with 125 ppm Zn showed the highest weights (values from Ca effect: 10.87 vs. 10.33 Kg d 14 and 21.20 vs. 20.37 Kg d 35; values from Zn effect: 10.97 vs. 10.24 Kg d 14 and 21.67 vs. 19.90 Kg d 35, respectively). A significant interaction was observed on average daily feed intake (ADFI) from 0 to 14d ($P = 0.04$), where piglets with 0.35% Ca and 125ppm Zn in the diet presented higher consumption compared to piglets with 0.35% Ca and 2,500 ppm Zn (327.13 vs. 261.20 g/d, respectively). In addition, an statistical trend for the interaction in FCR during pre-starter phase (0 to 14d; $P = 0.097$), where piglets with 0.95% and 2,500ppm Zn showed the highest ratios. There was no significant effect of the experimental treatments on the FCR of the starter phase (14 to 35d). It can be concluded that lower levels of Ca and Zn allow better growth of weaned piglets, suggesting that mineral supplementation has an important role on growth performance.

Key Words: calcium, pigs, zinc

0965 Evaluation of cold pressed soybean meal and pea protein as alternative amino acid sources in swine diets. J. Koepke*, *South Dakota State University, Brookings.*

Cold pressed soybean meal (CP-SBM) and a processed pea product (PP, 55% crude protein) were evaluated as potential alternative ingredients for use in swine diets. CP-SBM was produced from regular full fat soybeans that had been heat treated before cold-pressing to reduce trypsin inhibitors. 907 kg of heated soybeans produced approximately 775.6 kg of high oil (8%) meal and 131.5 kg soybean oil. Unlike solvent extracted SBM, CP-SBM can be produced on-farm and the oil byproduct sold as high commodity product. The PP was harvested from yellow peas that were mechanically milled and a portion of the dehulled split cotyledons was processed. A digestibility trial was conducted to determine the standard ileal digestibility (SID) of protein and amino acids in CP-SBM and PP in comparison to solvent extracted SBM. Six ileal-cannulated barrows (29.25 ± 1.5 kg BW) were used in crossover design with 4 collection periods of 7 d each (5 d acclimation and 2 d ileal collection of 12h/d). Pigs were randomly assigned, within period, to one of four experimental diets (CP-SBM, PP, SBM, and nitrogen-free) where CP-SBM, PP and SBM were included as the sole protein sources, respectively. Feed allowance per period was provided at 3 × maintenance energy requirement (197 kcal x $BW^{0.60}$/d) based on measured body weight at the beginning of each period. The SID of lysine (94.4 vs. 77.2 ± 1.9), arginine (96.7 vs. 83.2 ± 2.7), valine (89.3 vs. 73.6 ± 3.3), leucine (91.3 vs. 75.7 ± 2.9), isoleucine (90.9 vs. 77.4 ± 2.4) and threonine (88.3 vs. 67.0 ± 4.4) were higher ($P < 0.02$) in PP than CP-SBM. The SID of isoleucine (84.6 vs. 77.4 ± 2.4; $P = 0.107$), asparagine (82.3 vs. 72.6 ± 3.0, $P = 0.075$) and glutamine (85.9 vs. 77.4 ± 2.8, $P = 0.099$) tended to be higher in SBM compared to CP-SBM. There was no difference in SID between PP and SBM in any of the essential AA measured. Based on SID, both CP-SBM and PP may be used as an alternative amino acid source in swine diets while PP appears to be superior alternative than CP-SBM.

Key Words: cold-pressed soybean meal, pea protein, growth performance

0966 The effects of feeding low trypsin inhibitor soybean meal to broilers on growth performance. G. Hosotani*, B. Freitas, M. S. Kerley, and M. C. Shannon, *Division of Animal Sciences, University of Missouri, Columbia.*

A 21-d experiment was conducted to compare soybean meal (SBM) from low trypsin inhibitor to parent soybean cultivars on growth performance of broilers. One hundred and fifty 1-d-old male broilers (Ross 308) were randomly placed in battery cages and allocated to 6 dietary treatments with 5 replicates and 5 birds per replicate in a factorial arrangement of 3 SBM sources, solvent extracted conventional SBM (SOLV), cold-pressed conventional SBM (CON), and cold-pressed low trypsin inhibitor SBM (LTI) by laboratory-scale mechanical extraction. All SBM sources were either non-heated or heated in a forced-air oven at 120°C for 20 min. Diets were formulated to meet or exceed NRC (1994) and Aviagen nutrient requirements. Broilers were weighed and feed disappearance measured on d 7, 14, and 21. Statistical analyses were performed as a randomized complete block design using PROC GLM of SAS with significance level set at $P \leq 0.05$. Feeding sources of SBM resulted in differences in ADG, ADFI, and feed conversion ratio (FCR) in all measurements ($P < 0.05$). Overall, chicks fed LTI had intermediate ADG (36 g; $P < 0.0001$) compared to CON and SOLV (30 and 50 g, respectively), and FCR (1.38 vs. 1.54, and 1.19, respectively; $P < 0.0001$). Chicks fed LTI or HTI had lower ADFI compared to SOLV (49, 46, and 59 g, respectively; $P < 0.0001$). Heating SBM improved FCR on wks 1 and 2, resulting in overall improvement from 1.40 to 1.34 FCR ($P = 0.0017$). Interaction between SBM sources and heat treatment was not significant throughout the experiment. In conclusion, feeding LTI improved growth performance of broiler chicks compared to CON by 20% in ADG and 10% in FCR. We hypothesized that feeding LTI to broilers would result in similar growth performance of broilers fed SOLV. However, feeding either heated or non-heated LTI to broilers did not have similar growth performance as broilers fed SOLV, decreasing ADG by 28% and impairing FCR by 16%, most likely due to other anti-nutritional factors or nutritional characteristics that impaired growth performance of broiler chicks.

Key Words: broiler, performance, soybeans

0967 Nutritive value of cold-pressed camelina cake with or without supplementation of multi-carbohydrase in pig diets. T. A. Woyengo*[1], R. Patterson[2], and C. L. Levesque[1], [1]*South Dakota State University, Brookings,* [2]*Canadian Biosystems, Calgary, AB, Canada.*

Cold-pressed camelina cake (CPCC), a fibrous co-product of camelina seed pressing, is available for livestock feeding. However, information is also lacking on the effect of supplementing fiber-degrading enzymes (carbohydrases) to CPCC-based diets on nutrient utilization by pigs. Thus, the objectives were to determine the standardized ileal digestibility (SID) of AA and DE value of cold-pressed camelina cake (CPCC), and the effect of adding Multi-Carbohydrase to a CPCC-based diet for pigs. Six ileal-cannulated barrows (average initial BW = 36 kg) were fed 5 diets in 5 × 5 Latin square design with 1 added column to give 6 replicates per diet. A corn-soybean meal-soybean oil-based diet and the basal diet with corn, soybean meal, and soybean oil replaced by 25% CPCC in a 2 × 2 factorial arrangement with or without Multi-Carbohydrase (1,200 U of xylanase, 150 U of glucanase, 500 U of cellulose, 60 U of mannanase, 700 U of invertase, 5,000 U of protease, and 12,000 U of amylase/kilogram of diet; Superzyme CS, 1 g/kg). The fifth diet was N-free. The ratio of corn, SBM, and soybean oil in the basal diet was identical to the CCPC-containing diets to allow calculation of nutrient digestibility of CPCC by the difference method. On a DM basis, CPCC contained 42% CP, 10.5% ether extract, 12.2% crude fiber, 2.07% Lys, 0.73% Met, 1.64% Thr, and 0.51% Trp. The SID of Lys, Met, Thr, and Trp for CPCC were 43.5, 70.7, 44.8, and 55.3%, respectively. The DE value for CPCC was 3783 kcal/kg of DM. Multi-Carbohydrase supplementation did not affect the SID of AA and DE value for the CPCC-based diet. In conclusion, CPCC evaluated in the current study could be an alternative source of AA and energy in swine diets. However, Multi-Carbohydrase supplementation did not result in an additional benefit in nutritional value of the CPCC.

Key Words: pig, cold-pressed camelina cake, nutrient digestibility

0968 Optimization of alkali hydrolysis conditions to increase antioxidant availability in corn distillers grain. A. Daramola* and B. Min, *University of Maryland Eastern Shore, Princess Anne.*

Corn is one of the most abundant sources for antioxidants, such as phenolic compounds, among crops and they are well-concentrated into corn distillers grain (CDG) products without degradation. However, more than 70% of phenolics in CDG exist in the insoluble from bound to cell-wall-matrix, which could not be absorbed to exert their health benefits. The objective of this study was to evaluate combinations of alkali hydrolysis condition variables and determine the best combination of the variables to maximize amounts and antioxidant capacity of available phenolics in CDG for absorption. Wet distillers grains (WDG) were alkali-hydrolyzed using factorial combinations of the condition variables: NaOH concentration (0 (control), 0.6, 1.5, and 3.0 mol/kg WDG), incubation temperature (25, 50, and 80°C) and time (0.5, 2, and 4 h). WDG were mixed with NaOH solution at the ratio of 1:3 (w/v) and incubated in a temperature-controlled shaker. After incubation, the mixture was neutralized with HCl and centrifuged. Supernatants were extracted with ethyl acetate and precipitates were freeze-dried and extracted with 80%

ethanol to obtain soluble (FREE) phenolics. Residues were alkali-treated and extracted with ethyl acetate for matrix-bound (BOUND) phenolics. Antioxidant potentials (total phenolic and flavonoid contents and antioxidant capacity measured as oxygen radical absorbance capacity [ORAC]) of FREE and BOUND phenolics were evaluated. Data were analyzed by ANOVA and least square means were compared using PDIFF. Response surface analysis was used to determine the best combination of the condition variables. The antioxidant potential of FREE and BOUND phenolics in control without NaOH were not affected by incubation temperature and time ($P > 0.05$). As the condition variables increased, the antioxidant potentials increased significantly ($P < 0.05$). The biggest increases in antioxidant potentials of FREE phenolics were observed when NaOH concentration increased from 0.6 to 1.5 mol/kg WDG, incubation temperature from 50 to 80°C, and incubation time from 0.5 to 2 h, respectively ($P < 0.05$). When WDG was incubated with NaOH solution at 3.0 mol/kg WDG at 80°C for 4 h, FREE phenolics accounted for over 98% of the total amounts and antioxidant capacity in alkalized WDG. In addition, response surface analysis showed the best combination of alkali hydrolysis condition variables as NaOH concentration (2.55 mol/kg WDG), incubation temperature (69°C) and time (3.0 h) for producing alkalized WDG with maximally available bioactive phenolics, which could contribute to the improvement of farm animal health and productivity.

Key Words: corn distillers grain, alkali hydrolysis, antioxidants

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0969 Effects of high protein canola meal on digestibility of phosphorus and growth performance of weanling pigs. Y. She[*1], H. H. Salgado[2], D. Li[3], and H. H. Stein[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Laval Univ., Quebec City, QC, Canada, [3]CAU, Beijing, China.*

Two experiments were conducted to evaluate the nutritional value of high-protein canola meal (CM-HP) and conventional canola meal (CM-CV) in diets fed to weanling pigs. Experiment 1 was designed to compare the apparent total tract digestibility (ATTD) and the standardized total tract digestibility between CM-HP, CM-CV and soybean meal (SBM). Forty eight growing barrows (initial BW: 16.8 ± 1.18 kg) were placed in metabolism crates and allotted to a randomized complete block design using a 2 × 3 factorial arrangement with 8 replicate pigs per diet. Diets were based on CM-HP, CM-CV, or SBM, and 0 or 500 units of microbial phytase. Diets were provided for 12 d with total collection of feces over the final 5 d. Results indicated that as phytase was added to the diets, the ATTD and STTD of P increased ($P < 0.01$) from 41.9 to 57.5% and 45.1 to 60.8%, respectively, in CM-HP; from 40.8 to 60.5% and 44.5 to 64.3%, respectively, in CM-CV; and from 61.0 to 74.2% and 66.7 to 80.5%, respectively, in SBM. There were no difference in ATTD or STTD of P between CM-HP and CM-CV, but ATTD and STTD of P was greater ($P < 0.05$) in SBM than in CM-HP and CM-CV. In Exp. 2, 405 pigs (initial BW: 10.07 ± 1.41 kg) were randomly allotted to 9 dietary treatments with 9 replicate pens per treatment. There were 4 to 6 pigs per pen. The control diet was a corn-SBM diet. Four additional diets were formulated by adding 10, 20, 30, or 40% of either CM-HP or CM-CV to the control diet. Results indicated that increased inclusion rate of CM-CV increased (quadratic, $P < 0.05$) ADG of pigs. Increased inclusion rate of CM-HP or CM-CV decreased (linear, $P < 0.05$) ADFI, but increased (linear, $P < 0.05$) G:F. Pigs fed CM-CV had greater ($P < 0.05$) ADG and G:F than pigs fed CM-HP. In conclusion, there is no difference in the ATTD or STTD of P between CM-HP and CM-CV, and inclusion of up to 40% CM-HP or CM-CV has no negative effects on growth performance of weaned pigs from 2 wk post-weaning.

Key Words: canola meal, phytase, pigs

0970 Effect of heat stress on the apparent and standardized ileal digestibilities of amino acids in growing pigs. A. Morales[1], M. Perez[1], P. Castro[1], N. O. Ibarra[1], E. Avelar[1], L. H. Baumgard[2], and M. Cervantes[*1], *[1]ICA- Universidad AutÃ³noma de Baja California, Mexicali, Mexico, [2]Iowa State University, Ames.*

The exposure of pigs to heat stress (HS) impairs the small intestine digestive and absorptive capacities affecting in turn the AA digestibilities. A two 7-d periods experiment was conducted with 8 pigs (30 kg initial BW) surgically fitted with T-type cannulas at the terminal ileum to analyze the effect of HS on both the apparent (AID) and the standardized ileal digestibility (SID) of AA in pigs fed a wheat-SBM diet. A thermometer was placed inside the ileal lumen (IL) of all pigs to register the temperature at 15 min intervals. After recovery from surgery, all pigs were adapted to the diet and trained to consume the same amount of feed twice a day for 7d under thermal neutral (TN) conditions (22 ± 2°C). Following, the pigs were divided into 2 groups (4 pigs each); one was kept under TN conditions and the other group was exposed to natural HS (24 to 45°C) for 7d (period 1). In period 2, the ambient temperature conditions of the two groups were switched. Ileal digesta was continuously collected during 12 h on d 7 of each period. Chromic oxide was used as indicator of the intestinal digesta flow. The IL temperature was around 1.6°C higher in HS pigs ($P < 0.001$). The AID of AA (%) for the TN and HS pigs were: Arg, 90.6, 88.1; His, 88.7, 85.9; Ile, 84.8, 83.9; Leu, 86.9, 84.1; Lys, 86.8, 86.2; Met, 89.8, 89.1; Phe, 86.0, 84.8; Thr, 75.7, 74.1; Val, 82.8, 81.7, respectively. The SID (%) of AA for the TN and HS pigs were: Arg, 94.0, 92.0; His, 92.5, 90.2; Ile, 89.5, 88.1; Leu, 90.1, 88.6; Lys, 91.0, 90.1; Met, 94.4, 93.6; Phe, 90.4, 88.9; Thr, 86.0, 83.7; Val, 88.1, 86.5;, respectively. The AID of Arg and His was lower ($P <$

0.01) in HS pigs, and the SID of Arg and His, as well as Leu, was also lower in HS pigs. Neither the AID nor the SID of the remaining essential AA was affected by HS. In summary, these data show that ileal temperature increases in HS pigs, and that the digestibilities of essential AA are differentially affected in pigs exposed to natural HS conditions. Special attention should be given to Arg and His when formulating diets for growing pigs under HS conditions

Key Words: pigs, heat stress, amino acids, digestibility

0971 Effect of methionine sources and graded levels of sulfur amino acids on the growth performance of post-weaning piglets. F. Molist[*1], P. Buttin[2], M. Bouwhuis[1], and P. J. van der Aar[1], *[1]Schothorst Feed Research, Lelystad, The Netherlands, [2]Novus International, Brussels, Belgium.*

The aim of the experiment was to evaluate the effects of graded levels of sulfur amino acids (SAA) in the diet of weaned piglets, and to compare the effects of the source of added free-methionine (Met). The experiment was set up according to a 2 × 4 factorial arrangement, with two Met sources (DL-2-hydroxy-4(methylthio) butanoic acid, HMTBa; Novus Europe SA/NV, Belgium vs. DL-methionine, DL-Met; Adisseo, France) and four graded levels (−6, 0, +6, +12% of the requirement) of Met. All the diets were formulated to meet 2008 CVB requirements for weaning piglets for energy (NE 9.37 MJ/kg) and slightly limiting in standardized ileal digestible (SID) Lys (11 g SID Lys/kg). The basal diet (0%) was formulated at 0.6 SID SAA/SID Lys, and the different levels were obtained by the inclusion of the Met source on molar content of HMTBa compared to DL-Met in the commercial products. In total 480 piglets (Tempo × Topigs 20, Topigs Norsvin; boars and gilts) with an average BW of 7.35 ± 0.70 kg and an average age of 26 ± 1 d old entered the trial at the day of weaning. The piglets received a standard diet during the first 7 d. The experimental diets were fed ad libitum from d 7 post-weaning during 4 wk. Body weights (BW) were measured at weaning, on 7, 21, and 35 d post-weaning, and ADG, ADFI, and FCR were calculated accordingly. Data were analyzed as a 2 × 4 factorial arrangement in a randomized block design by analysis of variance (ANOVA), using GenStat® for Windows (17th edition). During d 7–21 of the trial, neither ADG nor ADFI were affected by the treatment. During d 21–35 of the trial, and overall (7–35 d), piglets supplemented with HMTBa showed a greater ADFI ($P = 0.046$), ADG ($P = 0.037$), and final BW ($P = 0.043$) with no effect of level nor interaction. In conclusion, there was no effect of level of Met or SAA on growth performance suggesting that SID Met and SID SAA were above the piglets' requirements. Piglets supplemented with HMTBa showed greater feed intake and subsequent growth than piglets receiving diets containing DL-Met.

Key Words: methionine, piglets

0972 Digestible calcium requirement for 100 to 130 kg pigs. L. A. Merriman[*1], C. L. Walk[2], C. M. Parsons[3], and H. H. Stein[3], *[1]University of Illinois, Urbana-Champaign, [2]AB Vista, Marlborough, United Kingdom, [3]University of Illinois at Urbana-Champaign, Urbana.*

An experiment was conducted to determine the digestible calcium requirement by pigs from 100 to 130 kg. Ninety pigs (average initial BW = 99.89 ± 3.34 kg) were randomly allotted to 15 experimental diets. Each diet was fed to 6 replicate pens using a randomized complete block design. Fifteen corn and soybean meal-based diets were formulated and all diets had the same concentrations of phytate and Na. Diets were formulated using a 3 × 5 factorial design with diets containing 0.11, 0.21, or 0.31% standardized total tract digestible (STTD) P and 0.12, 0.29, 0.46, 0.61, or 0.78% total Ca (0.08, 0.18, 0.29, 0.38, or 0.49% STTD Ca). The P concentrations ranged from 48 to 152% of the STTD P requirement and the Ca concentrations ranged from 27 to 173% of the total Ca requirement. Experimental diets were fed for 28 d and pigs were individually housed. Pig and feeder weights were recorded at the beginning and at the conclusion of the experiment to calculate ADFI, ADG, and G:F. On d 28, all pigs were euthanized and the right femur was extracted. Ash, Ca, and P concentrations were determined from the de-fatted, dried femurs. Results indicated that as dietary concentrations of STTD Ca increased, the ADFI and ADG decreased (main effects of Ca, $P < 0.05$), regardless of the dietary concentration of P. Models to predict ADFI [ADFI = 3.6782– 1.2722 × STTD Ca (%); $P = 0.001$] and ADG [ADG = 1.2141– 0.6230 × STTD Ca (%); $P = 0.008$] were dependent only on the concentration of STTD Ca, but not on the STTD of P. There were no effects by STTD Ca or STTD P on G:F indicating that the negative effects of STTD Ca on ADG was a result of reduced ADFI. Linear increases were observed for bone ash, bone Ca, and bone P as dietary concentrations of STTD Ca increased for all levels of STTD P (interaction, $P < 0.001$). In conclusion, results from the experiment support the current requirements (NRC, 2012) for Ca and STTD P, and feeding beyond the requirements for Ca (0.46% total Ca; 0.29% STTD Ca) or STTD P (0.21) is detrimental to growth performance of pigs.

Key Words: bone ash, calcium, pigs, phosphorus

0973 Effects of inclusion of canola meal in weanling pig diets containing different concentrations of energy. T. F. Pedersen[*1], Y. Liu[2], and H. H. Stein[3], *[1]Aarhus University, Aarhus, Denmark, [2]University of California, Davis, Davis, [3]University of Illinois at Urbana-Champaign, Urbana.*

The objective of the experiment was to determine effects of diet NE and addition of an exogenous enzyme on growth performance and physiological parameters of weanling pigs fed a corn-soybean meal (SBM) diet or diets containing high protein canola meal (CM-HP) or conventional canola meal (CM-CV). In total, 492 pigs (initial BW: 9.15 ± 0.06 kg) were used in a randomized complete block design with 9 replicate pens per treatment. A control diet based on corn and SBM and 4 diets containing 20 or 30% CM-HP or CM-CV were formulated; inclusion of choice white grease (CWG) was adjusted to maintain constant NE among diets. Four additional diets containing 20 or 30% CM-HP or CM-CV were formulated without adjusting CWG and NE in these diets was, therefore, reduced compared with the control diet. Three diets that were similar to the control diet and the diets containing 30% CM-HP or CM-CV without adjusted CWG were formulated, but a carbohydrase was included in these diets. Pigs were fed experimental diets for 22 d. Results indicated that ADG and G:F decreased (linear, $P < 0.05$) as CM-HP was included in diets with constant energy, but that was not the case if CM-CV was included in the diet or if diets were not formulated to a constant NE. There were also no differences in G:F or in final BW among pigs fed the control diet and pigs fed canola meal diets. Only minor and inconsistent effects of CM-HP or CM-CV on intestinal weight, gut fill, digesta pH, cecal VFA concentrations, and serum concentrations of urea N, total N, or albumin were observed. However, thyroid gland weight increased ($P < 0.05$) or tended to increase ($P < 0.10$) as the concentration of canola meal increased. Serum concentrations of IgG and total tract digestibility of GE were reduced (linear, $P < 0.05$) if CM-HP or CM-CV was included in the diets. No major effects of the carbohydrase were observed. In conclusion, up to 30% CM-HP or CM-CV may be used in diets fed to weanling pigs from 2 wk post-weaning without impacting growth performance and NE in diets containing canola meal does not have to be similar to that in corn-SBM diets.

Key Words: canola meal, energy concentration, pigs

0974 Effect of increasing concentrations of digestible calcium and digestible phosphorus on apparent total tract digestibility of calcium and phosphorus by pigs. J. C. González-Vega[*1], C. L. Walk[2], M. R. Murphy[1], and H. H. Stein[1], *[1] University of Illinois at Urbana-Champaign, Urbana, [2]AB Vista, Marlborough, United Kingdom.*

Two experiments were conducted to determine effects of increasing concentrations of digestible Ca and digestible P on apparent total tract digestibility (ATTD) of Ca and P in diets fed to pigs. In Exp. 1, 6 diets were formulated to contain 0.36% standardized total tract digestible (STTD) P and 0.32, 0.40, 0.48, 0.56, 0.64, or 0.72% STTD Ca, by including increasing quantities of calcium carbonate at the expense of cornstarch. Two additional diets contained 0.72% STTD Ca and 0.33% or 0.40% STTD P. A total of 80 pigs (initial BW: 13.12 ± 1.79 kg) were placed in metabolism crates and randomly allotted to the 8 diets with 10 replicate pigs per diet in a randomized complete block design. Results indicated that the ATTD of Ca and the ATTD of P decreased (linear, $P < 0.001$) as dietary STTD Ca increased. However, increasing dietary STTD P did not affect ATTD of Ca, but the ATTD of P increased (linear, $P < 0.05$) as dietary STTD P increased. In Exp. 2, 20 corn-soybean meal based diets were formulated with diets containing 4 concentrations of STTD P (0.15, 0.31, 0.39, or 0.47%) and 5 concentrations of STTD Ca (0.13, 0.27, 0.42, 0.57, or 0.72%). A total of 120 pigs (initial average BW: 29.45 ± 2.15 kg) were placed in metabolism crates and randomly allotted to the 20 diets in 6 blocks with 1 pig per diet in each block. Results indicated that ATTD of Ca in diets linearly increased ($P = 0.009$) as concentration of STTD Ca increased, but was not affected by the concentration of STTD P. However, the ATTD of P linearly decreased ($P < 0.001$) as the concentration of STTD Ca increased, but linearly increased ($P < 0.001$) as the concentration of STTD P increased. In conclusion, for pigs between 11 and 50 kg, the ATTD of Ca varies by the concentration of STTD Ca in diets, but is not affected by the concentration of STTD P. However, the ATTD of P is negatively affected by increasing concentration of STTD Ca, but increases as concentration of STTD P increases.

Key Words: calcium, phosphorus, pigs

0975 Trans-generational effect of feeding genetically modified mCry1Ac corn to laying hens and offspring on offspring growth and health. L. Chen*, R. Zhong, L. Zhang, L. Gao, and H. Zhang, *Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, China.*

The experiment was to assess the chronic effect of the transgenic corn lines containing the *mCry1Ac* gene from *Bacillus thuringiensis* strain (BT) to White Leghorn laying hens for 12 wk and their offspring from 1 d to 36 wk on offspring growth

and health. Healthy hens (n = 72 placed in cages; 3 hens/cage) were randomly assigned to 1 of 3 corn-soybean meal dietary treatments (8 cages/treatment) formulated with the following corn: 61.7% nontransgenic near-isoline control corn (CT), BT corn, and commercially available nontransgenic reference corn (RF) for 12 wk. After 12 wk, fertile eggs were collected daily and hatched for 21 d. A total of 240 offspring pullets were assigned to 3 dietary treatment for 36 wk, i.e., 1) CT corn-fed parental hens/CT corn-fed offspring pullets (CT/CT); 2) BT corn-fed parental hens/BT corn-fed offspring pullets (BT/BT); and 3) RF corn-fed parental hens/RF corn-fed offspring pullets (RF/RF). Each dietary treatment was assigned to 10 replicates with 8 offspring pullets per replicate for a total of 80 pullets per treatments. Body weight and egg quality of pullets were determined weekly. Offspring hens were harvested at the end of 36 wk (n = 8/treatment), and carcass yield and organ weights (heart, liver, spleen, lung, kidneys and ovary) were recorded; organs and intestines were sampled for histological analysis. Analysis of serum biochemistry parameters, hematology, and hormone were performed. Immune cell phenotypes of spleen and peripheral blood mononuclear cells were determined. No differences in body weight, egg quality and function of reproductive organs were observed between hens consuming the CT/CT diet and hens consuming the BT/BT diet. Intestinal histology and health were similar between the control and test groups. The relative weight of lung and kidneys of hens fed the BT/BT treatment was less than hens fed the CT/CT treatment ($P < 0.05$). Liver and kidney histology and health were not affected by the diet treatment. Offspring hens from the BT/BT treatment had greater duodenal goblet cells/villus ($P < 0.05$) and jejunal villus height/crypt depth ratios ($P = 0.06$). Similar organosomatic indices, serum biochemistry parameters, hematology, and hormone parameters did not indicate the characteristics of organ dysfunction. Immune response was not affected by the trans-generation feeding BT/BT diet. These results indicate that trans-generational consumption of the BT corn diets is not detrimental to hen growth and health.

Key Words: *Bacillus thuringiensis*, genetically modified, hen, *mCry1Ac* gene corn, trans-generational effect

0976 Effects of methionine or arginine supplementation and environmental temperature on performance, carcass traits and meat quality of finishing pigs. J. K. Htoo[*1], C. A. Garbossa[2], H. Silveira[2], L. G. Amaral[2], N. A. Barbosa[3], and V. S. Cantarelli[2], *[1]Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany, [2]Federal University of Lavras, Lavras, Brazil, [3]Evonik Industries do Brazil, São Paulo, Brazil.*

A 46-d study was conducted to determine the effects of methionine (Met) or arginine (Arg) supplementation in a thermal-neutral (24°C) or heat stressed (32°C) environment on performance, carcass characteristics and meat quality of finishing pigs. Seventy-two mixed-sexed pigs (PIC × DanBred; initial BW of 69.1 ± 0.11 kg) were assigned to 6 diet regimes using a 2 × 3 factorial arrangement with 3 dietary treatments [a basal diet (BD), the BD + 0.15% DL-Met or the BD + 0.40% L-Arg], and 2 environmental temperatures (24°C or 32°C) having 6 pen replicates (2 pigs/pen) per treatment. Diets were formulated based on corn, soybean meal and corn gluten meal using the analyzed ingredient AA contents and published standardized ileal digestible (SID) coefficients to meet AA requirements for both finisher 1 (0.76% SID Lys; 70–90 kg) and finisher 2 (0.69% SID Lys; 90–112 kg) phases. Pigs were fed the finisher 2 diets until they reached a predetermined market weight (115 kg). At slaughter, 36 pigs (6 pigs/treatment) were selected for carcass assessment. Samples of longissimus dorsi (LD) muscle were used for meat quality assessments. Data were analyzed using the MIXED procedure of SAS. There was no diet × temperature interaction for any variables ($P > 0.05$). Compared with 24°C, ADFI, ADG and G:F were lower ($P < 0.001$) under 32°C temperature during each phase and the overall 46-d period, except for the ADFI during finisher 2 period ($P = 0.056$). Overall, supplementing with 0.15% DL-Met or 0.40% L-Arg reduced ADFI ($P = 0.033$) and increased G:F ($P = 0.012$). Compared with 24°C, 32°C temperature increased ($P < 0.05$) chilled carcass yield and 24 h pH of carcass but decreased ($P < 0.05$) drip loss after 24 and 48 h and the number days to reach 115 kg BW. The 24 h pH of carcass tended to increase ($P = 0.053$) by 0.15% DL-Met addition but all other measured carcass parameters including lean percentage and backfat thickness were not affected by dietary treatments. The concentrations of cortisol and heat shock protein 70 (HSP70) in plasma and concentrations of thiobarbituric acid reactive substances and hydrogen peroxide in LD muscle were not affected by the dietary treatments or the environment temperature. These results indicate that heat stress reduces pig performance and may affect carcass quality. Additional L-Met or L-Arg supplementation in finisher pig diets may improve feed efficiency.

Key Words: arginine, methionine, temperature

0977 A protective effect of IGF-activated plasma protein (CTCgrow) on lipopolysaccharide-induced intestinal dystrophy in rats. M. Kwak[*1], J. Kim[1], J. M. Lee[2], S. W. Jung[2], and K. Y. Whang[1], *[1]Korea University, Seoul, The Republic of Korea, [2]CTC BIO, Seoul, The Republic of Korea.*

In livestock industry, dietary plasma protein has shown the improved growth performance of weaned animals and it seems to be more than nutrient content itself. The exact mechanism of plasma protein on enhancing growth performance is not fully understood yet, but dietary insulin-like growth factors (IGFs) in plasma protein might have an important role. But it has been also suggested that IGFs with binding protein

might attenuate the growth-promoting effects of IGFs. Therefore, we conducted an experiment to determine the protective effects of commercially available IGF-activated plasma protein product (by de-binding with protein, CTCgrow) on intestinal dystrophy induced by lipopolysaccharides (LPS). Forty-two rats (4 wk-old) were allotted into six treatments in a 2 × 3 factorial design. One factor was dietary supplementation (CON, control; PP, 50 g/kg of plasma protein; and aIGFPP, 3.4 g/kg of IGF-activated plasma protein) and the other factor was LPS-challenge (PBS or LPS). Basal diet was formulated based on NIH-31 diet. During 4 wk of feeding period, rats were allowed to the diets ad libitum and growth performance was recorded weekly. On Day 28, rats were injected with either LPS or PBS and growth performance was recorded every day for 3 d. At Day 3 post-injection, rats were sacrificed and gut morphological change was investigated in jejunum samples. Before LPS-challenge, body weight and feed intake of aIGFPP group were numerically higher than those of other groups. After LPS-challenge, aIGFPP alleviated the weight loss induced by LPS-challenge and showed significantly higher feed efficiency than PP ($P < 0.05$). In non-challenged groups, there were significantly higher villus height (VH) and VH:CD ratio and lower crypt depth (CD) in aIGFPP than other groups ($P < 0.05$). And the number of goblet cells per villus was also significantly higher in aIGFPP than other groups ($P < 0.05$). And there was a tendency that LPS-challenged groups showed lower VH and higher CD than non-challenged groups in respective dietary treatment groups. In LPS-challenged groups, VH and VH:CD ratio were numerically higher in CON and aIGFPP than PP. The number of goblet cells per villus was significantly higher in LPS-challenged aIGFPP than other LPS-challenged groups ($P < 0.05$). These results indicated that aIGFPP had a growth-promoting effect by improvement of intestinal morphology before LPS-challenge. Also aIGFPP demonstrated a protective effect on gut mucosal injury induced by LPS.

Key Words: rats, intestine, gut morphology, IGF, plasma protein

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0978 Effects of α-Galactosidase supplementation on the energy value of soybean meal and growth performance of weanling pigs. C. D. Espinosa*, *University of the Philippines Los Baños, Laguna, Philippines; University of Illinois at Urbana-Champaign, Urbana-Champaign.*

Two experiments were conducted to determine effects of supplementing diets with an α-galactosidase enzyme complex on the energy value of soybean meal (SBM), apparent total tract digestibility (ATTD) of nutrients in corn-SBM diets, and growth performance of weanling pigs. In Exp. 1, 40 barrows (PIC 337 × C24; initial BW 9.9 ± 1.9 kg) were randomly allotted to 5 dietary treatments with 8 pigs per diet. A basal diet consisting of 94.89% corn (as-fed basis) and 4 diets containing 70% of the basal diet and 30% (as-fed basis) SBM supplemented with 0, 100, 200, or 400 mg/kg of an α-1,6-galactosidase enzyme complex were formulated. Pigs were individually housed in metabolism crates that allowed for the total, but separate, collection of urine and fecal materials from each pig. Results indicated that addition of increasing concentrations of α-1,6-galactosidase enzyme complex increased (linear, $P < 0.05$) DE, and tended (linear, $P = 0.09$) to increase ME of SBM by approximately 300 kcal/kg (as-fed basis). The enzyme complex also improved ($P < 0.05$) the ATTD of ash and tended ($P < 0.10$) to improve the ATTD of DM, hemicellulose, OM, and crude fat. In Exp. 2, 378 pigs (PIC 337 × C24; initial BW 4.5 ± 1.8 kg) were randomly allotted to 1 of 3 dietary treatments with 21 pigs per pen and 6 pen replicates per treatment. The experiment lasted 10 d. Treatments included 2 diets (without or with the enzyme complex) formulated with the assumption that SBM contained 3344 kcal ME/kg (as-fed basis). The last diet was formulated assuming that the SBM contained 3644 kcal ME/kg if 100 mg/kg of the enzyme complex was also included in the diet. Inclusion of SBM was 18% in all diets. Results indicated that regardless of the presumed ME in SBM, addition of the enzyme improved ($P < 0.05$) total BW gain, tended ($P = 0.09$) to improve ADG, and tended ($P = 0.10$) to improve caloric efficiency when compared with the diet containing no enzyme. The cost of feed/kg of gain also tended ($P = 0.10$) to be reduced by addition of the enzyme complex to the diet. In conclusion, the α-1,6-galactosidase enzyme complex used in these experiments improved the energy value of SBM and the ATTD of nutrients, which may result in reduced cost of production per unit of gain.

Key Words: α-galactosidase, soybean meal, weanling pigs

0979 Use of crystalline amino acids in meal feeding does not affect nitrogen retention in growing pigs compared to protein-bound amino acids. S. A. Lee* and B. G. Kim, *Konkuk University, Seoul, The Republic of Korea.*

The present study was conducted to test the hypothesis that the supplementation of crystalline AA (CAA) affects the N retention for growing pigs in the meal feeding. Ten pigs with initial BW of 53.6 kg (SD = 2.7) were individually housed in metabolism crates. The pigs were allotted to 2 experimental diets according to a crossover design with 10 animals and 2 periods. Two experimental diets were formulated. A diet was mainly based on corn and soybean meal as N sources (protein-bound form-diet, PBD), and the CAA were supplemented to the PBD at the expense of 14.2% soybean meal (CAA-supplemented diet, CD). The supplementation levels of CAA were determined based on the standardized ileal digestible AA in the SBM. The daily amount of feed allowance per pig was determined as 3 times the maintenance energy of pigs within similar BW and an equal amount of the feeds was provided at 0730

and 1630 h. Total but separate collection of feces and urine was performed according to marker-to-marker and time-to-time methods, respectively. The amounts of excreted and retained N were determined based on the analyzed N contents in the fecal and urinary samples. Nitrogen intake of pigs fed the PBD and CD were 52.4 and 46.2 g/d ($P < 0.001$), respectively. The fecal N excretion (7.52 and 6.23 g/d, $P = 0.014$), digested N (44.9 and 39.9 g/d, $P < 0.001$), and retained N (24.9 and 22.2 g/d, $P = 0.014$) in the pigs fed the PBD were greater than in the pigs fed the CD. However, the apparent total tract digestibility of N and retention of N did not differ among the pigs fed 2 experimental diets. In conclusion, the use of CAA in the meal feeding did not affect the N retention in growing pigs compared to the protein-bound AA from the SBM.

Key Words: free amino acid, nitrogen retention, protein-bound amino acid

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0980 Effects of SILOHealth 104 supplementation on the growth performance of Ross 308 broiler chickens.

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Global consumption of poultry products has consistently increased over the past 30 yr, requiring producers to maintain chicken production to meet the demands. With the rising concern regarding the inclusion of antibiotics in feed, developing a viable alternative for poultry production is of a significant interest. Butyric acid, a short chain fatty acid, is the primary energy source for colonocytes and has shown potential as an alternative to in-feed antibiotics, including its antimicrobial activity and positive effects on production performance traits of broiler chickens. SILOHealth 104 (SILO S.P.A., Florence, Italy) is a commercial butyrate product mainly containing mono- and di-glycerides of butyrate with a small portion of mono- and di-glycerides of propionic, caprylic, capric, and lauric acids. Its effects on broiler performance have yet to be evaluated. Four hundred and eighty day old male Ross 308 birds were divided into different treatment groups with equal starting weights and fed a basal diet, or basal diet including 500, 1,000, 2,000, or 3,000 ppm of SILOHealth 104 for 35 d. There were no significant differences in overall average daily gain or feed:gain ratio with the addition of SILOHealth 104 to the diets ($P > 0.05$). At 5 wk of age, abdominal fat weight was reduced in birds supplemented with SILOHealth 104 in a dose responsive manner ($P < 0.05$), while breast muscle weight increased with supplementation up to 2000 ppm, with significant increases in 1000 ppm and 2000 ppm birds compared to controls ($P < 0.05$). Expression of both Forkhead box protein O4 and myostatin, two factors that can inhibit protein synthesis, were found to be significantly decreased in the breast muscle of all SILOHealth 104 birds compared to control birds ($P < 0.05$). These data suggest that the components of SILOHealth 104 can positively impact the deposition of muscle, while reducing abdominal fat deposition in broiler chickens.

Key Words: broiler, butyrate glycerides, breast muscle

0981 Effect of increasing *Buttiauxella* phytase dose to 2000 FTU/kg on phytate degradation and ileal AA digestibility in weaned pigs.

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This study determined the effect of increasing *Buttiauxella* phytase dose on phytate degradation and ileal AA digestibility in weaned pigs. Six treatments were tested including a nutritionally adequate positive control (PC); a negative control (NC) with reduction of 0.1% Ca, 0.14% digestible P and 35 kcal/kg ME vs. PC; NC supplemented with a *Buttiauxella* sp. phytase at 250, 500, 1,000 or 2,000 phytase units (**FTU**)/kg feed. One FTU was defined as the amount of enzyme required to release 1 µmol of iP per minute from sodium phytate at pH 5.5 at 37°C. Male pigs (Topigs × Pietrian, barrows, 20kg BW) were randomly allocated in metabolism crates (1 pig per crate) in 2 runs, 24 pigs in each run with a total of 8 replicates per treatment. Pelleted diets based on mixed grain (wheat, corn and barley) were fed for 9 d with 3 d adaptation, 5 d collection of feces and urine (for measuring apparent total tract digestibility [ATTD]) and 1 d to collect ileal digesta (for measuring apparent ileal digestibility [AID], TiO_2 as marker). The diets were supplied at 2.5 times energy requirement for maintenance in 2 equal meals per day, water was freely available. Treatment means were compared using Tukey's HSD, linear or nonlinear responses were determined using JMP 11 (SAS). Phytase at 2,000 FTU/kg showed greater ($P < 0.05$) nutrient digestibility vs. NC or PC for most of the parameters. Increasing phytase dose from 0 (NC) to 2,000 FTU/kg linearly improved ($P < 0.05$) ATTD of P, retainable P, Ca, DM, N, ME as well as AID of P, N, Lys, Met, Cys, Thr, Val, Ile, Leu and mean essential AA. While AID of Ca and Trp increased in a nonlinear manner. AID of phytate was 36, 39, 54, 67, 76, and 83%, respectively, for PC, NC, phytase at 250, 500, 1,000 and 2,000 FTU/kg feed ($P < 0.05$). The AID of phytate was linearly correlated with mean AID of AA ($P < 0.05$). In conclusion, increasing *Buttiauxella* phytase dose increased the level of phytate degradation, resulting in improved digestibility of AA and other nutrients. This demonstrated that increasing *Buttiauxella* phytase dose to 2,000 FTU/kg can lead to both phosphoric and extra-phosphoric effects.

Key Words: pigs, phytate degradation, AA digestibility

0982 Influence of dietary crude protein and phosphorus levels on the utilization of crude protein and phosphorus in growing pigs. P. Xue*[1] and O. Adeola[2], [1]*Purdue University, West Lafayette, IN,* [2]*Department of Animal Sciences, Purdue University, West Lafayette, IN.*

A study was conducted to determine the response of total tract utilization of CP and P to different CP and P levels in growing pigs. A total of 72 growing pigs (initial BW 20.9 ± 0.8 kg) were used in a randomized completely blocked design, with 9 treatments and four 10-d experimental periods giving 8 replicates per treatment. The pigs were blocked by BW and allotted to 9 treatments with a 3 × 3 factorial arrangement consisted of 3 CP levels (5.5, 9.7, or 13.9%) and 3 apparent total tract digestible P (ATTDP) levels (0.11, 0.19, or 0.27%). The CP level and ATTDP levels were adjusted using SBM and mono-calcium phosphate (MCP), respectively. Limestone was included to maintain the Ca: ATTDP ratio across diets. There was a 5-d adjustment period followed by a 5-d total collection period. Chromic oxide and ferric oxide were used as markers to time the initiation and termination of fecal collection, respectively. The daily feed intake was adjusted to 4% of the average BW of each block, in 2 equal daily feeding regimen at 0730 and 1730 h. Data was analyzed using PROC MIXED of SAS (9.4) and contrasts were used to test the linear and quadratic effects of increasing levels of P within each CP level, or vice versa. Digested P (g/d) was regressed against P intake (g/d) for each CP level to determine the true total tract digestibility (TTTD) of P in MCP. Digested P (g/d) increased linearly along with the increasing level of CP ($P < 0.05$). The determined TTTD of P in MCP for 5.5, 9.7, and 13.9% CP diets were 80.5, 82.6, and 87.9%, respectively. There were no statistical differences among the three TTTD estimates. In the nitrogen utilization results, increasing dietary P level decreased the urine nitrogen output ($P < 0.05$). In conclusion, the results indicated that dietary CP deficiency may limit total tract P digestion.

Key Words: crude protein, phosphorus, total tract digestibility

0983 Effects of Dakota gold and high fat commodity DDGS in a complete diet on pellet quality. A. D. Yoder*, *Kansas State University, Manhattan.*

Inclusion of dried distillers grains with solubles (DDGS) in pelleted feed is limited because of pellet quality. Including a reduced-fat DDGS instead of a higher fat DDGS may mitigate these negative effects. Thus, the objective of this experiment was to evaluate pellet quality when 2 different sources of DDGS were used in a pelleted complete feed. The experiment was set up as a 2 × 2 × 2 × 4 factorial arrangement with 2 sources of DDGS (reduced and high-fat DDGS), 2 pellet temperatures (65.6°C and 82.2°C), 2 inclusion rates (15% and 30%) and 4 Pellet Durability Methods (Standard Pellet Durability Index (PDI; ASABE S269.4, 2007), Modified PDI (three 19-mm hex nuts), Holmen NHP 100 for 60 s, and Holmen NHP 200 for 240 s) in a typical complete feed formulated for a finishing swine diet. Reduced-fat DDGS (Dakota Gold) was sourced from POET, LLC and high-fat DDGS was sourced from a local feed mill. Feed was pelleted on a 1 ton per hour pellet mill (CPM Model PM 1012–2) equipped with a 4.0 mm × 32 mm die. Throughput was held constant at 680 kg/hour. Each treatment was replicated 3 times. Data were analyzed using the GLIMMIX procedure of SAS. There was no interaction between any 2 variables of the experiment. The addition of Dakota Gold improved pellet quality by 5.2% points ($P < 0.05$). The PDI results were 88.0% and 82.8% for the Dakota Gold and 8% fat commodity DDGS, respectively. Inclusion level ($P = 0.71$) or conditioning temperature ($P = 0.103$) had no effect on PDI. The PDI method of analysis had the greatest effect on the results ($P < 0.05$). The result of Standard PDI, Modified PDI, Holmen NHP 100, and Holmen NHP 200 were 95%, 91%, 89%, and 67%, respectively. The NHP 200 method produced the lowest values primarily due to the long run time of the method. The feed industry should select the method that best models their feed manufacturing and delivery processes. The results of this experiment indicate that the addition of lower fat DDGS improves pellet quality, and the PDI method of analysis can significantly impact the results reported in the industry.

Key Words: pellet, DDGS, pellet durability index

0984 Oregano essential oil supplementation in gestation and lactation shortened birthing interval in primparous and multiparous sows. M. Renken, R. C. Thaler, and C. L. Levesque*, *South Dakota State University, Brookings.*

A total of 15 gilts and 26 sows (parity 2 to 5) were used to assess the impact of oregano EO (By-O-Reg, Advanced Ag Products) supplementation in gestation and lactation on farrowing characteristics (duration and birth interval), and sow and piglet performance. Females were assigned to 1 of 2 dietary treatments at breeding [0 or 2 g/d oregano EO supplementation]. Experimental diets were fed throughout gestation and lactation (21 d). Diets were offered once daily in gestation and twice daily in lactation, and oregano EO was added as a top dress with the AM feeding. Diets were formulated to meet or exceed nutrient requirements for sows/gilts in gestation (0.6% SID Lysine and 3280 kcal ME/kg) and lactation (0.9% SID Lysine and 3280 kcal ME/kg). Control sows (0 g/d EO) received soy hulls (the carrier for the EO) at 2 g/d. Assessment of sow performance included body weight and backfat (breeding, d 110 of gestation, d 1 of lactation, and at weaning), and lactation feed intake. Piglets were weighed at birth and at weaning. All farrowings were attended by a trained technician and farrowing duration was determined as the time between birth of the first and last piglets and piglet birth interval was

recorded. Data was analyzed as a RCB design with sow as the experimental unit. Sow performance was not affected by EO supplementation: mean body weight was 180.0 ± 8.9 kg and 233.7 ± 5.3 kg at breeding and d110, respectively and lactation feed intake was 7.09 ± 0.35. Gestation length tended to be shorter ($P = 0.11$) in EO supplemented sows (115.0 vs. 115.7 ± 0.3). Farrowing duration (3.5 ± 0.5 h) was not influenced by EO supplementation but birthing interval tended to be shorter ($P = 0.10$) in EO fed sows (14.0 vs. 20.2 ± 2.8 min/pig). Born alive (12.8 vs. 11.9 ± 0.8), stillborns (0.26 vs. 0.40 ± 0.17), piglet birth weight (1.33 vs. 1.36 ± 0.03 kg) and piglet weaning weight (7.38 vs. 7.26 ± 0.16 kg) were not influenced by maternal EO supplementation. Subsequent rebreeding interval tended to be increased ($P = 0.06$) in EO fed sows (4.7 vs. 4.5 ± 0.1 d). Oregano EO supplementation had little impact on sow and piglet performance but appeared to positively impact birthing interval and gestation length. A shorter birthing interval may reduce the risk of stillborns and limit the need for farrowing assistance.

Key Words: birthing interval, essential oil, sow

0985 Effects of casein on digestibility of amino acids in distillers dried grains with solubles fed to pigs.

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The objective of this experiment was to determine the true ileal digestibility (TID) of CP and AA in casein and to determine the effects of inclusion of casein in experimental diet on apparent ileal digestibility (AID) and standardized ileal digestibility (SID) of CP and AA in corn distillers dried grains with solubles (DDGS) fed to pigs. Eighteen barrows with an initial BW of 50.5 ± 4.5 kg were surgically fitted with T-cannula at the distal ileum and individually housed in metabolism crates. Pigs were allotted to triplicate 6 × 3 incomplete Latin square design with 6 dietary treatments and 3 periods. The 6 dietary treatments consisted of 3 diets formulated to contain 6, 10, or 14% casein; 2 diets prepared to contain 48% DDGS or 30.8% DDGS and 6% casein; and one nitrogen-free diet to determine the basal ileal endogenous losses of CP and AA. Each period lasted 7 d consisted of 5 d of adaptation period and 2 d of ileal digesta collection period. The AID of CP and all AA in casein were linearly increased ($P < 0.01$) with increasing dietary casein. The estimated TID of CP, Lys, Met, Thr, and Trp were 101% (SE = 3.2), 99.9% (SE = 2.12), 99.2% (SE = 1.17), 97.0% (SE = 3.23), and 98.8% (SE = 3.30), respectively. The AID and SID of Arg, Lys, Phe, and Trp in diet containing DDGS were less ($P < 0.01$) than those in diet containing DDGS and casein. There were no differences between the AID of CP, His, Ile, Thr, and Val in diet containing DDGS and those in diet containing DDGS and casein. However, the SID of CP, His, and Ile in DDGS diet were less ($P < 0.05$) than those in DDGS and casein diet. In conclusion, improving protein quality in experimental diets by inclusion of highly digestible protein sources such as casein may affect the SID of CP and AA in test ingredients of lower protein quality.

Key Words: digestibility, nutrient, swine

0986 Investigations of marker and fiber effects on energy and nutrient utilization in growing pigs.

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An experiment was conducted to investigate whether the apparent ileal and total tract digestibility of nitrogen and energy, and excretion patterns of indigestible markers were influenced by the type of marker and dietary fiber. Twenty barrows surgically fitted with T-cannula at the end of ileum were used in two experimental periods consisting of a 7-d adjustment period followed by a 3-d total fecal collection period and a 3-d ileal digesta collection period. Three diets were identically formulated except for 10% of the cornstarch (CS), corn bran (CB) or oat bran (OB). All three diets contained three index markers (5 g/kg chromic oxide [Cr_2O_3], 5 g/kg titanium dioxide [TiO_2], and 20 g/kg acid-insoluble ash [AIA]). Pigs were fed at 0800 h and 1600 h with 2 equally sized meals during the experimental period. The ileal digesta were collected every 3 h from 0900 h to 1700 h with 4 time periods (TP) on ileal digesta collection days. For all 3 markers, the marker concentration of CS diet was greater than OB diet, which had greater marker concentration than CB diet ($P < 0.001$). The marker concentration of the first ileal collection day (Day1) was significantly lower than the third day (Day3) for Cr_2O_3 ($P = 0.05$), TiO_2 ($P < 0.001$) and AIA ($P < 0.01$), respectively. The 3 markers were excreted in a similar pattern over 4 TPs for ileal digesta. The highest marker concentration appeared at the second TP (1200 h to 1500 h). The apparent ileal digestibility of energy (AIDE) and nitrogen (AIDN) of CB and OB diets was not affected by markers. For all 3 diets, the apparent total tract digestibility of energy (ATTDE) and nitrogen (ATTDN) determined by total collection method was greater ($P < 0.05$) than those determined by using inert digestibility markers. The ATTDE and ATTDN of CB diet calculated based on Cr_2O_3 were lower ($P < 0.05$) than those determined by TiO_2, but for OB diet, the ATTDE and ATTDN determined by AIA were greater ($P < 0.05$) than those determined by TiO_2. In conclusion, the marker distribution varied over time periods and was affected by fiber type, and the marker type may affect the estimate of total tract but not ileal digestibility of energy and nitrogen.

Key Words: markers, fibers, digestibility

0987 Evaluation of ileal energy digestibility of diets based on different grain species fed to growing pigs. P. Rosenfelder*, H. K. Spindler, E. J. P. Strang, E. DeGiorgi, M. Eklund, and R. Mosenthin, *University of Hohenheim, Institute of Animal Science, Stuttgart, Germany.*

It is well accepted that feed energy digested until the end of the ileum is more efficiently utilized by the pig than energy fermented microbially in the hindgut. Thus, ileal rather than fecal energy digestibility values may be closer to the actual energy available for maintenance and production, but data on ileal energy digestibility of cereal grains are scarce. The objective of the present study was to determine in growing pigs the ileal energy digestibility of diets based on 8 different genotypes of barley, rye, triticale, and wheat each. Therefore, 4 experiments were conducted with 8 or 9 ileally cannulated growing pigs (initial BW of 24 to 32 kg) each. The assay diets were formulated to contain 1 of the 8 genotypes of each grain species at an inclusion level of 95% (on as-fed basis). All diets were supplemented with plant oil, minerals and vitamins, and titanium dioxide as an indigestible marker. The experiments were either arranged as a row-column design with 8 periods of 6 d each and 9 pigs (for barley and wheat), or according to an 8 × 8 Latin square design with 8 periods of 6 (rye) or 7 d (triticale) and 8 pigs. Experimental periods comprised 4 (barley, rye, and wheat) or 5 d (triticale) for adaptation, followed by 2 d for ileal digesta collection. The daily feed intake amounted to 4% of pigs' average BW, corresponding to about 3 times the animals' energy requirement for maintenance (106 kcal of ME/kg of $BW^{0.75}$). On average, ileal energy digestibility amounted to 65, 67, 78, and 73% for barley, rye, triticale, and wheat diets and was different between grain species ($P < 0.05$). Ileal energy digestibility was different within the 8 rye diets ($P < 0.05$) with values ranging between 66 and 70%, but there were no differences in ileal energy digestibility within barley, triticale, or wheat diets. Differences in ileal energy digestibility within rye diets reflect variations in contents of fiber fractions of the rye genotypes, as higher contents of NDF, ADF, and different non-starch polysaccharide fractions resulted in a linear decrease in ileal energy digestibility ($P < 0.01$). In conclusion, triticale is superior in ileal energy digestibility compared to the other grain species.

Key Words: cereal grains, ileal energy digestibility, growing pigs

0988 The relationship between the expression of genes regulating appetite control and feeding behavior in pigs divergent in feed efficiency. S. Vigors[1], J. V. O'Doherty[2], A. K. Kelly[2], and T. Sweeney*[1], [1]*School of Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland,* [2]*School of Agriculture and Food Science, University College Dublin, Dublin 4, Ireland.*

More efficient pigs eat less than their less efficient counterparts, however the regulation of appetite and feeding behavior in the hypothalamus and intestine has not been well researched. Therefore, the objective of this study was to examine the association between residual feed intake (RFI) and feeding behavior with both hypothalamic and gut peptides involved in appetite control. Seventy-five male pigs (initial BW 22.4 kg [SD = 2.03]) were fed a standard finishing diet (13.8 MJ DE/kg and 9.5 g standard ileal digestible [SID] lysine/kg) during a 42 d period for the purpose of calculating RFI and evaluating feeding behavior. Following the calculation of RFI on Day 112, 8 high RFI (HRFI) and 8 low RFI (LRFI) pigs (average weight 85 kg, sem 2.8 kg), were slaughtered (115 d.o). Tissue was collected from the hypothalamus and small intestine to analyze the gene expression of neuropeptides and gut peptides associated with appetite control. Behavioral analysis confirmed that LRFI pigs ate less ($P < 0.0001$), spent less time eating per day ($P < 0.05$), had smaller meals ($P < 0.05$), and spent less time eating each meal than the HRFI pigs ($P < 0.10$). In the jejunum and ileum, the HRFI pigs had increased expression of glucagon-like peptide 1 receptor (*GLP-1R*) ($P < 0.05$), with no changes in the other measured gut or hypothalamic peptides ($P > 0.10$). While RFI was unrelated to neuropeptide gene expression, the amount eaten per feeder visit was positively correlated with cocaine and amphetamine related transcript gene expression (*CART*) in the periventricular nucleus ($r = 0.63$; $P < 0.01$). The expression of pro-opiomelanocortin (*POMC*) was negatively correlated with eating rate ($r = -0.62$; $P < 0.011$). In the duodenum the amount eaten per visit was positively correlated with the expression of cholecystokinin (CCK; $r = 0.56$) and *GLP-1R* ($r = 0.54$). In conclusion HRFI pigs had increases in activity related to feeding behavior and increased gene expression of *GLP-1R.* This study identified strong relationships between feeding behavior traits and the gene expression of the hypothalamic neuropeptides *CART, POMC* and the gut peptide *CCK* suggesting these neuropeptides are important in the control of feeding behavior in pigs.

Key Words: gut peptides, neuropeptides, pigs, residual feed intake

0989 Ileal amino acid digestibility in broiler chicken fed rice bran with or without carbohydrase and phytase. C. Gallardo*, J. C. Dadalt, J. C. da Silva Maciel de Souza, and M. A. D. T. Neto, *University of São Paulo, Pirassununga, Brazil.*

Exogenous enzymes improve feedstuffs used by poultry but information on amino acid digestibility is still limited. Apparent ileal digestibility (AID) and standardized ileal digestibility (SID) of amino acids (AA) in broiler chicks fed rice bran (RB) with or without multi-carbohydrase (MC; 35 U/g α-galactosidase, 110 U/g galactomannanase, 1,500 U/g xylanase and 1,100 U/g β-glucanase) and Phytase (Phy; 10,000 FTU/g) supplementation was investigated. A total of 245 male broilers (7 birds/pen) were fed with one low-protein diet and four corn-starch-based diets containing 30% of RB as sole source of protein in 2 (MC; 0 or 200 mg/kg) × 2 (Phy; 0 or 50 mg/kg) factorial arrangement. Low-protein diet (5% casein) was used to estimate endogenous AA losses. All diets contained Chromium (0.3%) as an indigestible marker. All birds were slaughtered on 21st for ileal digesta collection. Data were analyzed using the GLM procedure of SAS (Statistical Analysis System, version 9.2) for enzyme effects and probable interaction on digestibility. Compared to diet without enzymes, single inclusion of MC or Phy showed effect ($P < 0.05$) on AID and SID of AA. Absolute increases on AID and SID of AA, from MC + Phy supplementation, exceeded the single sum of the increases from MC or Phy supplementation. Averages of 17 AA from AID and SID were: 63.03% and 74.08% for RB without enzyme; 63.73% and 75.11% for RB with MC, 64.22% and 75.41% for RB with Phy, and, 64.65% and 75.98% for RB with MC + Phy, respectively. Interaction ($P < 0.05$) from MC × Phy was observed on AID for Arg, His, Thr, Val, Glu and Ser; and SID for Arg, His, Leu, Val, Asp, Glu and Ser; and a trend on AID for Asp ($P = 0.072$), and SID for Thr ($P = 0.051$) and Pro ($P = 0.080$). The beneficial effects from MC combined with Phy may be an effective strategy to improve AID and SID of AA in RB for broiler chicks.

Key Words: apparent, standardized, enzyme

0990 Effect of dietary net energy and digestible lysine levels on performance of weaned and starter pigs fed low protein-amino acids fortified diets. J. K. Htoo*[1] and J. Morales[2], [1]*Evonik Nutrition & Care GmbH, Hanau-Wolfgang, Germany,* [2]*PigCHAMP Pro Europa, Segovia, Spain.*

Two experiments were conducted to evaluate the effect of dietary NE and standardized ileal digestible (SID) Lys levels on performance of 7 to 10 kg pigs (Exp. 1) and 9 to 17 kg pigs (Exp. 2). In Exp. 1, 288 mixed-sex pigs (PIC; initial BW of 7.0 ± 0.45 kg) were assigned to 6 diet regimes using a 2 × 3 factorial design with 2 levels of SID Lys (1.35 or 1.42%) and 3 NE levels (10.00, 10.35 or 10.70 MJ/kg) for 14 d. In Exp. 2, 288 mixed-sex pigs (PIC; initial BW of 9.2 ± 0.39 kg) were assigned to 6 diet regimes using a 2 × 3 factorial design with 2 levels of SID Lys (1.22 or 1.32%) and 3 NE levels (9.75, 10.10 or 10.45 MJ/kg) for 21 d. For both studies there were 6 pen replicates (3 barrows and 3 gilts/pen) per treatment, and diets were based on corn, soybean meal and whey powder using the analyzed ingredient AA contents to meet requirements. There was no NE x SID Lys interaction for any measured parameter ($P > 0.05$) in both Exp. 1 and 2. In both Exp. 1 and 2, ADFI was not affected ($P > 0.05$) by SID Lys or NE levels. The amount of SID Lys (g/kg of gain) was not affected ($P > 0.05$) by the treatments in both studies. In Exp. 1, pig performance seemed to maximize at 1.42% SID Lys and 10.35 MJ NE. However, ADG and G:F were not affected by the NE level. Compared with 1.35% SID Lys, 1.44% SID Lys increased G:F (0.782 and 0.833; $P = 0.035$) but did not affect ADG (233 and 244 g/d; $P > 0.05$). In Exp. 2, pig performance seemed to maximize at 1.32% SID Lys and 10.10 MJ NE. The dietary NE level did not affect ADG and G:F. Increasing dietary SID Lys from 1.22 to 1.32% increased ADG (388 and 420 g/d; $P = 0.014$) but did not affect G:F (0.592 and 0.616; $P = 0.105$). These results indicate that performance of 7 to 10 kg pigs maximized when the diet contains 1.42% SID Lys and 10.35 MJ/kg NE (SID Lys:NE of 1.37 g/MJ). For 9 to 17 kg pigs, performance maximized at the dietary SID Lys of 1.32% and NE of 10.10 MJ/kg (SID Lys:NE of 1.31 g/MJ).

Key Words: lysine, net energy, performance

0991 Relationship between the microbiota in different sections of the gastrointestinal tract, and the body weight of broiler chickens. J. Lee* and C. Kong, *Konkuk University, Seoul, The Republic of Korea.*

In the poultry industry, many efforts have been undertaken to improve the growth performance of broiler chickens and identification and modulation of body weight (BW)-related bacteria could be one of the strategies to improve productivity. However, studies regarding the relationship between BW and microbiota are scarce. The objective of the present study was to investigate the relationship between BW and microbiota in different sections of the gastrointestinal tract (GIT), and explore the BW-related bacterial groups in broiler chickens. A total of twenty 18-d-old Ross 308 male broiler chickens were selected based on BW, and samples were collected individually from the 3 different sections of the GIT, which included the crop, ileum and cecum. Bacterial genomic DNA was extracted from the samples, and the V4 region of 16S rRNA gene was amplified. All the amplicons were then sequenced on Illumina MiSeq, and microbial communities were analyzed by using QIIME. In principal coordinate analysis, bacterial communities were clustered into three groups, based on the sections of GIT. Several BW-related bacterial groups were identified from linear regression analysis with R statistical package (version 3.0.3). At the genus level, *Streptococcus*

in the ileum ($r = -0.81$, $P < 0.001$) as well as *Akkermansia* in ileum ($r = -0.51$, $P = 0.023$) and cecum ($r = -0.55$, $P = 0.022$), were negatively related to BW, whereas *Bifidobacterium* in the ileum ($r = 0.49$, $P = 0.029$) and *Lactococcus* in the cecum ($r = 0.59$, $P = 0.006$) showed a positive correlation. The results from the present study showed that particular bacterial communities in the GIT were related to BW, and the study has broadened the understanding of the intestinal microbial ecosystem in broiler chickens.

Key Words: broiler chickens, gastrointestinal tract, microbiota

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0992 Nutrient profile and in vitro digestibility of cassava silages in swine. U. P. Tiwari*, and R. Jha, *University of Hawaii at Manoa, Honolulu, HI.*

Exploring and evaluating alternative feedstuffs to develop cost-effective and sustainable feeding program is of utmost need when market availability and price of conventional feedstuffs are variable. Cassava (*Manihot esculenta*) is a starchy tuber with high energy content while its leaves are rich in protein; thus combined parts of cassava can be a potential feedstuff for swine. Ensiling cassava parts may enhance its utilization in swine. Two independent studies were performed with cassava silages. First study evaluated different combinations of tubers and vines while second study evaluated different combinations of vines and molasses. In first study, 2 different lines of cassava (L_1 and L_2) and 2 sample types (100% tubers, T_{100} and 50% tubers and 50% vines, T_{50}) were ensiled over 3 periods (fresh [M_0], ensiled for 2 [M_2] and 3 [M_3] months). In second study, 2 different lines of cassava (L_1 and L_2) and 3 sample types (100% vines, V_0; 95% vines and 5% molasses, V_5; and 90% vines and 10% molasses, V_{10}) were ensiled for 2 mo. Nutrient profile of samples was analyzed using standard methods and digestibility was determined using an in vitro method (3 step enzymatic assay). With increasing the proportion of vine in the silage mix, ADF, NDF, and CP content increased ($T_{50} > T_{100}$) while starch decreased. However, ensiling resulted in a reduction of the CP, NDF, ADF and starch contents compared to the fresh samples. The CP content of L_2 (V_0M_0, V_5M_2, $V_{10}M_3$) was higher (15–18%) than L_1 (12–13%). The DM digestibility of $L_2T_{100}M_0$ (91%) and $L_1T_{100}M_0$ (86%) was higher ($P < 0.05$) than $L_2T_{50}M_0$ (76%) and $L_1T_{50}M_0$ (74%). Energy digestibility of $L_2T_{100}M_3$ (92%) and $L_1T_{100}M_3$ (87%) was higher ($P < 0.05$) than $L_1T_{50}M_3$ (69%) and $L_2T_{50}M_3$ (61%). Nutritional value of cassava silages decreased with increase in proportion of vines in the sample. However, digestibility was still at reasonable level. Thus, ensiling the combination of tubers and vines of cassava can be useful strategy to supply enough amount of feed for swine. However, ensiling period needs to be considered with combination of tubers and vines. Also, the pH of silage decreased with increase in ensiling period; feeding silage may provide gut health benefit, in addition to providing energy and other nutrients to swine.

Key Words: cassava silage, digestibility, swine

0993 Amino acid digestibility in feed ingredients fed to pigs. S. A. Lee*[1], J. Y. Ahn[2], A. R. Son[3], and B. G. Kim[1], *[1]Konkuk University, Seoul, The Republic of Korea, [2]Jeongeup, The Republic of Korea, [3]Konkuk University, Seoul, South Korea.*

The objective was to determine the standardized ileal digestibility (SID) of CP and AA in the cereal grains and various byproducts fed to growing pigs. Ten feed ingredients used in this study were barley (9.32% CP), lupin kernels (LK, 31.1% CP), and wheat (11.3% CP) as the cereal grains, and 2 sources of corn gluten feed [CGF 1 (21.6% CP) and 2 (24.6% CP)], corn gluten meal (CGM, 65.3% CP), lupin hulls (LH, 11.6% CP), rice bran (RB, 14.5% CP), soybean meal (SBM, 44.8% CP), and wheat bran (WB, 15.4% CP) as the byproducts. Eleven experimental diets were formulated to contain each ingredient as a sole source of N and an N-free diet was also prepared to estimate the basal endogenous losses of CP and AA. All diets also contained 0.5% chromic oxide as an indigestible index. The ileal digestibility of AA in the test ingredients was determined at 2 different locations. An incomplete 11 × 5 Latin square design was employed for each of 2 locations with 11 dietary treatments, 5 periods, and 11 animals. Eleven barrows with an initial BW of 62.1 ± 5.8 (location 1) and 66.7 ± 3.5 kg (location 2) were equipped with a T-cannula in the distal ileum. An experimental period consisted of a 4-d adaptation and a 2-d collection periods. Least square means were presented for the SID values. Values for the SID of CP in the barley, LK, wheat, CGF 1 and 2, CGM, LH, RB, SBM, and WB were 84.7, 90.5, 90.4, 77.4, 74.6, 89.5, 90.4, 74.4, 86.9, and 63.4% (SEM = 5.3, $P = 0.006$), respectively. Respective values for the SID of Lys were 75.5, 88.4, 83.9, 74.7, 62.4, 80.3, 83.9, 78.5, 88.0, and 71.2% (SEM = 3.3, $P < 0.001$), and the respective values for the SID of Met were 83.6, 88.7, 89.4, 85.7, 78.3, 88.9, 89.4, 85.3, 91.1, and 77.0% (SEM = 2.4, $P < 0.001$). In conclusion, the SID of Lys and Met in the barley, LK, wheat, CGF 1, CGM, LH, and RB did not differ compared to the SBM.

Key Words: amino acid, alternative feed ingredient, digestibility

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0994 Evaluation and development of the prediction equation for the gross energy in feed ingredients. A. R. Son*[1] and B. G. Kim[2], *[1]Konkuk University, Seoul, South Korea, [2]Konkuk University, Seoul, The Republic of Korea.*

The objective of this study was to evaluate the accuracy of a previously published equation and to develop novel prediction equations for the GE concentration in feed ingredients. Data from 297 corn, 550 corn gluten feed, 148 copra expellers, 222 copra meal, 486 palm kernel expellers, 102 rapeseed meal, and

130 soybean meal samples were used. The mean values of the feed ingredients were 10.4 ± 2.4%, 19.8 ± 9.6%, 4.44 ± 2.71%, 5.19 ± 2.17%, and 4230 ± 265 kcal/kg on an as-is basis for the moisture, CP, ether extract, ash, and GE concentrations, respectively. The predicted GE concentration of each ingredient was calculated using the published equation based on the chemical composition. To test the accuracy of the predicted GE concentrations, the regression analysis of the determined minus predicted GE concentration against the predicted GE concentration was conducted, which was able to verify the bias in the predicted values. The correlation and multiple regression procedures of SAS were used to generate the novel prediction equations. According to the results of regression analysis for the accuracy of the published equation, the intercept (−230.3; SE = 4.8 and $P < 0.01$) and slope (0.062; SE = 0.031 and $P < 0.05$) was different from 0. The recommendable regression equations for the GE concentration (kcal/kg on an as-is basis) in the feed ingredients were: Eq. 1 = 4598– (51.6 × moisture) + (37.7 × ether extract) with root mean square error = 181, R^2 = 0.537, and $P < 0.001$; Eq. 2 = 4537– (54.2 × moisture) + (11.0 × CP) + (46.5 × ether extract)– (32.6 × ash) with root mean square error = 166, $R^2 = 0.612$, and $P < 0.001$. All independent variables are in % on an as-is basis. In conclusion, the previously published equation may overestimate the GE concentrations in the feed ingredients used in this study. On the basis of the novel prediction equations, the moisture and ether extract concentrations can be good independent variables to estimate the GE concentration in the feed ingredients.

Key Words: feed ingredient, gross energy, regression equation

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0995 Effect of supplemental citrulline on thermal and production parameters during heat stress in growing pigs.

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Heat stress (HS) compromises intestinal barrier function, and citrulline improves gut health in rodent models. Therefore, objectives were to characterize effects of citrulline supplement (CIT) on physiological and production responses during HS. Supplements were fed twice daily at 0600 and 1800 h and consisted of 20 g of cookie dough without citrulline (CON) or with 0.13 g/kg BW L-citrulline (CIT; 99.3% purity; MP Biomedicals, Santa Ana, CA). Forty crossbred gilts (30 ± 2 kg) were assigned to 1 of 5 supplemental-environmental treatments: 1) thermoneutral (TN; 23.6 ± 0.1°C) ad libitum fed (AL) with CON (TN-AL; $n = 8$), 2) TN pair-fed (PF) with CON (PF-CON; $n = 8$), 3) TN PF with CIT (PF-CIT; $n = 8$), 4) HS AL with CON (HS-CON; $n = 8$), and 5) HS AL with CIT (HS-CIT; $n = 8$). Acclimation lasted 4d while all pigs received the CON supplement. During period 1 (P1; 7d), pigs were kept in TN and fed AL their respective diets. During period 2 (P2; 60 h), HS-CON and HS-CIT animals were fed AL and exposed to cyclical HS (33.6 to 38.3°C) while TN-AL, PF-CON, and PF-CIT remained in TN and were fed either AL or PF to their HS counterparts to negate the effect of dissimilar nutrient intake. Feed intake was measured daily and BW was obtained 1 d before P1, d7 of P1, and at P2 conclusion. Rectal temperature (Tr), skin temperature (Ts), and respiration rate (RR) were obtained once daily at 1800 h during P1 and thrice daily at 0600, 1200, and 1800 h during P2. Pigs exposed to HS had increased Tr (0.8°C), Ts (4.7°C), and RR (47 bpm) relative to TN pigs ($P < 0.01$). HS-CIT pigs had decreased RR (7 bpm, $P = 0.04$) and a tendency for decreased Tr (0.1°C, $P = 0.07$). Feed intake decreased ~15% in HS relative to TN-AL pigs ($P < 0.01$) and did not differ between HS and PF pigs ($P > 0.10$). P2 ADG decreased 18 and 62% in HS and PF pigs, respectively, relative to TN-AL pigs. PF-CIT pigs tended to have increased (0.12 kg/d; $P = 0.09$) ADG compared to PF-CON pigs. Gain:feed was similar between TN-AL and HS pigs but decreased 30% in PF relative to TN-AL pigs ($P < 0.01$). No effects of CIT on production variables during HS were detected. In summary, CIT modestly affected the thermal response but had no effect on production parameters during HS, but tended to increase ADG during limit-feeding.

Key Words: heat stress, citrulline

0996 Effect of microencapsulated blends of organic acids on growth performance, nutrient digestibility, and fecal microflora in pigs.

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The microencapsulated blend of organic acids (MO) allowed slow-release of active ingredients and prevented the immediate disappearance of compounds on exiting the stomach. A total of 90 pigs [(Landrace × Yorkshire) × Duroc] with an average initial BW of 6.47 ± 0.27 kg (21 d) were used in a 154-d trial. Pigs were allotted to 3 treatments with 6 replicates/treatment and 5 pigs/pen. Dietary treatments included: 1) CON, basal diet, 2) MO1, CON + 0.1% MO (weanling phase) and 0.025% MO (growing-finishing phase), 3) MO2, CON + 0.2% MO (weanling phase) and 0.05% MO (growing-finishing phase). Individual pig BW and the feed consumption of each pen were monitored to calculate the ADG, ADFI, and G:F. Chromium oxide (2 g/kg) was added to the diets to determine the ATTD of DM, N, and GE. All data were analyzed using the GLM procedures of SAS (SAS Inst. Inc., Cary, NC). Orthogonal comparison was conducted using polynomial regression to measure the linear and quadric effects. Tukey's range test was used to compare the means of treatments, and $P < 0.05$ was considered to be significant. Pigs BW was higher ($P < 0.05$) in MO2 than CON on d 21 (14.39 vs. 13.94 kg), d 42 (25.98 vs. 27.05 kg), and d 154 (109.32 vs. 114.09 kg). From d 0 to 21, 22 to 42, 0

to 42, and 0 to 154, pigs in MO2 had higher ($P < 0.05$) ADG (377 vs. 356 g, 603 vs. 573 g, 490 vs. 464 g, 699 vs. 667 g) than CON. Increased ($P < 0.05$) G:F was detected in MO2 compared with CON from d 84 to 154 (0.369 vs. 0.343) and d 0 to 154 (0.430 vs. 0.408). Linear effect ($P < 0.05$) was observed on BW, ADG, and G:F at the same time. Pigs in MO2 had higher ($P < 0.05$) ATTD of DM (83.67 vs. 81.82%, 76.63 vs. 72.29%) than CON on d 21 and 42. Linear effect ($P < 0.05$) was also observed on the ATTD of DM on d 21 and 42. Fecal *Lactobacillus* concentration (7.70 vs. 7.45 $\log_{10}$cfu/g) was increased ($P < 0.05$) by MO2 compared with CON on d 42. Linear and quadratic effects ($P < 0.05$) were also observed on *Lactobacillus* concentration on d 42. In conclusion, the inclusion of 0.2% MO can increase BW, ADG, the ATTD of DM, and fecal *Lactobacillus* counts in weanling pigs, in addition, 0.05% MO can increase G:F in finishing pigs.

Key Words: growth performance, microencapsulation, pigs

0997 Effect of multispecies probiotic supplementation source on growth performance and meat quality traits in growing-finishing pigs.

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In South Korea, using antibiotics as growth promoters in animal feeds has been forbidden since 2011. Probiotics have received considerable attention as suitable alternatives of antibiotics to promote growth in pig industry. The study was conducted to investigate the effects of multispecies probiotic (*B. coagulance* [1×10^9 cfu/g], *B. lichenformis* [5 × 10^8 cfu/g], *B. subtilis* [1 × 10^9 cfu/g], and *Clostridium butyricum* [1 × 10^8 cfu/g]) supplementing with corn based meal on growth performance and meat quality traits in growing-finishing pigs. A total of 75 pigs ([Landrace × Yorkshire] × Duroc) with initial body weight (BW) of (23.3 ± 1.42) kg. Pigs were randomly allocated to the three treatment groups with 5 replicate pens per treatment, 5 pigs (3 barrows, 2 gilts) per pen. The following three treatments were used: CON (Basal diet), T2 (CON + 0.01% multispecies probiotic), and T3 (CON + 0.02% multispecies probiotic). These dietary treatments were given as Phase I (Week 6), Phase II (Week 12), and Phase III (Week 16) to analyze growth performance. Orthogonal polynomial contrast was conducted to measure the linear and quadratic effects for increasing the multi-species probiotic levels on all measurements. Statistical significance was considered when P value was less than 0.05. Higher level of (0.02%) multispecies probiotic supplementation had linearly increased effects on BW ($P = 0.030$) at wk 16 and also significant differences on average daily gain and gain:feed ($P < 0.05$) without effects of average daily feed intake ($P > 0.05$) in treatments with probiotic supplementation at entire experiment. Significant effects ($P < 0.05$) were observed on increased apparent total tract digestibility of dry matter (DM, $P = 0.004$), nitrogen (N, $P = 0.012$), energy (E, $P = 0.055$) at wk 16 in diets with probiotic supplementation, 0.02% multispecies probiotic inclusion in diets showed reduced level of *E. coli* ($P = 0.011$, 0.013) and increased significant difference on *Lactobacillus* counts ($P = 0.004$, 0.005) respectively at wk 6 and 16, live meat quality traits of back fat thickness ($P = 0.004$, at wk 16) and lean meat percentage ($P = 0.006$, at wk 12), blood glucose ($P = 0.028$, at wk 6) level, RBC ($P = 0.013$, at wk 16) levels, NH_3 emission ($P = 0.010$, at wk 16) and sensory evaluation of color ($P = 0.001$), firmness ($P = 0.031$). These results suggested improving effects of dietary multispecies probiotic on growth performances, apparent total tract digestibility, balancing the management of desired fecal micro biota, reduced NH_3 gas emission, and sensory evaluation of meat quality in growing-finishing pigs.

Key Words: *Bacillus* spp., *Clostridium butyricum*, pig performances

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0998 Effects of dietary red ginseng on growth performance, nutrient digestibility, blood profile, meat quality, and carcass grade in growing-finishing pigs.

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This study was conducted to determine the effect of dietary red ginseng on growth performance, nutrient digestibility, blood profile, meat quality, and carcass grade in growing-finishing pigs. A total of 120 crossbred pigs ([Landrace × Yorkshire] × Duroc) with an average body weight of 21.77 ± 1.88 kg were used in 22 wk experimental period. Pigs were randomly assigned to 3 treatments with 8 replications (5 pigs per replication). Dietary treatments included: 1) CON, basal diet; 2) TRT1, CON + 0.1% fermented red ginseng; 3) TRT2, CON + 0.2% fermented red ginseng. All data were analyzed as a randomized complete block design using mixed procedures of SAS. In the current study, no significant difference was observed on average daily gain (ADG), average daily feed intake (ADFI), and gain to feed ratio (G/F) among treatments at 10th, 18th and 22th weeks. However, pigs fed with TRT1 diet (657 g) had higher ADG ($P < 0.05$) than those fed with CON diet (634 g) at sixth week. Overall, a significant increase ($P < 0.05$) in ADG was observed in TRT1 treatment (550 g) compared with CON treatment (542 g), and no effect was observed on ADFI, FCR, and G/F. Apparent total tract digestibility (ATTD) of dry matter (DM) in TRT1 treatment (81.46) was higher ($P < 0.05$) than that of CON treatment (78.03). In addition, ATTD of nitrogen (N) in pigs fed with TRT1 diet (81.89) was higher ($P < 0.05$) compared with pigs fed with CON diet (76.08) and TRT2 diet (77.37). No significant difference was observed in the ATTD of energy (E) among treatments at sixth

and 10th weeks. Supplementation of red ginseng in TRT1 treatment significantly decreased ($P < 0.05$) drip loss at d 1 (1.38), d 5 (4.60) and d 7 (7.01) post slaughter. On d 9, drip loss of CON treatment (13.92) was considerably lower than TRT1 treatment (8.68) and TRT2 treatment (11.12). Meantime, drip loss of TRT2 treatment (11.12) was significantly higher than TRT1 treatment (8.68). In conclusion, results of the present study indicated that supplementation of red ginseng enhanced growth performance, nutrient digestibility and decreased meat drip loss, with no significant effect on blood profile and carcass grade in finishing pigs.

Key Words: growing-finishing pigs, growth performance, red ginseng

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0999 Effect of protected organic acid blend with medium chain fatty acid on growth performance, nutrient digestibility, blood profiles, meat quality, fecal micro flora and fecal gas emission in finishing pigs. D. H. Nguyen*, T. S. Li, S. D. Upadhaya, H. N. Tran, and I. H. Kim, *Department of Animal Resource & Science, Dankook University, Cheonan, South Korea.*

A total of 105 finishing pig ([Yorkshire × Landrace] × Duroc) with an average BW of 51.0 ± 3.33 kg were used in 10 wk trial to evaluate the effect of protected organic acid blend on finishing pigs. Pigs were randomly allotted to one of three dietary treatments (7 replication pens with 5 pigs per pen) in a randomly complete block design based on their initial BW. Dietary treatments were: 1) CON (basal diet); 2) MC1 (CON + 0.1% protected organic acids); 3) MC2 (CON + 0.2% protected organic acids). Protected organic acids contained 17% fumaric acid, 13% citric acid, 10% malic acid and 1.2% medium chain fatty acid (capric and caprylic acid). BW and feed were recorded at the beginning, on week 5 and week 10 of the experimental period to calculate ADG, ADFI and G:F. Fresh fecal samples were collected at sixth week and 12th week for calculation of DM, N, and energy digestibility by adding 0.2% chromium oxide before 1 wk. All data were subjected to the GLM procedures of SAS and differences among treatments were separated by Tukey's multiple range test with a $P < 0.05$ indicating a significance. In the current study, overall, the inclusion of MC1 and MC2 led to greater ADG (861, 864 vs. 827 g/d; $P < 0.05$). Administration of MC2 improved G:F compared with CON treatment (0.354 vs. 0.337; $P < 0.05$). However, no difference ($P > 0.05$) was observed in ADFI of pigs fed MC1 and MC2 compared with CON. Pigs fed MC1 and MC2 diets led to higher ($P < 0.05$) IgG concentration at the end of 5 wk. At the end of 10 wk higher concentration of IgG was seen in MC1 treatment compared with CON treatment ($P < 0.05$). Administration of MC1 and MC2 treatments led to higher *Lactobacillus* counts and lower *E.coli* counts compared with CON ($P < 0.05$). During the end of the experiment, a decrease in fecal ammonia emission was observed with MC2 treatment ($P < 0.05$). Supplementation of protected organic acid increased ($P < 0.05$) the drip loss at d5 and d7 of meat evaluation. In conclusion, protected organic acid supplementation enhanced growth performance, reduce ammonia gas emission and improve gut microbial population in finishing pigs.

Key Words: finishing pig, growth performance, protected organic acids

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1000 Effect of dietary melamine concentrations on performance and tissue melamine residue in male broiler chickens. J. H. Kim[1] and D. Y. Kil[*2], [1]*Chung-Ang University, Anseong-si, The Republic of Korea,* [2]*Chung-Ang University, Anseong-si, South Korea.*

We investigated the effect of dietary melamine concentrations on performance and tissue melamine residue in male broiler chickens. A total of 504 1-d-old male broiler chicks were housed in 42 battery cages for a 5-wk feeding trial. Birds were randomly allotted to 1 of 7 dietary treatments with 6 replicated cages. Dietary melamine concentrations were set to 0, 250, 500, 750, 1,000, 5,000, or 10,000 mg/kg by adding purified form of melamine ($\geq$ 99.0%) at the expense of the sand. At the end of the experiment, 3 birds from each treatment were euthanized. Kidney and breast samples were collected for melamine residue analysis. Results indicated that the BW and BW gain for birds fed diets containing 10,000 mg/kg melamine were less ($P < 0.01$) than those fed diets containing 0, 250, 500, 750, 1,000, or 5,000 mg/kg melamine. There were no differences in feed efficiency and mortality among treatments. Kidney melamine residue for 10,000 mg/kg treatment group was greater ($P < 0.01$) than for 0, 250, 500, 750, or 1,000 mg/kg treatment groups. The 10,000 mg/kg treatment group had greater ($P < 0.01$) melamine residues in breast muscle than other treatment groups. Orthogonal polynomial contrast test revealed that increasing melamine concentrations of diets decreased BW, BW gain (linear and quadratic, $P < 0.05$), and feed intake (linear, $P < 0.01$). Increasing melamine concentrations of diets increased (linear, $P < 0.01$) melamine residues in the kidney and breast. According to food safety issue (WHO), melamine concentrations of human food should be limited less than 2.5 mg/kg. Thus, based on linear regression analysis between dietary melamine concentrations and breast melamine residue ($y = 0.0071x - 1.7956$, $R^2 = 0.89$), the upper limit of melamine concentrations of diets for male broiler chickens was estimated to be 605 mg/kg. In conclusion, 10,000 mg/kg melamine is toxic to male broiler performance. Dietary melamine concentrations for male broiler chickens should be limited approximately less than 600 mg/kg in terms of human food safety.

Key Words: dietary melamine, male broiler chicken, tissue melamine residue

1001 Effect of dietary melamine concentrations on performance and tissue melamine residue in female broiler chickens. J. H. Kim[1] and D. Y. Kil[*2], [1]*Chung-Ang University, Anseong-si, The Republic of Korea,* [2]*Chung-Ang University, Anseong-si, South Korea.*

An experiment was conducted to investigate the effect of dietary melamine concentrations on performance and tissue melamine residue in female broiler chickens. A total of 504 1-d-old female broiler chicks were housed in 42 battery cages for a 5-wk feeding trial. Birds were randomly allotted to 1 of 7 dietary treatments with 6 replicated cages. Dietary melamine concentrations were set to 0, 250, 500, 750, 1,000, 5,000, or 10,000 mg/kg by adding purified form of melamine ($\geq$ 99.0%) at the expense of the sand. At the conclusion of the experiment, 3 birds from each treatment were euthanized by CO_2, and then kidney and breast samples were collected for melamine residue analysis. Results indicated that the BW, BW gain, and feed intake (FI) for birds fed diets containing 10,000 mg/kg melamine were less ($P < 0.01$) than those fed diets 0, 250, 500, 750, 1,000, or 5,000 mg/kg melamine. There were no differences in feed efficiency and mortality among treatments. Kidney and breast melamine residue for 10,000 mg/kg treatment group were greater ($P < 0.01$) than other treatment groups. Orthogonal polynomial contrast test revealed that increasing melamine concentrations of diets decreased (linear and quadratic, $P < 0.05$) BW, BW gain and FI (linear, $P < 0.01$). Increasing concentrations of melamine in diets from 0 to 10,000 mg/kg decreased (quadratic, $P < 0.05$) feed efficiency. Increasing melamine concentrations of diets increased (linear and quadratic, $P < 0.01$) melamine residues in the kidney and breast. According to food safety issue (WHO), melamine concentrations of human food should be limited less than 2.5 mg/kg. Thus, based on linear regression analysis between dietary melamine concentrations and breast melamine residue ($y = 0.0054x - 1.3291$, $R^2 = 0.94$), the upper limit of melamine concentrations of diets for female broiler chickens was 709 mg/kg. In conclusion, 10,000 mg/kg melamine is toxic to female broiler performance. Dietary melamine concentrations for female broiler chickens should be limited approximately less than 700 mg/kg in terms of human food safety.

Key Words: dietary melamine, female broiler chicken, tissue melamine residue

1002 A plant extract with manganese, Vali MP®, decreased adipogenesis in 3T3-L1 pre-adipocytes by modulating adipogenic gene expression and cellular energy level. S. W. Choi[*1], J. Kim[1], S. W. Jung[2], and K. Y. Whang[1], [1]*Korea University, Seoul, The Republic of Korea,* [2]*CTC BIO, Seoul, The Republic of Korea.*

As animals grow, the rate of fat deposition increases and results in a decreased feed efficiency. To improve lean growth, dietary modulation (low energy and high protein) and metabolic modulator are applied for finishing pigs. One of successful metabolic modulators is a β-adrenergic agonist, which increases leanness by improving protein synthesis. However, the use of β-adrenergic agonist for pork production are banned in many counties due to bio-safety issue. Vali MP® is a natural product consisting of plant extracts and manganese and showed improved lean growth and decreased fat deposition when supplemented in finishing pig diet. However, direct effect on adipogenesis is not fully understood. We investigated effect of Vali MP® on adipogenesis by using 3T3-L1 mouse pre-adipocytes. Murine pre-adipocytes (3T3-L1) were differentiated into adipocyte by switching media (DMEM with 10% FBS, 1% antibiotics, 10 μM cortisone, 0.5 mM methylisobutylxanthine, and 1.0 ug/mL insulin) for 2 d, and then media was changed adipocyte maintenance medium (DMEM with 10% fetal bovine serum, 1% antibiotics and 1.0 μg/mL insulin) for another 2 d. Cells were maintained in DMEM with 10% fetal bovine serum and 1% antibiotics) for 4 more days. After a total of 8 d differentiation, cellular triglyceride (TG) content was determined by Oil Red-O staining, cDNA was constructed for quantitative real-time PCR and cell lysates were prepared for immunoblotting. During differentiation, Vali MP® (10% in PBS) solution was added to the final concentration of 0, 0.05, 0.10, and 0.2% through the adipocyte differentiation. TG accumulation was not affected at 0.05% Vali MP® supplementation, however 0.10% and 0.20% Vali MP® supplementation decreased TG accumulation by 25% and 90%, respectively. At 0.05% Vali MP® supplementation, gene expression level of SREBP1C was not changed, but PPAR-γ and CEBPα, and fatty acid synthase were increased ($P < 0.05$). As Vali MP® concentration was increased (0.10% and 0.20%), these gene expression levels were decreased at dose dependent manner ($P < 0.05$). Protein expression level of AMPK (cellular energy gauge) was not affected by Vali MP® supplementation, but phosphorylated AMPK was increased and resulted in increased phosphorylated acetyl-coA carboxylase (inactive form; $P < 0.05$). Collectively, these data indicate Vali MP® decreases adipogenesis by affecting adipogenic gene expression and cellular energy status (AMPK). The results suggest a possible molecular mechanism of lean growth promoting effects of Vali MP® in finishing pigs. However, the molecular mechanism of Vali MP® on myogenesis should be addressed.

Key Words: ValiMP(*R*), anti-adipogenesis, 3T3-L1

1003 Effects of dietary lysophospholipids (LipidolTM) on intestinal morphology and gene expression of inflammatory cytokines in weaned rats.

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Weaning is a stressful condition for animals and negatively affects growth performance by increasing dystrophy of intestinal villi. This intestinal dystrophy attenuates nutrient absorption and barrier function. Lysophospholipids (LPLs), biosynthesis metabolites, are glycerophospholipids in which one acyl chain is lacking and thus only one hydroxyl group of the glycerol back bone is acylated. LPLs can diffuse rapidly into the lipid parts of membrane due to the relatively small hydrophobic part and increase permeability of membrane by altering fluidity of membrane. Therefore, we hypothesize that supplementation of LPLs products (Lipidol^{TM}) can modulate nutrient absorption and barrier function of intestine, and an experiment was conducted to investigate relieving effects of LPLs against weaning stress. Twenty-one rats (4 wk-old) were allotted into 3 dietary treatments (Control, NIH-31 diet; LEC, NIH-31 diet with 2 g of lecithin/kg of feed; and LPL, NIH-31 diet 2 g of LPLs/kg of feed). After 4 wk of feeding period, jejunum samples were collected and gene expression of inflammatory cytokines (IL-1, IL-4, IL-6, IL-10, IL-12β, and TNF-α) and tight junction proteins (β-catenin and ZO-1) were determined by qRT-PCR. Body weights and feed intakes were measured weekly. Serum biochemical markers (triglyceride, total cholesterol, and blood urea nitrogen) were measured. And jejunum morphology (villus heights, crypt depths, and the number of goblet cells) was also observed. Growth performance (body weight, average daily gain, average daily feed intake, and feed efficiency) was not affected by dietary treatments. There were numerically lower triglyceride and higher total cholesterol in LPL than other groups but no difference was found in blood urea nitrogen among 3 treatments. There were no differences in levels of IL-1, IL-4, IL-6, IL-10, IL-12β, and TNF-α, and ZO-1 expression among 3 treatments. But β-catenin expression was increased in LPL than other treatments ($P < 0.10$). Jejunal villus height were also numerically higher in LPL and villus heights:crypt depths ratio was significantly higher in LPL than other groups ($P < 0.05$). The number of goblet cells per villus was also significantly higher in LPL than other groups ($P < 0.05$). The results of this experiment demonstrated LPLs improved the gut health in villus heights and villus heights:crypt depths ratio after weaning. Also gut barrier function was improved with higher number of mucous producing cells. The healthier intestine should be able to absorb more nutrients with better efficiency, thus a reduced weaning-related growth check is expected.

Key Words: rats, intestine, gut morphology, lysophospholipids

1004 Effect of protected sodium butyrate and nutrient concentration on early phase of broilers.

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The study was conducted to compare the effect of sodium butyrate protected with PFAD sodium salt (GUSTOR N'RGY) with three different nutrient concentration diets on growth performance. A 3 × 2 factorial design was used with a basal diet based on wheat, barley and soybean meal with three different nutrient concentrations and with or without additive. The tested treatments were: CON (3,000 kcal AMEn/kg, 22.02% CP and 11.6 g/kg dig Lys) and CON-1 (CON with a reduction of 60 kcal AMEn/kg and 2.3% of amino acids), CON-2 (CON with a reduction of 120 kcal AMEn/kg and 4.6% of amino acids), N'RGY (CON diet with GUSTOR N'RGY at 1kg/t), N'RGY-1 (CON-1 diet with 1 kg of N'RGY/t) and N'RGY-2 (CON-2 diet with 1 kg of N'RGY/t). A total of 252 Cobb 1-d-old males broiler chickens were used in the study. Birds were housed in 36 floor pens of seven animals, such that there were 6 replicates/treatment. The treatments were randomly distributed among the pens. Mash feeds and water were offered ad libitum. The study lasted 21 d and the weight of animals and feed from each pen were recorded at d 0 and at d 21. Data were analyzed by ANOVA using the GLM procedure of SAS. Both nutrient concentration and feed additive inclusion affected the performance variables. There were no differences between CON and CON-1 on BW, ADG and FCR. However, CON-2 had lower BW than CON-1 (BW: 831 g ab, 860 g a and 805 g b, $P = 0.03$; ADG: 37 g/day ab, 39 g/d a and 36 g/d b, $P = 0.03$) and worst FCR than CON and CON-1 (1.51 b, 1.52 b and 1.57 a, $P = 0.007$). Animals fed diets with the addition of N'RGY had higher BW (850 g vs. 813 g, $P = 0.03$), ADG (38 g/d vs. 36 g/d, $P = 0.03$), ADFI (52 g/d vs. 51 g/d, $P = 0.01$) and better FCR (1.51 vs. 1.56, $P = 0.003$). It can be concluded that the reduction of energy and amino acids reduce animal performance on its second step, and that the use of GUSTOR N'RGY is able to improve the results of performance in the early phase of chickens.

Key Words: protected sodium butyrate; nutrient concentration; broilers

1005 Use of aromatics plants in the diet on performance of broilers in Colombia. L. Bernal*, *La Salle University, Bogotá, Colombia.*

Poultry production has major challenges to streamline animal productivity, improve intestinal health, create safe and of good nutritional quality protein for human consumption. Plant diversity of Colombian tropical plant species has not evaluated in animal feed and which may have beneficial antiseptic properties in the productive parameters and intestinal health of chickens. The aim of this study was to evaluate the inclusion of the leaves of two plants from Choco, Santa Maria (*Piper peltatum*) and basil (*Ocimum basilicum*) on performance of broilers Ross 308 line in Colombia. The experiment was conducted in the San José de Guausa farm, located in the municipality of Chia, Cundinamarca Department. Two hundred chickens Ross 308 commercial line a day were used. Birds were evaluated for an experimental of 42 d. Four treatments were evaluated. Control (CON, basal diet): animals were fed a diet of corn-soybean meal without aromatics plants; treatment two, animals that received the control diet with the inclusion of 0.05% basil leaves (ABH); treatment three, animals fed with 0.05% leaves of Santa Maria (SMB) and treatment four diet by including 0.025% (ABH) and 0.025% (SMB). The production parameters evaluated were feed intake (g), weekly weight (g), feed conversion and weight gain (g). The experimental design was completely random, distributed in four treatments, five replicates per treatment, and 10 animals per repetition. Data variables were asked ANOVA, and to detect between treatment means the Tukey test was employed in the SAS statistical package. As a result of this study, significant difference ($p < 0.05$) was found between treatments for the weekly weight, bird average daily gain and feed conversion, ABH was the treatment with the best results in week seven for the weight (2362 vs. 2155, 2297, 2346 g), weight gain (79 vs. 59, 71, and 76 g) and feed conversion (2.079 vs. 2.23, 2.42, 3.74). These results suggest that the diet with the addition of 0.05% of ABH can benefit the productive parameters of chickens level weight, weight gain and feed conversion, which favors animal productivity.

Key Words: aromatics plants, growth performance, feed conversion

1006 Dietary antioxidants, chromium and betaine supplementation can improve lactation performance of sows during summer. J. J. Cottrell[1], F. Liu[1], D. J. Henman[2], K. O'Halloran[2], and F. R. Dunshea*[1], *[1]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Australia, [2]Rivalea Australia Pty Ltd, Corowa, Australia.*

Heat stress (HS) causes considerable losses to the global pig industry with lactating sows being particularly sensitive. There is strong evidence that nutritional supplements may provide means of ameliorating HS and so the aim of the present study was to investigate the effects of some dietary additives on lactational performance of lactating sows during summer. Eighty seven multiparous sows were fed either a wheat-based control (CON, $n = 31$) or a supra-nutritional antioxidant diet (AO, $n = 56$) for an 18 d lactation period during summer in southern Australia. All sows were housed in lactation stalls within open-sided lactation sheds. The CON diet contained NRC recommendations for all nutrients including selenium (0.15 mg/kg) and Vitamin E (44 IU/kg) while the AO diet was fortified with selenized yeast (0.4 mg/kg Se), Vitamin E (95 IU/kg), chromium picolinate (400 ppm Cr) and betaine (2 g/kg). All of these nutritional supplements have been demonstrated to ameliorate some of the physiological responses to HS in sheep and/or pigs in our laboratory. The daily temperatures during this summer study were from 15.8 ± 3.67°C to 31.9 ± 5.00°C. Sow weight and backfat were measured from 9 d before farrowing and at weaning, and individual piglet and litter weight were measured at farrowing and weaning. When the outside temperature exceeded 30°C, the respiration rate of all sows was measured in the afternoon. Appropriate blocking ensured there was no dietary effect on initial weight (301 ± 27.7 kg) on entry into the facility. Sows fed the AO diet lost less backfat (4.1 vs. 2.2 mm for CON and AO, $P = 0.047$) and live weight (−41.6 vs. −33.4 kg, $P = 0.021$) between entry into the facility and weaning than those sows fed the CON diet despite there being no effect on feed intake (5.63 vs. 5.87 kg/d, $P = 0.20$). There was also no dietary effect on litter weight at weaning (82.7 vs. 83.2 kg, $P = 0.91$) or number of piglets at weaning (10.2 vs. 9.9 piglets, $P = 0.42$) although average piglet weight at weaning tended to be greater for the sows fed the AO diet (8.05 vs. 8.47 kg, $P = 0.078$). Respiration rate increased by 4.0 breaths per min for every degree above 30°C ($P = 0.001$) but was unaffected by diet ($P = 0.88$). In conclusion, dietary Se, Cr, betaine and Vitamin E supplementation can reduce backfat and live weight loss of lactating sows during summer.

Key Words: antioxidants, lactating sow, heat stress

1007 Effects of dietary melamine on growth performance, organ weight, and blood melamine concentrations in pigs. K. R. Park* and B. G. Kim, *Konkuk University, Seoul, The Republic of Korea.*

The objective of current experiment was to determine the effects of dietary melamine on growth performance, organ weights, and blood melamine concentration for pigs. Twelve barrows with an initial BW of 19.8 kg (SD = 2.2) were randomly allotted to 4 dietary treatments in a completely randomized design. Four experimental diets were prepared to contain 0, 1, 2, or 4% of melamine based on the commercial corn and soybean meal based diet. The pigs were individually housed in metabolism crates and fed the experimental diets during 21 d of trial. Body weight and feed intake were recorded on d 7, 14, and 21. The daily feed allowance was approximately 2.7 times the estimated energy requirement for maintenance and divided into 2 equal meals at 0700 and 1600 h. The blood samples were obtained on d 7, 14, and 21 from each pig to analyze the melamine concentration. To exclude the effects of feed intake, blood melamine concentration relative to ADFI was calculated in each pig. At the end of the experimental period, all pigs were euthanized for collecting heart, kidneys, liver, and lungs. The collected organs were weighed and the organ weight relative to BW was calculated to exclude effects of BW. From d 0 to 7, the ADG, ADFI, and G:F linearly decreased ($P < 0.05$) as dietary melamine concentration increased. From d 7 to 14, linear decrease ($P < 0.05$) of ADG and ADFI and quadratic decrease ($P < 0.05$) of ADG was observed with increasing dietary melamine concentration. However, there were no linear and quadratic effects of dietary melamine concentration on G:F from d 7 to 14. During the overall period, the ADG, ADFI, and G:F linearly decreased ($P < 0.05$) as dietary melamine concentration increased. The weight of organs relative to BW was not affected by the concentration of dietary melamine. The blood melamine concentration relative to ADFI linearly increased ($P < 0.05$) as dietary melamine concentrations increased on d 7, 14, and 21. In conclusion, increasing levels of melamine in diets fed to pigs linearly decreased the growth performance and increased blood melamine concentration.

Key Words: blood, melamine, organ

1008 Effects of dietary melamine on growth performance and blood and urinary melamine concentrations in pigs. K. R. Park* and B. G. Kim, *Konkuk University, Seoul, The Republic of Korea.*

The objective of current experiment was to determine the effects of dietary melamine on growth performance and melamine concentration in blood and urine for pigs. Nine barrows with an initial BW of 35.9 kg (SD = 2.1) were randomly allotted to 3 dietary treatments in a completely randomized design. Three experimental diets were mainly based on wheat and soybean meal and were formulated to contain 0, 1, and 2% of melamine. The pigs were individually housed in metabolism crates and fed experimental diets during 12 d of trial. Body weight and feed intake were recorded at the end of the experimental period. The pigs had free access to feed and water. Blood samples were obtained on d 12 from each pig to analyze the melamine concentration. Urine was collected from 1100 h on d 7 to 1100 h on d 9, and urinary melamine concentration and average daily urinary melamine excretion were determined. To exclude effects of feed intake, melamine concentration in the blood samples, urinary melamine concentration, and average daily urinary melamine excretion relative to ADFI were calculated. The ADG and G:F were not affected by increasing dietary melamine concentrations. However, ADFI linearly decreased ($P < 0.05$) and tended to quadratically decrease ($P = 0.081$) with increasing dietary melamine concentration. The melamine concentration in the blood samples relative to ADFI linearly increased ($P < 0.05$) as dietary melamine concentration increased. The urinary melamine concentration, urinary melamine concentration relative to ADFI linearly and quadratically increased ($P < 0.05$), and the daily melamine excretion relative to ADFI linearly increased ($P < 0.05$) and tended to quadratically increase ($P = 0.071$) with increasing dietary melamine concentration. In conclusion, the addition of melamine to diets fed to growing pigs decreased feed intake and increased blood and urinary melamine concentrations.

Key Words: growth performance, swine, urine

1009 Feed additives reduced diarrhea occurrence in a medication-free postweaning pig diet. Z. Yang*[1], X. Wang[1], F. Chi[2], and S. Ching[2], *[1]College of Animal Science, Shandong Agricultural University, Tai-an, China, [2]Amlan International, Chicago, IL.*

Because of concerns about the use of antibiotics in animal diets and zinc oxide pollution in China in recent years, we conducted a trial to evaluate 2 feed additives (FA1, FA2) in an antibiotic and ZnO free diet in post-weaning pigs. One hundred-sixty newly weaned nursery pigs (30-d-old, 8.67" ± 0.35 kg body weight) were randomly allotted to 4 TRTs with 10 pigs per pen and 4 replications. The 4 TRTs were: Control (CON); CON+FA1 (0.25%); CON+FA2 (0.15%); and CON+FA1 (0.25%)+FA2 (0.15%). A mineral-based product, FA1 (MD-09™) has been shown to reduce wet droppings in poultry. The second product, FA2 (NeoPrime™) was designed to enhance gut health. The control feed was a corn-SBM basal diet formulated to meet or exceed NRC recommendations and contained no antibiotic or ZnO at levels higher than needed to meet the Zn requirement. A two-phase-feeding program with phase I from d 0 to 14 and phase II from d 15 to 28 was used in the study. Body weight and feed intake were measured weekly to determine ADG, ADFI, and FCR. Fecal scores were recorded daily using a 0 to 5 scale (0-solid to 5-watery). Fecal

samples were collected at 14 and 28 d post-weaning and fecal microorganisms were analyzed. Data were analyzed using ANOVA procedure of SAS (SAS 9.2) with pen as the experimental unit. Post-weaning pigs supplemented with FA1 and FA2 had numerically higher ADG (0.42 and 0.45 vs. the CON 0.33) and significantly increased ADFI (0.67 and 0.71 vs. the CON 0.56) ($P < 0.05$) during the 4-wk experimental period resulting in better FCR 1.64 and 1.61 vs. the CON 1.68. Feeding FA1 or FA2 significantly reduced ($P < 0.05$) the diarrhea index from a 4.31 score in the CON to 0.84 and 0.93, respectively. Fecal samples of pigs fed the diet with FA1 had higher *Lactobacilli* counts on both d-14 and d-28 ($P < 0.05$), lower *E. coli* on d-14, and lower *Salmonella* on d-28 ($P < 0.05$). Supplementing FA2 to post-weaning pigs significantly reduced *E. coli* and increased*Lactobacilli* on both d-14 and d-28 of tested period ($P < 0.05$). Fecal *Salmonella*counts were numerically lower in the FA2 group on both d-14 and d-28. In conclusion, FA1 or FA2 can be used as feed additives to reduce diarrhea, improve growth performance, and improve microorganism profiles in the intestine of post-weaning pigs.

Key Words: gut health, growth performance, diarrhea, post-weaning pigs

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1010 Optimization of B vitamins for improving the quality of fermented feed with response surface methodology. Z. Yang*[1] and X. M. Wang[2], *[1]College of Animal science, Shandong Agricultural University, Taian, China, [2]College of Animal science, Shandong Agricultural University, Tai-an, Shandong, Taian, China.*

To investigate the optimization of vitamin B_1, B_2 and B_{12} that were inoculated to improve the quality of fermented feed. Central composite design of response surface methodology (RSM) was employed to optimize vitamin B_1 content (X_1: 0.6~1.0 mg/kg), vitamin B_2 content (X_2:0.6~1.8 mg/kg) and vitamin B_{12} content (X_3: 9~15 μg/kg). After 72 h solid-state fermented (SSF), samples from three fermented feed/pen and 6 replicate pens/treatment were obtained to evaluate the pH value, dry matter recovery (DMR) and reducing-sugar content. Results indicated that the data of pH value, DMR and reducing-sugar were adequately fitted into 3 s-order polynomial models ($P < 0.05$). The vitamin B_1, B_2 and B_{12} were found to have significant linear, quadratic and interaction effects on the pH value, DMR and reducing-sugar ($P < 0.05$). The optimal extraction conditions were predicted to be vitamin B_1 content of 0.65 mg/kg, vitamin B_2 content of 1.29 mg/kg and vitamin B_{12} content of 12.02μg/kg. The pH value, DMR and reducing sugar were predicted by RSA to be 4.09, 91.57, and 6.46%, respectively. These detection indexes what obtained through the verification experiment were close to the predicted values significantly ($P < 0.01$). The establishment of such a model provides a good experimental basis with employing RSM for optimizing the inoculation amount of vitamin B_1 (0.65 mg/kg), vitamin B_2 (1.29 mg/kg) and vitamin B_{12} (12.02μg/kg) to improve the quality of fermented feed.

Key Words: B vitamins, pH, dry matter recovery, reducing-sugar, fermented feed

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1011 Changes in pH of digestive tract and cecal microflora composition in broilers fed with probiotic and prebiotic supplementation (SynerAll). A. Ipek* and A. Sozcu, *Faculty of Agriculture, Department of Animal Science, Uludag University, Bursa, Turkey.*

This study was conducted to investigate the changes in the pH of the digestive tract and cecal microflora composition in broilers fed a combination of probiotic and prebiotic supplementation (PPS) (SynerAll; Global Nutritech LLC, Richmond, VA). A total of 720 1-d-old Cobb 500 broiler chicks were randomly assigned to four treatment groups: Control (no PPS), Group 1 (0.5 kg PPS/ton), Group 2 (1 kg PPS/ton), and Group 3 (2 kg PPS/ton). The combination of probiotics and prebiotics included live *Saccharomyces cerevisiae* (strain NCYC R618), mannan, and glucan. Each experimental group consisted of six replicates, each containing 30 chicks (15 female and 15 male). At 42 d of age, the pH and dry matter of the digestive tract (crop, proventriculus, gizzard, ileum), the pH of feces, and cecal microflora composition (*Lactobacillus* spp. and total *E. coli* spp.) were determined. Data were analyzed using the GLM Procedure of SAS. The crop and gizzard had the lowest ($P < 0.05$) pH values in Group 2 (4.35 and 2.24, respectively) compared to the Control (5.90 and 3.28, respectively), Group 1 (4.88 and 2.91, respectively), and Group 3 (4.63 and 2.78, respectively). The pH of the ileum was higher ($P < 0.01$) for the Control (6.64) than for Group 1, Group 2, and Group 3 (5.38, 5.18, and 5.42, respectively). Dry matter and pH of feces were similar among the treatment groups ($P > 0.05$). The count of *Lactobacillus* spp. increased more in Group 2 (7.97 log CFU/g wet digesta) and Group 3 (6.90 log CFU/g wet digesta) than the Control (1.30 log CFU/g wet digesta) and Group 1 (1.43 log CFU/g wet digesta; $P < 0.01$). Total *E. coli* spp. count was higher ($P < 0.05$) in the Control and Group 1 (8.90 and 7.67 log CFU/g wet digesta, respectively) compared to Group 2 and Group 3 (3.47 and 4.20 log CFU/g wet digesta, respectively). Increasing the dose of SynerAll resulted in increased counts of *Lactobacillus* spp. and decreased counts of total *E. coli* spp. in the cecal microflora. In conclusion, supplementation of SynerAll to broiler diets had a positive effect on the pH of digestive organs and cecal microflora composition, which may increase the performance of broilers.

Key Words: broiler, probiotic, prebiotic, pH, cecal microflora

1012 Effects of dietary inclusion of probiotics and prebiotics (SynerAll) on growth performance and serum biochemical parameters in broilers.
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This study was conducted to investigate the effects of the dietary inclusion of probiotics and prebiotics (PPS) (SynerAll; Global Nutritech LLC, Richmond, VA) on broiler growth performance and serum biochemical parameters. A total of 720 1-d-old Cobb 500 broiler chicks were randomly assigned to four treatment groups: Control (no PPS), Group 1 (0.5 kg PPS/ton), Group 2 (1 kg PPS/ton), and Group 3 (2 kg PPS/ton). The combination of probiotics and prebiotics included live *Saccharomyces cerevisiae* (strain NCYC R618), mannan, and glucan. Each experimental group consisted of six replicates, each containing 30 chicks (15 female and 15 male). Growth performance, live weight gain, and feed conversion rate were determined between d 1–21 and d 22–42. At 42 d of age, serum biochemical parameters (heterophil (H), lymphocytes (L), monocytes, eosinophils, basophils) were analyzed and the H:L ratio was calculated. Data were analyzed using the GLM Procedure of SAS. Final live body weight on d 42 was the highest ($P < 0.01$) for Group 2 (3238.6 g) and the lowest ($P < 0.01$) for the Control (2818.5 g). Final body weight was 6.8%, 14.9%, and 5.8% higher ($P < 0.01$) for Group 1, Group 2, and Group 3, respectively, when compared to the Control. Feed consumption was lower ($P < 0.01$) for Group 2 and Control (1683.5 and 1727.2 g/bird, respectively) compared to Group 1 and Group 3 (1926.3 and 1935.4 g/bird, respectively). Dietary inclusion of PPS affected the feed conversion ratio ($P < 0.01$). The feed conversion ratio was the highest for the Control (2.04) and the lowest for Group 2 (1.72). It was intermediate for Group 1 and Group 3 (1.88 and 1.97, respectively). Mortality rate was not statistically significant among treatment groups ($P > 0.05$). Serum biochemical parameters and H:L ratio were similar among treatment groups ($P > 0.05$). These findings demonstrated that SynerAll can be used in broiler diets to improve weight gain and profitability.

Key Words: broiler, probiotic, prebiotic, live weight, blood parameters

1013 Changes in pH of digestive tract and cecal microflora composition in broilers fed with probiotic and prebiotic supplementation, SynerAll.
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This study was conducted to investigate the changes in pH of the digestive tract and cecal microflora composition in broilers fed a combination of probiotic and prebiotic supplementation (PPS) (SynerAll; Global Nutritech LLC, Richmond, VA). A total of 720 1-d-old Cobb 500 broiler chicks were randomly assigned to four treatment groups: Control (no PPS), Group 1 (0.5 kg PPS/ton), Group 2 (1 kg PPS/ton), and Group 3 (2 kg PPS/ton). The combination of probiotics and prebiotics included live *Saccharomyces cerevisiae* (strain NCYC R618), mannan, and glucan. Each experimental group consisted of six replicates, each containing 30 chicks (15 female and 15 male). At 42 d of age, the pH and dry matter of the digestive tract (crop, proventriculus, gizzard, ileum), the pH of feces, and cecal microflora composition (*Lactobacillus* spp. and total *E. coli* spp.) were determined. Data were analyzed using the GLM Procedure of SAS. Crop and gizzard had the lowest ($P < 0.05$) pH values in Group 2 (4.35 and 2.24, respectively) compared to the Control (5.90 and 3.28, respectively), Group 1 (4.88 and 2.91, respectively), and Group 3 (4.63 and 2.78, respectively). The pH of the ileum was higher ($P < 0.01$) for the Control (6.64) than Group 1, Group 2, and Group 3 (5.38, 5.18, and 5.42, respectively). Dry matter and the pH of feces were similar among treatment groups ($P > 0.05$). The *Lactobacillus* spp. count increased more in Group 2 (7.97 log CFU/g wet digesta) and Group 3 (6.90 log CFU/g wet digesta) than the Control (1.30 log cfu/g wet digesta) and Group 1 (1.43 log CFU/g wet digesta; $P < 0.01$). The total *E. coli* spp. count was higher ($P < 0.05$) in the Control and Group 1 (8.90 and 7.67 log CFU/g wet digesta, respectively) compared to Group 2 and Group 3 (3.47 and 4.20 log CFU/g wet digesta; respectively). Increasing the dose of SynerAll resulted in increased counts of *Lactobacillus* spp. and decreased counts of total *E. coli* spp. in the cecal microflora. In conclusion, supplementation of SynerAll to broiler diets had a positive effect on the pH of digestive organs and cecal microflora composition, which may increase the performance of broilers.

Key Words: broiler, probiotic and prebiotic, pH, cecal microflora

1014 Supplementation of chestnut tannins in artificially infected weaned piglets. G. Bee*, S. Thanner, G. Marion, and A. Gutzwiller, *Agroscope Institute for Livestock Sciences, Posieux, Switzerland.*

Weaning is a critical stage for piglets that is associated with disturbances in the intestinal microflora and pre-disposes them to gastrointestinal tract infections such as enterotoxic *E. coli* F4 (ETEC) infections and the development of post-weaning diarrhea. The continuous use of large amounts of antibiotics in animal production has led to the increased occurrence of resistances, so alternative solutions become urgent. Hydrolyzable tannins (HT) are known to have antimicrobial properties. The aim of this study was to determine the effect of HT from chestnut added to a standard starter diet on the prevalence of diarrhea in weaned piglets artificially infected with ETEC. The trial was arranged as a 2 × 2 factorial design and was performed with 72 piglets, weaned at 23 to 31 d of age. Piglets were allocated within weaning body weight and litter to the treatments and housed as pairs in pens. From the day of weaning, piglets had ad libitum access to either a control (**C**) or a 1% tannin (T) supplemented diet. Four days after weaning, 18 C and 18 T piglets received a 5-mL ETEC suspension of 10^8 CFU/ml orally, while the other 18 C and 18 T piglets received 5 mL of a PBS solution. For 14 d after infection, fecal score was assessed daily using the following score scheme: 1 = dry, pelleted feces; 2 = molded feces; 3 = moist, cow-dung appearance; 4 = diarrhea; 5 = watery diarrhea. Once per week, the piglets were weighed and the feed disappearance per pen was determined. In the first week after infection, the fecal score and the number of days in diarrhea were reduced ($P < 0.01$) in the T group (2.7 ± 1.24 and 2 ± 1.9 d, respectively) compared with the C group (3.1 ± 1.32 and 3 ± 2.4 d, respectively). However, average daily weight gain and feed disappearance were similar ($P > 0.05$) between the infected groups in the first week after infection (T: 0.4 ± 0.70 kg/piglet/d; C: 0.2 ± 0.27 kg/piglet/d; T: 517 ± 157.5 g/pen/d; C: 488 ± 193.7 g/pen/d) as well as in the second week after infection (T: 0.9 ± 1.25 kg/piglet/d; C: 0.6 ± 0.69 kg/piglet/d; T: 1043 ± 385.4 g/pen/d; C: 946 ± 347.5 g/pen/d). There was no difference in the frequency of antibiotic treatment between the C and T groups (2 out of 36 T piglets and 2 out of 36 C piglets suffering from watery diarrhea for 4 d received antibiotic treatment), and none of the T and C piglets died. In conclusion, the HT extract reduced the severity of diarrhea in the first week after infection but had no effect on growth performance.

Key Words: ETEC infection, post-weaning diarrhea, piglet

1015 Curcumin prevents hepatotoxic effects of Aflatoxin B1 associated with inhibition of cytochrome P450 isozymes genes in chick liver. L. Sun*, N. Zhang, M. Zhu, L. Zhao, and D. Qi, *College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China.*

The involvement of cytochrome P450 (CYP450) isozymes in curcumin-mediated protection against aflatoxin B_1 (AFB_1)-induced adverse effects in broilers remains unclear. This study was designed to establish if curcumin could alleviate AFB_1-induced hepatotoxic effects and then to determine if these effects were due to changes in the CYP450 isozymes expression in the livers of chicks. 120 1-d-old male Avian broilers were assigned to 4 groups with 5 replicates of 6 birds to be included in a 2 by 2 factorial trial, in which the main factors included supplementation of AFB_1 (<5 vs. 100 μg/kg) and curcumin (0 vs. 150 mg/kg) in a corn/soybean-based diet for 4 wk. The liver histology, antioxidant enzymes, and mRNA of CYP450 isozymes in liver were analyzed. Administration of AFB_1 induced liver injury, which was indicated by induced hepatic necrosis and bile duct hyperplasia at wk 2. AFB_1 also decreased ($P < 0.05$) hepatic activities of catalase and glutathione peroxidase, while increasing ($P < 0.05$) exo-AFB_1–8,9-epoxide (AFBO)-DNA concentration. Curcumin supplementation was found to prevent the changes induced by AFB_1 in broilers. Moreover, the mRNA of the enzymes responsible for the bioactivation of AFB_1 into AFBO, which included CYP1A1, CYP1A2, CYP2A6, and CYP3A4, were induced ($P < 0.05$) in liver microsomes after 2 wk exposure to AFB_1. These alterations induced by AFB_1 were prevented by curcumin supplementation. In summary, dietary curcumin supplementation protected chicks from the AFB_1-induced liver injury, potentially through the synergistic actions of increased antioxidant capacities, and inhibition of the pivotal CYP450 isozyme-mediated activation of AFB_1 to toxic AFBO.

Key Words: curcumin, aflatoxin B_1, CYP450, AFBO-DNA, chicks

1016 Effects of humic acid supplementation on pig growth performance, Nitrogen digestibility, odor, and ammonia emission. C. H. Ponce[*1], C. Arteaga[2], and A. Flores[2], [1]*Escuela de Medicina Veterinaria, Colegio de Ciencias de la Salud, Universidad San Francisco de Quito USFQ, Quito, Ecuador,* [2]*Departamento de Ciencias de la Vida y Agricultura, Universidad de las Fuerzas Armadas ESPE, Sangolqui, Ecuador.*

An experiment was conducted to evaluate the effects of the level of supplementation of humic acid salts (HF) on pig performance, nitrogen digestibility, odor, and ammonia emissions from manure. A total of 150 piglets were used in a completely randomized block design (10 pens/treatment and 5 piglets/

pen) and assigned into 3 experimental treatments: 1) control, without HF supplementation (0HF), 2) supplementation of 2 g/pig/day of HF (Huminfeed; 2HF), and 3) supplementation of 4 g/pig/day of HF (Huminfeed; 4HF). Commercial diets were fed ad libitum in a pellet form in 2 phases, from weaning (21 d) to d 49 (pre-starter) and from d 49 to 70 (starter). Growth parameters were measured weekly. Total fecal and urine samples were collected form 3 pens/treatment on d 14 of the experiment for 5 consecutive days to measure nitrogen digestibility. On d 20 of the experiment, fecal samples mixed with urine samples (1:2) were placed into plastic containers to measure ammonia emissions over 48 h. Additionally, fecal samples were collected to measure odor characteristics. Overall, body weight, ADFI, ADG, and the G:F ratio were not altered by HF supplementation ($P > 0.59$). Nitrogen intake and N fecal excretion were linearly decreased as HF increased ($P < 0.01$). Apparent total nitrogen digestibility increased linearly as HF increased ($P = 0.02$). However, N retention was not different across treatments ($P > 0.37$). There was a tendency toward decreased NH_3 emission from manure from the 4HF treatment over 48 h ($P = 0.09$). Odor hedonic tone and odor intensity from manure were significantly reduced by HF supplementation ($P < 0.01$). Results from this experiment suggest that there are benefits of HF supplementation on odor parameters, NH_3 emissions, and N digestibility without altering pig growth performance.

Key Words: ammonia emissions, growth performance, humic acids

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1017 A standardized blend of capsicum and turmeric oleoresins given during late gestation improves the performance of sows vaccinated against *E. coli*.

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Previous research projects have demonstrated that a standardized protected blend of capsicum and turmeric oleoresins (XT, Xtract® Nature, Pancosma, Switzerland) had an immune-modulating effect and could potentiate and complement the effects of vaccines in poultry. However, similar data were not available in swine. The objective of this trial was to evaluate if the supplementation of XT in late gestation could improve the performance of sows vaccinated against *E. coli* during farrowing and lactation. A total of 1531 sows vaccinated against *E. coli* at 80 d of gestation and regrouped in 3 successive bands were involved. Sows in phases 1 and 3 were fed an unsupplemented basal diet (CT, $N = 529$ and 329, respectively), whereas animals in the second phase were provided the same basal diet supplemented with 200 g/t XT ($N = 673$) from 80 until 110 d of gestation. In terms of sow performance, the proportion of piglets born/litter was recorded at farrowing as well as piglets' mortality during lactation. Colostrum was also collected at birth ($N = 14$ and 16, respectively, for the XT and CT groups) for analysis of total protein, albumin, and globulins. Data were analyzed by analysis of variance, considering the effect of the treatment for colostrum quality, and the effects of the treatment, parity, and their interaction for performance outcomes. Results showed that XT increased the levels of total proteins by +5.0% in colostrum ($P = 0.04$), and this was mainly driven by a greater concentration in globulins (+5.0%, $P = 0.08$). XT enhanced the proportion of piglets born alive per litter (92.6% vs. 90.7%, respectively, for XT and CT; $P < 0.01$). This effect was more pronounced in sows of parity 1 or 2 (+2.2%, $P = 0.02$) than in sows of parity 3 or more (+1.9%, $P = 0.06$). The treatment did not affect the piglets' mortality during suckling, but there was a treatment*parity effect on this outcome: litters in primiparous and parity 2 sows had reduced mortality when fed XT compared to CT (10.1 vs. 12.5%, $P = 0.01$). These results suggest that XT supplementation to vaccinated sows during late gestation has the potential to improve nutrient supply to the progeny, litter performance at farrowing, and litter size at weaning.

Key Words: performance, vaccinated sows, Xtract

1018 Evaluation of biodegraded and undegraded plantain peels as replacement to wheat offal in broiler production.

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This study evaluated the replacement of wheat offal with biodegraded and undegraded plantain peels in raising broilers. Plantain peels were biodegraded using fungus, and three diets were formulated. Diet I with 12% wheat offal was the control, and in diets II and III, wheat offal was replaced with undegraded and biodegraded plantain peels. Ninety day old broilers were randomly assigned to these diets, which were replicated thrice and lasted for 8 wk. During this feeding trial, data on the performance characteristics of the birds were collected. Blood samples were also taken at the eighth week for analysis, and all data generated were subjected to analysis. Results revealed that body weight gain was similar ($P = 0.05$) across the diets at both starter and finisher phases, implying that the energy and protein content of the diets were not below the maintenance requirements. The broilers fed control diets had a similar feed intake to those on the degraded plantain peel diet, but it was significantly ($P < 0.05$) higher than those on the undegraded plantain peel diet at the starter phase, while at the finisher phase the intake was similar across the diets possibly due to age. Feed conversion ratio had a similar pattern to intake at both phases. Among the serum metabolites observed, the glucose, total protein, cholesterol, urea, creatinine, and the enzymes were all significantly affected by the diets and were mostly within normal range. Morphological analysis of the birds revealed significant effects of treatments on the

heart, proventriculus, gizzard, lung, spleen, liver, and intestine. The carcass analysis revealed that the shank, wing, back, and the head of the control and those fed diet II were similar and higher than those fed diet III, but the breasts of broilers on diet III were better than those on diets I and II. The mortality that occurred could not be traced to diets. Biodegraded or undegraded plantain peels could be used as a replacement for wheat offal weight for weight in broiler production without adversely affecting performance characteristics, morphology, blood parameters, and carcass analysis.

Key Words: plantain peels, broilers, performance characteristics

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1019 Effect of lysophospholipids supplementation in different energy diets on growth performance, nutrient digestibility, milk composition, litter performance, and fecal score in lactating sows.

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Emulsifiers are substances that stabilize mixtures and prevent oil and water from separating, which is good for the digestion of lipids. This study was conducted to evaluate the effect of dietary emulsifier (lysophospholipids, LPL) supplementation with different energy diets in lactating sows. A total of 32 multiparous sows (Landrace × Yorkshire) were used in a 21-d experiment. On d 110 of gestation, sows were weighed and moved into the farrowing facility, randomly assigned in a 2 × 2 factorial arrangement with two levels of Lipidol (0 and 0.1%; Lipidol contains 3% LPL) and two level of metabolizable energy (3265 and 3165 kcal/kg) according to their BW. Individual sows were weighed and scanned for backfat thickness to determine weight and backfat loss. Chromium oxide (0.2%) was added to the diet as an indigestible marker to determine ATTD of DM, N, and GE. Milk crude fat (Method 960.39; AOAC, 2007) was measured according to the Association of Official Analytical Chemists. Lactose was assayed using an enzymatic method. Data were analyzed as a randomized complete block design with a 2 × 2 factorial arrangement using the GLM Procedure of SAS (SAS Inst. Inc., Cary, NC). A probability level of $P < 0.05$ was considered to be significant. Body weight loss (18.6 vs. 15.1 kg) and backfat thickness loss (2.4 vs. 1.9 mm) were decreased ($P < 0.05$) by LPL supplementation. Backfat thickness (17.0 vs. 14.5 mm) at weaning was higher ($P < 0.05$) in sows fed LPL supplementation diets. The ATTD of DM (84.4 vs. 83.2%), N (83.6 vs. 82.5%), GE (82.9 vs. 82.1%), and crude fat (80.1 vs. 79.2%) in sows fed LPL diets was increased ($P < 0.05$) compared with those fed non-LPL diets. Sows fed the high energy diets had higher ($P < 0.05$) milk fat (11.3 vs. 10.0%) on d 10 and milk lactose (4.6 vs. 3.9%) on d 20 than those fed the low energy diets. Milk fat (11.3 vs. 9.9%) and lactose concentrations (4.6 vs. 4.0%) in LPL supplementation treatments were increased ($P < 0.05$) compared with non-LPL treatments on d 10 and d 20, respectively. Interactive effects ($P < 0.05$) between energy and LPL were observed on milk fat concentration on d 10. In conclusion, LPL addition decreased body weight loss and backfat thickness loss and improved nutrient digestibility and milk fat as well as milk lactose concentrations. Additionally, LPL and energy can interactively increase milk fat concentration in lactating sows.

Key Words: growth performance, lysophospholipids, sow

1020 Effect of crystalline silicon dioxide in piglet feed on growth performance with different levels of growth promoters.

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Silicon dioxide is a common mineral that can be found under different forms (crystalline or amorphous) and is also found in many clays and diatomaceous earth. The purpose of this trial was to assess, in a factorial 2×2 arrangement, the growth performance of piglets reared with a feeding program including, or not, a crystalline silica-based feed supplement (SI) with or without antibiotics as growth promoters (AGP; chlortetracycline and high levels of Cu and Zn in Phase 1 and chlortetracycline in Phase 2). All diets were formulated to be iso-caloric and iso-nitrogenous. An ANOVA was performed on zootechnical parameters with the pen as the experimental unit for all analyses. Effects of AGP, SI, block (based on sex and body weight), and interaction between AGP and SI were included in the statistical model. A total of 252 piglets with body weights of 7 kg were reared until 24 kg of body weight and allocated into 36 pens. According to these results, groups fed with AGP showed improved weight gain, feed intake, and feed conversion during Phase 1, while no significant effect was observed during Phase 2. Concerning the effect of SI, feed intake was improved by 4.13% during the overall nursery period, compared to groups without SI (729 versus 700 g/day; $P < 0,05$). In addition, groups fed SI showed an average daily gain of 3.26% higher than animals without SI during the same period (607 versus 588 g/day; $P < 0.05$). This effect leads to an improvement of 2.2% in piglet's weight at the end of the post-weaning phase (24.52 versus 23.99 kg; $P < 0.05$). It was concluded that under our trial conditions, adding crystalline silicon dioxide to piglet feed (0.02%) increase feed intake, growth rate, and piglet weight at the end of the nursery period. This mineral additive could offer potential economic benefits to swine producers.

Key Words: silicon, silica, piglet

BEEF CATTLE NUTRITION SYMPOSIUM: A LOOK AT THE LATEST BEEF CATTLE NRC RECOMMENDATIONS

1021 Overview of the process and changes in the eighth edition of the Nutrient Requirements of Beef Cattle. M. L. Galyean*, *Texas Tech University, Lubbock.*

The National Research Council's (NRC) series on *Nutrient Requirements of Beef Cattle* has been an essential information resource for practicing nutritionists and academicians for decades. Standards set by NRC publications have improved the economic and environmental sustainability of the beef industry, and each revision has provided a stimulus for further research. The committee responsible for the eighth edition invested more than 2 yr in producing a revision that would meet the high standards set by previous publications in the series. Following the Statement of Task, the committee updated the seventh revised edition by reviewing the scientific literature on the nutrition of beef cattle for all life phases and various production settings. Several new sections were added, including beef cattle production systems, food quality, and safety; ruminant anatomy and digestion; carbohydrates; lipids; compounds that modify digestion and metabolism; nutrition and the environment; and byproduct feed ingredients. Chapters from the seventh edition were updated, with substantial effort to provide improved prediction equations for modeling nutrient supply and metabolism. Specifically, new equations for predicting microbial protein synthesis and recycled nitrogen that is incorporated into microbial products were added. New information was included relative to the role of sulfur in beef cattle production, particularly as it relates to high-sulfur byproduct feeds. Greater clarity is provided on recommendations for provision of vitamin E in various production settings, and new equations were provided for the prediction of feed intake by growing/finishing beef cattle. The body condition score-based system was changed to include a fixed percentage of shrunk BW change per unit of BCS, and updated guidelines for adjustments to dietary ME values associated with the use of ionophores are provided. A new chapter is devoted to the potential effects of livestock operations on the environment, and prediction equations for nutrient excretion and enteric methane production are included. Byproduct feeds are described in much greater detail, and a statistically based evaluation of a feed composition data from commercial laboratories is provided. The new computer model, with options for empirical and mechanistic solutions, is more intuitive and user-friendly than software provided with the seventh edition. The eighth edition of the *Nutrient Requirements of Beef Cattle* is a major revision that should have a significant effect on beef cattle research and production over the next decade.

Key Words: beef cattle, nutrient requirements, revision

1022 The eighth revised edition of the Nutrient Requirements of Beef Cattle: maintenance and growth. J. S. Caton*[1], C. R. Krehbiel[2], M. L. Galyean[3], and L. O. Tedeschi[4], *[1]Department of Animal Sciences, North Dakota State University, Fargo, [2]Oklahoma State University, Stillwater, [3]Texas Tech University, Lubbock, [4]Texas A&M University, College Station.*

The objectives of this review are to discuss updates to maintenance and growth components of the eighth revised edition of the Nutrient Requirements of Beef Cattle. From an energy supply standpoint, the traditionally held relationship of DE to ME (ME = DE × 0.82) needs to be reassessed. Maintenance requirements are computed by adjusting the base NEm requirement for breed, lactation, and heat loss vs. heat production (HE), which is ME intake minus retained energy (RE). Adjustments for animal insulation and environmental conditions are considered. The NEm requirement is computed based on the basal metabolism coefficient (a1) and adjustment factors for previous temperature (a2), breed (BE), lactation(L), gender, and previous plane of nutrition (COMP) as follows: NEm = $SBW^{0.75}$ × (a1 × BE × L × COMP × SEX + a2), where a1 = 0.077 and is the basal metabolism coefficient in Mcal/$kg^{0.75}$ daily, BE is breed factor, L is lactation factor, COMP = 0.8 + (BCS – 1) × 0.05 and is the NEm adjustment for previous nutrition, SEX is gender effect (1.15 bulls vs. 1 for others), a2 = 0.0007 × (20 – Tp) with a2 being the acclimatization factor in Mcal/$kg^{0.75}$ daily, and Tp is the previous temperature in °C. The seventh revised edition of the Beef NRC adjusted the a1 coefficient by 10% for all *Bos indicus* cattle; in the revised edition, this adjustment is removed for Nellore cattle. Previous adjustments to NEm for cold or heat stress are retained in the revised version, but users are cautioned on applying current equations, and this is an area of research need. Previous adjustments for the physical activity of grazing have been removed in the eighth revised edition, and additional research is needed on energetic costs of physical activity. Methods to estimate MP for maintenance remain unchanged. Growth equations from the previous NRC were retained. Additional data were used to evaluate equations for predicting retained energy and protein, with resulting satisfactory accuracy for predicting RE, but improvements are needed for predicting retained protein. Serial slaughter data measuring body composition in modern cattle with and without growth technologies are needed. Problems and barriers associated with accurately predicting NE and protein requirements for growth were delineated and discussed.

Key Words: energy, maintenance, protein

1023 The eighth revised edition of the Nutrient Requirements of Beef Cattle: reproduction.

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The eighth Revised Edition includes updates to the calculation of body energy (BE) and protein reserves in beef females, empty BW (EBW, kg) change per BCS, and Mcal of BE change per BCS. Energy and protein requirements for the maintenance and growth of bulls, heifers, and cows and for milk production remain largely unchanged from the seventh Revised Edition. Replacement heifer target weights at the beginning of the breeding season are unchanged from the seventh Revised Edition (55% for dual purpose or dairy breeds, 60% for *Bos taurus*, and 65% for *Bos indicus*), but the eighth Revised Edition model allows the user to change this variable. A more complete description of BCS 1 through 9 has been created, and a BCS decision tree has been added. A discussion regarding the effect of cow nutrition on fetal and developmental programming has been added to the narrative. While the previous body reserves model assumed a variable BW change per BCS, the new body reserves model assumes a fixed BW change per BCS, and it is computed as 7.105% of the empty body weight at BCS 5. Within the model, the user can modify the 7.105% adjustment. For primiparous females, based on limited data, an adjustment factor of 1.6 × 7.105% is suggested for the EBW change needed to increase 1 BCS. Similarly, it is suggested that an adjustment factor of 0.4 × 7.105% be used for EBW change needed to lose 1 BCS for primiparous females. Energy content of 1 kg cow weight gain in the eighth Revised Edition has been changed from a constant of 5.826 Mcal/kg of SBW to a variable number ranging from 3.69 for a BCS 1 cow to 7.99 Mcal/kg of SBW for a BCS 9 cow. The estimated DMI calculation for cows in the model remains unchanged, but a DMI calculation based on neutral detergent fiber (NDF) intake, as a percentage of BW, has been added to the model output for user evaluation of DMI. It is often suggested that 1.1% be used for low- to medium-quality forages. Only minor adjustments have been made to the vitamin and mineral (Co) requirements for reproducing beef females.

Key Words: beef cattle, reproduction, requirements

1024 The eighth revised edition of the Nutrient Requirements of Beef Cattle: protein and metabolic modifiers.

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The eighth Revised Edition includes updates to the proteins and digestive and metabolic modifiers sections of the report reflecting new information since the seventh Revised Edition was published. The MP system was adopted in the seventh Revised Edition. It accounts for rumen degradation of dietary protein and separates requirements into the needs for ruminal microorganisms and the needs of the animal. Rumen degradable protein (RDP) provides ruminal microorganisms with various sources of nitrogen (N). In contrast, ruminally undegraded protein (RUP) is not hydrolyzed in the rumen. The amount of RDP required is based on prediction of synthesis of microbial CP (MCP). Published data from studies using cattle fitted with intestinal cannulas were used to develop and evaluate empirical equations for the prediction of MCP based on total digestible nutrient intake (TDNI), fat-free TDNI (FFTDNI), and CP intake as independent variables. Equations based on TDNI and FFTDNI are provided to estimate MCP depending on the ether extract percentage of the diet. The MP supply is absorbed amino acids from protein digested in the intestine and supplied by microbial protein and RUP. Reported values for RUP digestibility are variable, but most estimates for forages are less than 60%. The digestibility of RUP for forages was decreased from 80% to 60%. Regression analysis of literature data based on the dual-labeled urea isotopic approach was used to update equations to estimate urea N kinetics. A more complex rumen model is needed to include recycling directly in the beef cattle nutrient requirements model. A number of feed additives and other compounds that improve animal health and the efficiency of nutrient use, increase growth rate, and decrease the environmental impact of beef cattle were reviewed. These include compounds that alter rumen fermentation, additional aspects of gastrointestinal tract function, or post-absorptive metabolism. Review of feed additives with the potential to provide an alternative to inclusion of dietary antibiotics, such as plant secondary metabolites, direct-fed microbials, and feed enzymes, was included. Ionophores change microbial populations in the rumen and improve feed efficiency. Predicted DMI is decreased by 3% when monensin is fed. In addition, dietary ME was increased by 2.3 or 1.5% for monensin or lasalocid, respectively, to account for improvements in ADG and feed efficiency when feeding ionophores.

Key Words: beef cattle, ionophores, microbial protein synthesis, urea recycling

1025 The eighth revised edition of the Nutrient Requirements of Beef Cattle: minerals, vitamins, and water. T. E. Engle*[1], J. S. Caton[2], M. L. Galyean[3], L. O. Tedeschi[4], N. A. Cole[5], C. R. Krehbiel[6], G. E. Erickson[7], K. A. Beauchemin[8], R. P. Lemenager[9], and J. H. Eisemann[10], *[1]Colorado State University, Fort Collins, [2]Department of Animal Sciences, North Dakota State University, Fargo, [3]Texas Tech University, Lubbock, [4]Texas A&M University, College Station, [5]USDA Agricultural Research Service, Bushland, TX, [6]Oklahoma State University, Stillwater, [7]University of Nebraska, Lincoln, [8]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [9]Purdue University, West Lafayette, IN, [10]North Carolina State University, Raleigh.*

The objective of this review is to briefly discuss the updates made to the minerals, vitamins, and water sections contained in the eighth revised edition of the Nutrient Requirements of Beef Cattle publication. Relevant data for determining mineral, vitamin, and water requirements for beef cattle published since the seventh revised edition as well as recommendations from recently published NRC publications were added where appropriate. Although long identified as essential components in the diets of beef cattle and required for many biochemical reactions, the interactions among minerals, vitamins, water, and metabolic processes are extremely complex. The minerals chapter provides an update of macro- and micro-mineral requirements for beef cattle and discusses factors that can affect mineral requirements as well as mineral-specific diseases that can influence beef cattle production. New information has been added relative to the role of sulfur in beef cattle production that focuses on factors affecting sulfur requirement and maximum tolerable concentrations of sulfur. Dietary cobalt requirements were increased from 0.10 to 0.15 mg Co/kg DM for all classes of beef cattle, and maximum tolerable concentrations of certain minerals were adjusted based on published data. The vitamins chapter provides an update of beef cattle vitamin nutrition, with new information regarding fat- and water-soluble vitamins. Of special note is the greater clarity that has been provided with respect to recommendations for provision of vitamin E in various production settings. The review articulates issues associated with specific deficiencies and excesses and suggests areas for additional research. New research focusing on the influence of diet type, physiological status, and stress would be useful to more accurately predict the vitamin and mineral requirements of beef cattle. Of the six essential nutrient classes, water is the single most important nutrient for beef cattle. The water chapter provides an update of equations to predict water intake by beef cattle and discusses certain factors that influence water intake, including the role of water quality in beef cattle production. In Chapter 19, the water intake model includes a response surface regression to predict water requirements for different effective temperature indexes for growing and finishing beef cattle.

Key Words: beef cattle, minerals, vitamins, water

1026 The eighth revised edition of the Nutrient Requirements of Beef Cattle: environmental issues. N. A. Cole*[1], K. A. Beauchemin[2], G. E. Erickson[3], L. O. Tedeschi[4], and M. L. Galyean[5]. *[1]USDA-ARS Conservation and Production Research Laboratory (retired), Bushland, TX, [2]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [3]University of Nebraska, Lincoln, [4]Texas A&M University, College Station, [5]Texas Tech University, Lubbock.*

Since publication of the of seventh Revised Edition of the *Nutrient Requirements of Beef Cattle*, (1996/2000), there has been growing concern among producers, regulators, and the general public about the impacts of livestock operations on the environment. Beef cattle typically retain less than 20% of the nutrients they consume. The remainder is lost via feces, urine, or respiration. The effects of these excreted nutrients, as well as pharmacologically active compounds (PAC) and pathogens on ground waters, surface waters, air quality, global climate change, environmental sustainability, land use, biodiversity, and quality of life are potentially affected by nutritional and management programs used by producers. Although environmental concerns normally revolve around concentrated animal feeding operations, some effects can also be a concern in extensive systems, such as pasture-based cow-calf and stocker operations. This new chapter in the eighth Revised Edition summarizes the environmental concerns associated with beef production in North America and reviews the latest scientific approaches to mitigation. Possible dietary effects on surface and ground water and air quality are discussed. Water quality concerns include the loss of nutrients, such as nitrates and phosphorus and PAC, to ground and surface waters. Air quality issues of greatest concern include emissions of ammonia and the greenhouse gases methane and nitrous oxide. Empirical equations are provided to estimate the excretion of organic matter, nitrogen, and phosphorus and for emissions of ammonia and enteric methane. A nonlinear equation is recommended to calculate the proportion of total nitrogen that is excreted in urine. Enteric methane production of cattle is highly dependent on factors such as forage quality, forage concentration, DMI, dietary fat, ionophores, and grain processing; therefore, multiple empirical equations are proposed to estimate enteric methane production from cattle fed high-forage, medium-forage, and low-forage diets. The effects of many co-products, such as distiller's grain, on enteric methane are variable and dependent on the control diet composition. By more precisely feeding and supplementing

livestock to meet their nutrient requirements, excess nutrient losses can be decreased. Under practical conditions, however, the use of precision feeding systems to manage environmental impacts is limited and challenged by factors such as: 1) inherent biological inefficiencies in the animal, 2) variability in animal performance and/or nutrient requirements, 3) variability in composition of feed ingredients, 4) high nutrient concentrations in many co-products, and 5) other factors.

Key Words: environment, beef cattle, nutrients, greenhouse gas, ammonia

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1027 The eighth revised edition of the Nutrient Requirements of Beef Cattle: byproducts and feed composition.

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Byproduct feeds are important in beef cattle production, often providing cost-effective energy and protein. The focus of the review in the eighth revised edition was on corn and soy byproducts, as corn and soybean production are the two largest crops produced in the U.S. Use of distillers grains plus solubles, distillers solubles, corn gluten feed, Sweet Bran (Cargill corn milling, Blair, NE), soybean hulls, and glycerin was reviewed. The focus for grain milling byproducts (distillers and gluten feed) was on protein characteristics and use as a protein or an energy supplement and to replace grain in finishing diets. Effects of initial grain used to produce ethanol on distillers grains characteristics was also reviewed. The associative effects of using grain milling byproducts was reviewed to illustrate the important interactions of corn processing, roughage inclusion, and dietary inclusions relative to energy content realized from distillers grains and corn gluten feed. Similar to the seventh Revised Edition of the Beef NRC, a comprehensive feed composition review was conducted. Data were summarized from 3 commercial laboratories that included 170 feeds. Nutrient data on DM, ash, TDN, DE, ME, NEm, NEg, sugar, starch, fat, NDF, ADF, lignin, CP, RDP, RUP, soluble CP, ADIN, and minerals (Ca, P, Mg, K, Cl, S, Co, Cu, I, Fe, Mn, Mo, Se, and Zn) were provided. Considerable effort was made to ensure feeds had proper nomenclature and to avoid duplication by evaluating normal distribution, mean, and SD. Feeds with less than 20 entries were removed from the database. Likewise, nutrient values greater or less than 3.5 SD were removed from the database but only for that nutrient within a particular feed. Once the final data were available, mean, SD, and sample size were calculated and reported, and composition data for these 170 feeds was included in the computer model database. Feed composition data should only be used as a guide in the absence of feed analysis and to indicate which nutrients are variable and may require assay before formulation. These data can also be used to compare analyzed nutrients to a known database. Additionally, grazed forages from different regions were provided from the literature and focused on masticate collections when available. Grazed forage data only include TDN, NDF, and CP but illustrate how season and region can affect grazed forage quality.

Key Words: beef cattle, byproducts, feed composition

1028 The eighth revised edition of the Nutrient Requirements of Beef Cattle: development and evaluation of the mathematical model.

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The beef cattle nutrient requirements model (BCNRM) is a spreadsheet-based computer software program compatible with Microsoft Excel 2007 or earlier versions. The BCNRM contains two levels of solutions (empirical = ELS and mechanistic = MLS) to compute the supply of energy and nutrients to the animal. The calculation of animal requirements for energy and nutrients is the same for ELS and MLS. In the ELS, users can choose to use tabular values for ME and NE or compute NE, ME, and DE from tabular TDN. Methane (CH_4) is computed based on empirical equations that combine animal and dietary chemical information. In contrast, the MLS computes TDN based on: 1) rumen digestibility of five carbohydrate pools (CA = sugars, CB1 = starch, CB2 = pectin, CB3 = available NDF, and CC = unavailable carbohydrate) and three protein pools (PA = NPN, PB = soluble CP, and PC = ADIN), assuming their fractional degradation rates (kd, %/h) and a fractional passage rate (kp, %/h) for each feed; 2) intestinal

digestibilities for CB1, CB2, and PB for each feed; and 3) endogenous matter production for each feed. Then, similar to ELS, NE, ME, and DE are computed from TDN. In the MLS, CH_4 is computed based on the stoichiometric relationship of VFA produced in the rumen. The BCNRM includes an optimizer to assist with diet formulation and balancing, an ability to perform stochastic modeling, and a table generator that allows the user to create tables of nutrient requirements through an optimization procedure. The BCNRM was compared with NRC (1996, 2000) levels of solution 1 (L1) and 2 (L2) using data from 20 experiments (n = 2539 pen-fed animals). For ME-allowable gain, ELS and L1 predictions were nearly identical (r^2 of 0.999, root of mean square error (RMSE) of 0.018 kg/d, and accuracy (Cb) of 0.998). The MLS predictions tended to be greater than L2 predictions by approximately 0.158 kg/d, though there was a strong correlation between them (r^2 of 0.999 and Cb of 0.9). The opposite was observed for MP-allowable gain, and MLS and L2 predictions were nearly identical (r^2 of 0.999, RMSE of 0.023 kg/d, and Cb of 0.998) while ELS and L1 predictions differed by 0.234 kg/d (r^2 of 0.975 and Cb of 0.9). A stochastic simulation (n = 5000) predicted 122 and 97 g CH_4/d for ELS and MLS, respectively, with a 67% prediction overlap.

Key Words: computer, modeling, simulation, spreadsheet

NON-NUTRITION: THE FUTURE OF NUTRITION?

1029 Why the intersection of microbiology and neurobiology matters to animal health: microbial endocrinology as a means to examine the host-microbiota interface. M. Lyte*, *Iowa State University, Ames.*

Microbial endocrinology represents the intersection of two seemingly disparate fields, microbiology and neurobiology, and is based on the shared presence of neurochemicals that are exactly the same in structure in the host as well as in the microorganism. The ability of microorganisms not only to respond to but also to produce many of the same neurochemicals that are produced by the host, such as during periods of stress, has led to the introduction of this evolution-based mechanism that has a role in the pathogenesis of infectious disease as well as the microbiota-gut-brain axis. Production of neurochemicals by microorganisms usually employs the same biosynthetic pathways as those utilized by the host, indicating that acquisition of a neurochemical-based signaling system in the host may have been acquired due to lateral gene transfer from microorganisms. Such recognition of a common shared signaling system suggests that there is a common mechanistic pathway by which the host may interact with the microbiota in a bi-directional fashion influencing aspects of both disease and health. In the case of infectious disease pathogenesis, the consideration of a microbial endocrinology-based mechanism in which infectious bacteria can directly respond to host-derived neurochemicals, such as those present during periods of stress, has demonstrated, for example, that the prevalent use of catecholamine-based synthetic drugs in the clinical setting contributes to the formation of biofilms in indwelling medical devices, leading to increased morbidity and mortality. At the same time, the ability of the microbiota to produce neurochemicals that constitute the host's own neuronal signaling systems means that a common pathway exists for the microbiota to influence host neurophysiology. One of the most prevalent examples by which neurochemical production by microbiota may influence the host's brain and ultimately behavior can be seen with the increasing use of probiotics as a means to influence behavior. Numerous probiotics in current use produce large amounts of neurochemicals, such as GABA, which are known to have well-recognized roles in behavior. That both the host and microorganism produce and respond to the same neurochemicals means that there is bi-directionality contained within the theoretical underpinnings of microbial endocrinology. Such a shared pathway argues for a role of microbiota-neurochemical interactions in animal health.

Key Words: gut endocrinology, microbiome

1030 The gut microbiome as a virtual endocrine organ: implications for host physiology and behavior. G. Clarke*, *University College Cork, Cork, Ireland.*

The gut microbiome exerts a marked influence on multiple aspects of host physiology including not just host metabolism and body composition but also brain function and behavior. This impact relates to its ability to produce or indirectly control a large range of hormonal agents that can play a regulatory role in the activity of local and distal systems and organs. Dysfunction of the hypothalamic–pituitary–adrenal (HPA) axis in particular has been a striking consequence to disrupting the gut microbiota in preclinical studies. The translational relevance of these findings is apparent in stress-related disorders, such as irritable bowel syndrome. Unlike other endocrine organs, however, the gut microbiota exhibits compositional plasticity and can itself be subject to fluctuation as a result of stressors or dietary factors with implications for the associated functionality. This includes stress experienced prenatally, postnatally, and during adulthood. Farm animals regularly encounter a variety of such stressors related to handling practices, weaning, housing systems, and transport that potentially affect welfare and productivity. While optimizing nutrition to promote the gold standard assembly and maturity of the microbiota is one option to counteract the detrimental impact of stress exposure, more targeted interventions may be necessary at various critical points of control across the lifespan. Understanding how best to manipulate the gut microbiota to control host physiological

and behavioral responses could have important implications in multiple settings, including the prevention or treatment of stress-related disorders. Expanding this research to farm animals may pave the way for new strategies to enhance animal health and to meet farm production targets.

Key Words: endocrinology, gut physiology, microbiome

1031 Threats to gut health in production animals.

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Demand for meat protein is steadily increasing due to an expanding population and increasing wealth in populous nations. With finite supplies of arable land under increasing pressure, productivity gains through increased efficiency of animal production are essential for future food security. However, regulations and public opinion have restricted the use of hormone supplements and antibiotics for growth enhancement. There is thus a focus on other non-nutrient additives, including phytonutrients. The gastrointestinal mucosa is a major determinant of feed conversion efficiency, as it represents the first line of defense against enteric pathogens and is susceptible to disruption by events, such as weaning, environmental (notably heat) stress, and infection. Heat stress is increasing with global warning and a shift of agricultural production into tropical regions; in feedlot cattle and in intensive pig faming, it can cause decreases in feed intake and growth, and in extreme cases may result in death. The gut leakiness of heat exposure is associated with oxidative stress in the intestine, which is manifested by compromised glutathione peroxidase activity and increased levels of oxidized glutathione. A further threat to gut health is rapid and early weaning. Rapid weaning is required to maintain breeding productivity and effective herd management. However, it causes stress that is not associated with gradual weaning, which occurs for animals in the wild. The weaning transition in farmed pigs is accompanied by adverse changes in intestinal morphology, including villus atrophy, increased crypt depth, reduced absorptive capacity, and reduced brush border enzyme activity. The weaned animals lose weight, some animals die, and those that lose significant weight lag behind their litter mates in weight gain. In pigs, first litters show greater post-weaning deficits. The third major threat, which is exacerbated by heat or post-weaning stress and by intensification of production, is reduced resistance to enteric pathogens. Intestinal bacterial infections can reduce average growth rates by as much as 40%. The major hormone that promotes mucosal growth and repair is glucagon-like peptide 2 (GLP-2), which is released from L-type enteroendocrine cells. These cells bear receptors that are potential targets for food additives. In addition, a number of phytonutrients and other food additives have antioxidant or mucosal protective qualities, for example cinnamaldehyde and selenium. There is need to further advance understanding of mucosal biology and the actions of non-nutrient additives in production animals to improve gut health, animal health, and productivity.

Key Words: gut health, mucosal integrity, heat stress, weaning, enteritis

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1032 The gut microbiome and its role in the development and function of newborn calf gastrointestinal tract.

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Microbial colonization plays important roles in neonatal gut health. However, studies on gut microbial composition and how it can shape host function during early life in ruminants are limited. Here, we report some of our recent efforts in studying host-microbial interactions in neonatal calves focusing on small intestines collected from animals from soon after birth to 6 wk of age. The use of molecular-based approaches revealed extensive colonization of the gut with active microbiota during birth. Composition of the newborn gut microbiota was significantly different from the maternal microbiota in the birth canal and the environmental microbiome. Further differences in diversity were observed between tissue-attached (epimural) and content-associated microbiomes. Epimural communities consisted primarily of *Pseudomonadaceae* and *Propionibacteriaceae*, whereas *Propionibacteriaceae*, *Prevotellaceae*, *Ruminococcaceae*, *and Lachnospiraceae* dominated luminal contents. Within the first week of life, *Veillonellaceae* and *Lachnospiraceae* dominated epimural communities, while *Bacteroidaceae*, *Clostridiaceae*, and *Lactobacillaceae* dominated content communities. Investigation of calf small intestinal transcriptomes using RNA-seq revealed that the expression of immune-related genes at birth was different from three other developmental stages (week 1, 3, & 6) in the jejunum and ileum. The expression of genes related to tight junction proteins, antimicrobial peptides, NOD-like receptors, regulatory T cell markers, and cytokines underwent dynamic changes within the first week of life along with the observed changes in microbiome. This suggests that the first week postpartum is a critical developmental period for the intestinal epithelial barrier, and development of the mucosal immune system may be responding to the changing microbial composition. This conclusion is supported by evidence of strong correlations between expression of mucosal immune-related genes and total bacterial population in different gut regions at different ages. This study provides evidence that the establishment of the small intestinal-specific microbiota begins during

birth, and its composition deviates significantly from the dam's microbiota. This process may be modulated primarily by host selection. The establishment of such "individualized" gut microbiota may be an important regulator of gut tissue and immune function development. Our findings provide fundamental knowledge regarding host-microbial interactions in neonatal calves and may support future development of more effective strategies to improve neonatal gut health.

Key Words: calf, gut health, mucosal immunity

1033 From pre- to post-weaning: the adaptations of the gastrointestinal tract of the young calf.

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The ruminant gastrointestinal tract (GIT) faces the challenge of protecting the host from luminal contents and pathogens while supporting the absorption and metabolism of nutrients for growth. The GIT of the calf in early-life undergoes some of the most rapid microbial and structural changes documented in nature, and it is these adaptations in GIT function that make the young calf susceptible to gastrointestinal disease and disorders. Despite these challenges, the GIT of the calf has a certain degree of plasticity and can sense nutrient supply and respond to bioactive ingredients. For example, the pre-weaned calf can adapt to meal size by altering abomasal emptying as a means of controlling nutrient delivery to the intestine, thereby stabilizing blood metabolites. Despite this plasticity, research has historically focused on the transition during weaning and characterizing ruminal papillae development using microscopy. Through the use of molecular-based approaches, we have recently shown that delaying the age of weaning and providing a step-down weaning protocol is associated with a more gradual shift in ruminal microbiota to a post-weaned state. In addition to ruminal adaptations during weaning, nutrient flow to the lower gut changes dramatically during weaning, coinciding with a wide array of structural and microbiological changes. A study examining structural and gene expression changes suggests that the lower gut of the dairy calf undergoes alterations that may reduce barrier function when solid feeds are consumed. Additionally, a recent in vivo calf study revealed that the weaning transition increases total gut permeability of the calf. Interestingly, some evidence suggests that the upper and lower gut are able to communicate with the forestomach, meaning that a nutrient can be sensed in the lower gut and cause subsequent adaptations in the forestomach. An improved understanding of how diet, microbiota, and functional ingredients interact to impact growth and barrier function of the intestinal tract would greatly benefit the industry. A mechanistic understanding of such adaptations would also aid in the formulation of specific management regimens and provision of the functional ingredients required to support or enhance gut function in young calves.

Key Words: calf, gastrointestinal tract, weaning, functional nutrition

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1034 Metabolic effects of dietary pungent spices on the gut in animal models.

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The beneficial influence of pungent spices was examined in experimental rats on (i) the fluidity of intestinal brush border membrane (BBM), (ii) the activity of intestinal membrane bound enzymes, and (iii) ultrastructural alterations in the intestinal epithelium. Groups of Wistar rats were maintained on dietary black pepper (0.5%), red pepper (3.0%), ginger (0.05%), and spice bioactive compounds—piperine (0.02%) and capsaicin (0.01%)—for 8 wk. A membrane fluidity study using an apolar fluorescent probe showed increased BBM fluidity in all of the spice fed animals. This was corroborated by decreased cholesterol: phospholipid ratio in jejunal and ileal regions of the intestine. These dietary spices stimulated the activities of BBM enzymes—glycyl-glycine dipeptidase, leucine amino peptidase, and γ-glutamyl transpeptidase in jejunal mucosa, suggesting a modulation in membrane dynamics due to the apolar spice bioactive compounds interacting with surrounding lipids and hydrophobic portions in the protein vicinity. Scanning electron microscopy of the intestinal villi in these spice treatments revealed alteration in the ultrastructure, especially an increase in microvilli length and perimeter, which would mean a beneficial increase in the absorptive surface of the small intestine, providing for an increased bioavailability of micronutrients. Thus, dietary spices—black pepper, red pepper, and ginger were evidenced to induce alteration in BBM fluidity and passive permeability property, associated with the induction in the increased microvilli length and perimeter, resulting in an increased absorptive surface of the small intestine. Everted segments of duodenum, jejunum, and ileum portions of small intestines isolated from rats fed piperine, capsaicin, and ginger containing diets for 8 wk were examined for ex vivo uptake of iron, zinc, and calcium from incubations containing digesta of finger millet. A higher uptake of iron, zinc, and calcium by the intestinal segments from spice-fed animals was observed. The increase in the mineral uptake was the highest for calcium with >100%. Higher in vitro absorption of β-carotene in the intestines was evidenced in all spice-fed animals. Dietary piperine and ginger increased the uptake of β-carotene by 147 and 98%, respectively, while increases in absorption were 59 and 27% in black pepper and red pepper fed animals, respectively. An

animal study conducted to evaluate the influence of dietary spice compounds—piperine, capsaicin, and ginger—on the absorption of orally administered β-carotene and its conversion to vitamin A revealed significantly increased β-carotene concentration in the serum, liver, and intestine of piperine and ginger fed rats, suggesting improved absorption of β-carotene. Retinol concentration was not however changed in these animals, suggesting that bioconversion of β-carotene to vitamin A was not similarly influenced. The higher intestinal uptake of iron, zinc, and β-carotene as a result of consumption of pungent spices could encourage a strategy to reduce the deficiency of these micronutrients prevalent in populations dependent on plant-based foods.

Key Words: gut health, nutrient absorption, spices

1035 Phytonutrients as non-nutritive feed additives to enhance growth and host immunity in broiler chickens. H. Lillehoj*[1] and S. Oh[2], [1]*ARS USDA, Beltsville, MD,* [2]*USDA, Beltsville, MD.*

The gut represents a continuously evolving ecosystem where a dynamic interaction between host immune, neuroendocrine, and enteroendocrine cells and the gut microbiota influences normal physiological development and homeostasis. New antibiotic regulatory policies and cage-free rearing systems in poultry production now challenge animal scientists to think outside of the box to develop alternative strategies for sustainable animal agriculture. This presentation will discuss using dietary phytonutrients to enhance poultry growth and modulate innate immunity against enteric pathogens. Phytochemicals are non-nutritive, plant-derived chemicals, many with disease-preventing properties. A growing body of scientific evidence has demonstrated that many of the health-promoting activities of phytochemicals are mediated through their ability to improve host defense against microbial infections and tumors. During the last 10 yr, our research has provided science-based evidence for the beneficial effects of certain phytochemicals in the poultry immune system. Many of these phytonutrients are now commercially used to increase poultry growth and reduce disease-associated losses. Furthermore, our latest study demonstrated that dietary phytonutrients influence the intestinal microbiome through "crosstalk" with the host immune system to maintain gut homeostasis and gut health. These studies collectively suggest that dietary feeding of certain phytonutrients reduces the negative consequences of enteric diseases, in part, through alteration of the gut microbiome.

Key Words: plant extracts, poultry, immunity

1036 Phytonutrients as additives in ruminants: the unexpected target organ. J. Oh[1], E. H. Wall[2], D. M. Bravo[2], and A. N. Hristov*[3], [1]*The Pennsylvania State University, University Park,* [2]*Pancosma, Geneva, Switzerland,* [3]*Department of Animal Science, The Pennsylvania State University, University Park.*

Plants produce an extensive array of organic compounds derived from secondary metabolism that may be useful in animal nutrition because of their chemical makeup. These plant-derived bioactive compounds, also referred to as phytonutrients or phytobiotics, have been shown to express antimicrobial activities against a wide range of bacteria, yeast, and fungi and have been investigated as rumen modifiers in animal nutrition. Reports have concluded that phytonutrients may inhibit deamination of amino acids and methanogenesis in the rumen and shift fermentation toward propionate and butyrate. Responses, however, have been highly variable. Most of the experiments have been conducted in vitro. Although in vitro data are useful for screening purposes, the true value of phytonutrients for altering rumen microbial fermentation and ultimately enhancing animal production must be assessed in vivo and in long-term experiments. Some phytonutrients, due to their phenolic nature, are likely less susceptible to microbial degradation in the rumen and, similar to observations in monogastric species, may exhibit activities postruminally. For example, depending on dose, 15 to 30% of capsaicin from capsicum oleoresin administered intraruminally was estimated to escape ruminal degradation. Thus, phytonutrients, such as garlic, curcumin, and capsicum, which have modulatory effects on both the innate and adaptive immune systems in monogastric animals, may exhibit similar properties in ruminants if protected from ruminal fermentation. This opens a new area of research on the effects of phytonutrients on the immune system, physiology, and health of ruminant animals. Studies with dairy cows have shown that some phytonutrients delivered postruminally increase subtype T cells in peripheral blood (CD4+) related to adaptive immunity. More recent reports indicated that capsicum increased energy-corrected milk yield and facilitated immune cells related to acute phase responses in high-producing dairy cows. In another study with dairy cows, a rumen-protected capsicum product tended to increase milk yield and increased feed efficiency. Increased insulin sensitivity during a glucose tolerance test in that study suggested that capsicum may redirect glucose for lactose synthesis and milk production. Data also suggest that capsicum may be enhancing fat mobilization in early lactation. Further research is needed to elucidate the effect and mode of action of phytonutrients on immune function and animal energetics. Overall, the effects of phytonutrients on immunity, health, and productivity of ruminant animals observed in short-term, crossover studies are encouraging but need to be confirmed in

long-term, production experiments.

Key Words: phytonutrients, postruminal effect, immune response, insulin sensitivity, dairy cow

1037 Non-nutrients in swine health and production.

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Demand for animal proteins in human food consumption is rising globally at an unprecedented rate. Swine products occupy an important position in the structure of animal proteins. Thus, the improvement of swine health in future swine production systems will be critical to increase global food production. A group of health technologies have been applied to powerfully improve swine health and production, including age segregation, all-in/all-out pig flow, biosecurity measures, sanitation, vaccination, and others. In addition, the regular use of antibiotics in pig diets has been proven to improve health and productive performance, as shown by volumes of scientific literature and decades of practical experience. Recently, a novel concept, non-nutrients, was illuminated to describe a group of dietary compounds, which has no nutrient contribution to animals but has physiological activities beyond provision of bioavailable nutrients. Antibiotics are also counted in the category of non-nutrients. Emerging evidence suggested that these non-nutrients provided benefits for animal health and production through different modes of action: regulating nutrient digestibility or absorption and modulating microbial ecology in the digestive tract and/or immune responses. For example, dietary supplementation of artificial sweeteners prevents enteric disorders and enhances the growth and performance of early weaned pigs by increasing the expression of the intestinal glucose transporter SGLT1 and glucose absorption. Different types of exogenous enzymes, such as phytase, xylanases, proteases, etc., may be used in swine diets to improve nutrient digestibility of all stages of pigs when certain endogenous enzymes are insufficient. Interest is growing in the use of probiotics and/or prebiotics to increase the populations of desired microbes in the digestive tract and thereby provide benefits on pig health and performance. They may achieve this goal either by continuously introducing the target microbes into the digestive tract or by providing substances that specifically favor the growth of the target microbes over competitors. Moreover, plant extracts can be additional tools that producers use to keep pigs healthy and reduce the impacts of disease. Dietary supplementation of certain plant extracts may enhance the disease resistance of pigs by improving gut mucosal integrity and optimizing immune response. In the near future, the importance of using non-nutritional dietary components for maintaining pig health will be increased, as such use of antibiotics will be progressively restricted in many countries.

Key Words: health, non-nutrients, pigs

1038 Manipulation of gut morphology and gut immunity in swine using novel, naturally sustainable bioactives.

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As health and environmental regulations increase the constraints on the use of in-feed antibiotics and minerals in swine husbandry, the search for novel bioactives from sustainable natural resources increases. A wealth of chemodiversity in nature has arisen from plants and animals developing protective molecules to survive in varying complex biosystems. Many of these molecules have anti-inflammatory, antimicrobial, and/or antioxidant properties, which help the host to survive a wide spectrum of environmental challenges. We hypothesize that these non-nutritive molecules can be used in the diet to support the developing gastrointestinal tract of the piglet. The mammalian gastrointestinal tract is a dynamic environment, where a symbiotic relationship exists between the immune system, the resident microbiota, and the digestive system. The development of the immune system begins in-utero and is further developed following the colonization of the GIT with microbiota during birth and postnatal life. The early establishment of this relationship is fundamental to the development and long-term maintenance of gut homeostasis, with unfavorable alterations in the composition of the microbiota, known as dysbiosis, being implicated in many conditions. The weaning period of the piglet under modern husbandry conditions is very prone to dysbiosis in the gastrointestinal tract, resulting in a period of post-weaning diarrhea. It involves complex dietary, social, and environmental stresses that interfere with gut development and is characterized by a reduction in feed intake and growth, atrophy of small intestine architecture, up-regulation of intestinal inflammatory cytokines, alterations in GIT microflora, diarrhea, and heightened susceptibility to infection. In this review, we discuss advances in our understanding of the immune mechanisms by which the dynamic interplay of the intestinal microbiota and its host normally favors a homeostatic, symbiotic relationship, and how feeding novel, naturally sustainable bioactives from marine flora and fauna and milk can be utilized to support this symbiotic relationship in times of challenge. The overall aim of our research program is to provide dietary support to ensure an appropriate level of immune reactivity in the gut to accommodate the presence of beneficial and dietary microorganisms, while allowing effective immune/inflammatory responses to clear pathogens. A variety of natural sustainable bioactives has been identified that target different components of the gastrointestinal tract environment. Modes of action vary from commensal microbial stimulants, targeted antimicrobial activity, gut barrier repair, mucosal structure (villous architecture, absorptive capacity, nutrient transporters), and mucosal anti-inflammatory

activity. Interestingly, ingestion of combinations of these bioactives can enhance bioavailability lower down in the colon.

Key Words: swine, natural, sustainable, bioactive, gut health

PHYSIOLOGY AND ENDOCRINOLOGY

1039 WS Influence of sampling location and pregnancy on composition of the microbiome associated with the reproductive tract of the ewe.

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The objective of this study was to investigate the microbiome of the vagina, uterus, and embryo and determine the effects of pregnancy status and a maternal pregnancy recognition antagonist treatment. We hypothesized that location, pregnancy status, and maternal pregnancy recognition antagonist treatment would result in significant differences in the bacterial microbiome of the reproductive tract in sheep. Mini osmotic pumps were placed surgically into the uterus and loaded with control (PBS, $n = 9$) or treatment (AMD3100, $n = 7$). AMD3100 is an antagonist for maternal pregnancy recognition. Samples were collected for microbiome analysis from the vagina, uterus, and embryo. AMD3100 and PBS had no effect on microbiome composition ($P > 0.98$). Sampling location had the greatest effect on bacterial population ($P > 0.01$). *Firmicutes*, *Proteobacteria*, and *Actinobacteria* were the most predominant phyla ($P < 0.01$) present in the vagina while *Proteobacteria*, *Firmicutes*, and *Actinobacteria* were present in the uterus ($P < 0.01$). The genus of bacteria present in the uterus and vagina supported the phylum data. *Corynebacterium* was more prevalent than *Finegoldia* in the vagina ($P < 0.01$), while the prevailing genus in the uterus was *Bradyrhizobium* ($P < 0.01$). The pregnancy status of ewes did not differ by phylum; however, the genus *Finegoldia* was greatest in nonpregnant ewes ($P < 0.01$). Treatment effects were not observed on embryo microbiome phylum ($P < 0.90$) or genus ($P < 0.88$). Results show further research is needed to understand the relationship between the reproductive tract microbiome and ewe fertility.

Key Words: metagenome, sheep, uterus, vagina

1040 Use of doppler ultrasound and infrared thermography to evaluate scrotal insulation in Braford bulls.

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The objective of this study was to evaluate the flow dynamics of scrotal surface temperature (SST) by infrared thermography in Braford bulls submitted to scrotal insulation. In addition, bulls were also evaluated for velocity parameters (V), pulsatility index (PI), and resistance index (RI) using Doppler ultrasound. All procedures were approved by the Ethical Committee for Care and Use of Experimental Animals (Project 19656/2014/58, CEUA/UEL). All animals had a breeding soundness examination at the beginning of the experiment. Eight Braford bulls were used at the age of 18 mo and randomly divided into four different groups, as follows: the control group not subjected to insulation (CON; $n = 2$), scrotal insulated bulls for 72 h (G72, $n = 2$), scrotal insulated bulls for 96 h (G96, $n = 2$), and scrotal insulated bulls for 120 h (G120, $n = 2$). Infrared thermography and Doppler data were collected at four different periods: after removal of scrotal insulation (M0), 10 min after removal of scrotal insulation (M10), 30 min after removal of scrotal insulation (M30), and 60 min after removal of scrotal insulation (M60). Data were analyzed using ANOVA, *t* test (paired), and Pearson correlation with a significance level of 5%. No differences were observed between insulated treated groups. Rectal temperature (38.5 ± 0.4) was higher compared to scrotal surface (32.7 ± 0.8; $P < 0.05$). Scrotal insulated animals showed higher testicular temperature at M0 (33.0 ± 0.7) compared to M10, M30, and M60 periods (30.2 ± 1.3, 31.6 ± 1.5, 30.6 ± 1.0, respectively; $P < 0.05$). We observed no difference in PI and RI indexes between evaluation periods after scrotal insulation. However, blood flow velocity (cm/sec) showed differences between M10 (17.1 ± 4.22) compared to the M0, M30, and M60 periods (12.5 ± 5.1, 14.3 ± 4.5, 14.3 ± 2.9, respectively; $P < 0.05$). A positive correlation (93.1%) was observed between PI and RI ($P < 0.05$) variables. The scrotal insulation changes the temperature and the blood flow velocity; however, after 60 min of insulation, these parameters are already reestablished. We conclude that Doppler ultrasound can be used to evaluate scrotal blood flow variations during scrotal heat stress induction in Braford bulls.

Key Words: Doppler ultrasonography, infrared thermography, scrotal insulation

1041 Diurnal vaginal temperature cycles of Senepol and crossbred beef heifers with different hair coat types and colors under tropical conditions.

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This study evaluated the influence of hair coat type and color on vaginal temperature (VT) regulation of beef heifers. The VT was recorded in five slick haired, red colored Senepol (SENEPOL); six slick haired, light colored crossbred (SLICK); and four wild-type long haired, light colored crossbred (REGULAR) heifers, every 5 min for four consecutive days. Crossbred heifers were obtained from Charbray × Senepol × Charolais crosses. Air temperature and relative humidity were recorded in synchrony with VT, and the thermal humidity index (THI) was determined. Heifers were kept in a large paddock with access to natural shade. After averaged by hour, data were analyzed by the GLIMMIX and CORR procedures of SAS. To study the possible lag time in the relationship between the THI and the TV, the correlations were performed taking into consideration the THI recorded previous to the VT in 1-hour intervals (from 1 to 24 h earlier). Hair type-color interacted with the time of day to affect VT, with REGULAR heifers presenting greater VT values than SLICK and SENEPOL from 2200 to 2400 h (39.33 ± 0.03, 38.84 ± 0.01, and 38.74 ± 0.02°C, respectively). During the remaining daily time period (0100 to 2100 h), similar VT values were observed in the REGULAR, SLICK, and SENEPOL heifers (38.75 ± 0.01, 38.62 ± 0.01, and 38.51 ± 0.01°C, respectively; $P > 0.05$). The greatest positive correlations between THI and VT were obtained when evaluating the THI value from 7 h earlier in SENEPOL ($r = 0.25$; $P < 0.0001$) and SLICK ($r = 0.30$; $P < 0.0001$) and from 8 h earlier in REGULAR ($r = 0.32$; $P < 0.0001$) heifers. Regardless of coat color, the slick hair phenotype allowed heifers to minimize their daily increase in body temperature in comparison with their long haired counterparts. We suggest introducing genes for the slick phenotype of the Senepol into other Puerto Rican beef breeds as a means of reducing the negative impact of heat stress.

Key Words: coat color, slick hair, vaginal temperature

1042 Associations between the environmental conditions and vaginal temperature in wild-type and slick-haired Puerto Rican Holstein cows.

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The physical barrier created by the hair coat between the skin and the environment has been reported to reduce heat dissipation in wild-type-haired (WT) *Bos taurus* cattle exposed to hot and humid weather. However, slick-haired (SLICK) cattle have demonstrated the ability to maintain lower body temperatures under similar conditions. Thus, the present study aimed to evaluate if the air temperature (AT), relative humidity (RH), thermal humidity index (THI), solar radiation (SR), wind speed (WS), and gust speed (GS) have a different relationship with vaginal temperature (VT) in Holstein cows with different hair coat types during the summer in Puerto Rico. Twenty-four lactating cows [11 WT; 176.31 ± 32.65 d in milk (DIM); 2.06 ± 1.44 lactations and 13 SLICK; 175.62 ± 42.78 DIM; 2.19 ± 0.96 lactations] were evaluated. The WT and SLICK classifications were confirmed in previous genotyping studies. Data loggers (Onset Computer Corporation, Bourne, MA, USA) recorded environmental variables as well as VT values in synchrony every 5 min for 7 consecutive days. After averaged by hour, data were analyzed by the GLIMMIX procedure of SAS. The CORR procedure of SAS was used to analyze the data collected every 5 min. Time and hair type interacted ($P = 0.0026$) to affect VT. From 1800 to 0700 h and from 0900 to 1600 h, the WT cows presented, on average, 0.31°C greater VT values than their SLICK counterparts ($P = 0.0032$). During the 0800 h ($P = 0.0584$) and 1700 h ($P = 0.0619$) VT values tended to be, on average, 0.20°C greater in WT than in SLICK cows. In WT cows VT was correlated with AT ($r = 0.43$; $P < 0.0001$), RH ($r = –0.38$; $P < 0.0001$), THI ($r = 0.45$; $P < 0.0001$), SR ($r = 0.16$; $P < 0.0001$), WS ($r = 0.38$; $P < 0.0001$), and GS ($r = 0.38$; $P < 0.0001$). In the SLICK group, greater correlation coefficients were obtained between VT and AT ($r = 0.50$; $P < 0.0001$), RH ($r = -0.44$; $P < 0.0001$), THI ($r = 0.53$; $P < 0.0001$), SR ($r = 0.24$; $P < 0.0001$), WS ($r = 0.46$; $P < 0.0001$), and GS ($r = 0.46$; $P < 0.0001$). Our results suggest that the slick-haired phenotype allows cows to have a more direct relationship between their skin and the environment, providing for greater heat dissipation and a lower body temperature.

Key Words: heat stress, slick-haired, vaginal temperature

1043 Impact of heat stress and metabolic endotoxemia on porcine ovarian function. M. J. Dickson*, K. L. Bidne, B. J. Hale, C. L. Hager, J. T. Seibert, L. H. Baumgard, J. W. Ross, and A. F. Keating, *Iowa State University, Ames.*

Heat stress (HS) results from an imbalance of thermal energy, and economic losses due to HS cost the U.S. swine industry approximately $900 million annually. HS negatively influences a variety of parameters affecting reproduction: spontaneous abortion, longer wean-to-estrus interval, delayed puberty, reduced litter size, and total number born, all of which culminate in seasonal infertility. Additionally, HS compromises intestinal integrity ultimately leading to metabolic endotoxemia (ME) and increased systemic lipopolysaccharide (LPS), an endotoxin originating from the cell wall of gram-negative bacteria. Toll-like receptor 4 (TLR4) is a membrane bound receptor protein that binds LPS, initiating a signaling cascade that involves phosphorylated nuclear factor kappa B (pNFκB) and pro-inflammatory cytokine release. Acyloxyacyl hydrolase (AOAH) cleaves the lipid A moiety from LPS and is thereby involved in LPS detoxification. We hypothesized that ME contributes to seasonal infertility in swine. The study objectives were to characterize the impact of HS and ME on ovarian function. Twelve post-pubertal gilts (126.0 ± 21.6 kg) were synchronized for 14 d by orally administering Matrix® to ensure that gilts were heat-stressed during the follicular phase of the estrous cycle. Immediately after Matrix® withdrawal, gilts were split in two groups ($n = 6$) and exposed to cyclical HS or thermal neutral (TN) conditions for 5 d and then sacrificed. Gilts were exposed to either constant TN conditions (20.3 ± 0.5°C) or cyclical HS (25.4– 31.9°C) to imitate a diurnal heat load pattern. Ovaries were collected at the end of the experimental period and TLR4, pNFκB, and AOAH protein abundance were quantified in whole ovarian lysate. Relative to TN ovaries, HS increased ($P < 0.05$) TLR4 (16%) and pNFκB (11%) protein abundance. There was no difference in AOAH abundance ($P > 0.05$) between TN and HS ovaries. This data suggests that the ovary is responsive to ME and that HS can induce a pro-inflammatory environment in the ovary, which could contribute to compromised fecundity in heat-stressed swine. This work was supported by the National Pork Board.

Key Words: heat stress, immune function, ovary

1044 Heat stress induces distinct lipidomic profile in differentiating porcine adipocytes. H. Qu[1] and K. M. Ajuwon*[2], *[1]Purdue University, West Lafayette, IN, [2]Department of Animal Sciences, Purdue University, West Lafayette, IN.*

Heat stress results in enhanced lipid deposition in pigs. However, the effects of heat stress (HS) on adipocyte lipidome and metabolome are largely unknown. Understanding the effects of heat stress on the lipid profile will increase understanding of heat stress sensing and signaling mechanisms. To study this, we applied a combination of liquid chromatography-mass spectrometry (LC-MS) based metabolomic and lipidomic profiling approaches to identify and characterize the lipid classes in differentiating pig adipocytes. Porcine preadipocyte (stromovascular cells) were differentiated either under control (37°C) or HS (41.5°C) temperature conditions for 9 d. HS increased triglycerides and decreased monoacylglycerols ($P < 0.05$) accumulation. HS also increased concentrations of glycerophosphocholines, glycerophosphoserines, glycerophosphoglycerols, and glycerophosphoinositols than in control ($P < 0.05$). The specific lipidomic signatures in HS indicates that metabolic pathways centered around diacylglycerol (DAG) metabolism may be impacted by HS in pig adipocytes, perhaps as part of an adaptive mechanism. The observed changes in phospholipid composition may help to regulate cellular metabolism, membrane characteristics, and signal transduction pathways for enhanced adaptation to HS. Overall lipidomic analysis revealed that HS induces a unique lipidomic profile in adipocytes.

Key Words: pig adipocytes lipidomics LC-MS

1045 Impact of temperature fluctuations in cooled-fresh semen on fertility of lactating dairy cows. A. H. Souza*[1], H. J. Bessoff[2], and E. Danzeisen[3], *[1]Ceva Animal Health, Libourne, France, [2]Dairy Management Solutions, Tulare, CA, [3]Global AG Alliance, Tulare, CA.*

The objective of this study was to evaluate whether deviations from ideal semen storage temperature of cooled-fresh semen could affect conception results (CR) in lactating dairy cows. A temperature recording system (LogTag® analyzer, Trix8 data logger model) was placed in the semen shipping-container from its initial shipping to the dairy (located in the Central California Valley) and continuously until breeding time. Temperature was recorded for breedings that took place from June 2015 to December 2015 at every 30 s interval with a 0.01°C of accuracy. Ideal storage temperature for fresh semen was assumed to be from 1.7 to 7.2°C. Then, the cumulative amount of time within the 24 h before AI in which semen temperature deviated to below the lower limit and/or above the high temperature limit was utilized in the Glimmix (SAS 9.3) logistic model to evaluate the impact of temperature fluctuations on

CR. A total of 2306 AI records were available for CR analysis. Variables considered in the logistic regression model were herd, parity number of the cow, days in milk at AI, year-month of AI, service sire, AI technician, temperature deviations from below and above ideal limits, and cow-within herd, which was included in the model as a random variable. As expected, most deviations from ideal storage temperature were due to above threshold temperature faults; and those were more common in summer months, particularly during months of June and August, occurring more commonly from 8AM to 1PM. Interestingly, semen storage deviations to above temperature limits appeared to have less impact ($P > 0.10$) on CR than when temperature deviated to below the lower limits ($P = 0.03$). As a result, CR was 36.2% when the temperature deviated less than 5% of the daily time above the temperature threshold limit and had a nonsignificant minor decrease to 35.1% when temperature deviated over 20% of the daily time above the upper temperature limits. In contrast, CR significantly decreased from 35.8% when semen deviated less than 5% of the time toward below lower temperature limits, to 31.3% when temperature deviated more than 20% of the daily time to below the lower temperature limit. In conclusion, it appears that exposing cooled-fresh semen to colder temperatures below 1.7°C was more detrimental to the fertility of dairy cows.

Key Words: fresh semen, storage temperature, fertility

1046 Effects of a 48 h feed withdrawal on intraperitoneal core body temperature in growing pigs. J. S. Johnson*[1], N. M. Chapel[2], and C. J. Byrd[2], *[1]USDA-ARS Livestock Behavior Research Unit, West Lafayette, IN, [2]Purdue University, West Lafayette, IN.*

In response to increasing ambient temperatures, pigs often reduce their feed intake (FI) to decrease metabolic heat production and maintain euthermia. Although the effects of reduced FI on swine body composition, metabolism, growth rate, and reproductive parameters are well-documented, little is known regarding the direct effects of feed withdrawal on core body temperature response. Therefore, the study objective was to determine the effects of a 48 h feed withdrawal on the intraperitoneal core body temperature response in growing pigs. Eight barrows (35.9 ± 1.9 kg BW) were housed in TN conditions (22.30 ± 0.22°C) and exposed to four 24 h periods: 1) PT (pre-treatment ad libitum feeding), 2) FW1 (1–24 h feed withdrawal), 3) FW2 (25–48 h feed withdrawal), and 4) RF (ad libitum re-feeding). Barrows were used in an effort to reduce the body temperature variability associated with gonadal steroid production. Intraperitoneal core body temperature (T_{core}) was recorded in 10 min intervals using implanted Thermochron temperature recorders. Data were analyzed using the PROC MIXED procedure in SAS 9.4. Overall, T_{core} was reduced ($P < 0.01$) during FW1 (40.30°C) and FW2 (40.28°C) compared to PT (40.59°C) and RF (40.60°C), but no differences were observed between the FW1 and FW2 or the PT and RF periods. Minimum T_{core} was reduced ($P < 0.01$) during FW1 (39.86°C) and FW2 (39.81°C) compared to PT (40.34°C) and RF (40.28°C), but no differences were observed comparing the FW1 and FW2 or the PT and RF periods. No maximum T_{core} period differences ($P = 0.32$) were observed. During FW1, a linear reduction ($P < 0.01$; −0.03°C/h) from maximum (h1) to minimum (h21) T_{core} was observed. Between h 24 of the FW2 period and h 1 of the RF period, T_{core} was linearly increased ($P < 0.01$) by 0.66°C. Feed withdrawal increased ($P < 0.01$) the T_{core} variance and range during FW1 (0.07 and 0.96°C, respectively) and FW2 (0.07 and 0.90°C, respectively) compared to the PT period (0.02 and 0.50°C, respectively) and during the FW1 compared to the RF period (0.02 and 0.69°C, respectively). No T_{core} variance or range differences were detected between the PT and RF periods or the FW1 and RF periods. In summary, a 48 h feed withdrawal directly reduced T_{core} in growing pigs, and this T_{core} reduction recovered within the first hour of re-feeding.

Key Words: pigs, feed withdrawal, core body temperature

1047 The effect of exercise on heat tolerance and first lactation in pregnant Holstein heifers. J. Johnson*, P. L. Steichen, and T. G. Rozell, *Kansas State University, Manhattan.*

A primary source of stress for dairy cattle is associated with the environment, particularly heat, and therefore a considerable amount of research has been done in an attempt to find ways of reducing heat stress. Exercise improves heat regulation in humans and horses; thus, the objectives of this study were to determine if an exercise regimen could improve thermo-tolerance and subsequent milk production during the hot part of the summer in Kansas. Pregnant Holstein heifers ($n = 24$) were randomly assigned to 2 treatment groups: exercise (EX; $n = 12$), and exercise-control (EC; $n = 12$; walked with exercise heifers to exerciser but held in a holding pen). An exercise regimen was implemented through May and June, 4 d per wk in the afternoon for approximately 30–45 min using a motorized 8-panel walker. Data were collected on fitness test d 0, 28, and 56 of the experiment in which heifers were exercised for 23 min, 10 of which were spent at a greater intensity (5.63 KPH). Intra-vaginal temperature, skin temperature, respiration rates, and heart rate were recorded. Weekly measurements of skin temperature, respiration rates, and rectal temperatures were also recorded and post-parturition milk production and milk components were determined. All data were analyzed using PROC MIXED. Respiration rates and heart rates were not affected by exercise treatment on fitness test days or during weekly measurements ($P > 0.10$). Time spent in body temperature zone 3 (> 40.0°C) during the 23-min fitness test and 1 h following fitness test tended to be greater for EC than EX (87% vs. 76%; $P < 0.10$). Average

body temperature of the hour following fitness tests was significantly less in EX than EC (40.48°C vs. 40.83°C; $P < 0.05$) on d 28. On fitness test Day 28, EX heifers tended to have reduced skin temperatures at the thurl post-exercise compared with EC ($P < 0.10$). Exercised heifers had reduced skin temperatures of the cheek, withers, and thurl compared with EC during week 7 ($P < 0.05$). Exercise resulted in greater milk protein % and solids-not-fat % ($P < 0.05$) compared with EC, but there was no difference in monthly milk production in the first 150 d of lactation ($P > 0.10$). These results indicate that exercise in pregnant dairy heifers may improve heat tolerance, and improve milk quality during first lactation.

Key Words: exercise, heat tolerance, milk quality

1048 Effect of exercise on ovarian function in cycling gilts.

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Exercise can alter reproductive function in the mare. To identify this phenomenon in other species, the effects of daily exercise on ovarian function was evaluated in cycling gilts. A total of 18 gilts (mean age = 225 ± 8.3 d) were treated orally with a synthetic progestin, and subsequently injected with a gonadotropin to synchronize estrous cycles. Gilts were then trained to follow a target and run voluntarily along an 80 m track. Thereafter, gilts were randomly assigned to either an exercise or control group. Exercised pigs were worked twice daily for 6 min each period, during the last 10 d of the estrous cycle. Each exercise period consisted of an average distance of 0.25 km at an average speed of 6.0 km/h. Rectal temperatures increased from values of 38.5 ± 0.3°C at rest to a mean of 38.8 ± 0.4°C immediately after exercise ($P < 0.05$). Respiration rates also increased from 30.8 ± 3.5 to 59.7 ± 12.6 breaths/min ($P < 0.05$). Cortisol was measured in saliva the day before the exercise protocol started and 5 and 9 d later. Cortisol concentrations were higher ($P < 0.05$) in exercised pigs at 5 and 9 d compared to controls. Gilts were slaughtered 2 d after the onset of estrus and reproductive organs were collected. No differences were found among treatments in the total number of follicles, corpus hemorragica, or corpora lutea. Exercised gilts had more medium (18.5 vs. 7.6; $P < 0.01$) and small (24.6 vs. 20.1; $P < 0.05$) sized follicles compared to control gilts. Cumulus-oocyte complexes were aspirated from small follicles (< 2 mm in diameter), medium follicles (3–6 mm) and large follicles (> 6 mm) and classified by quality based on a qualitative scale considering the number of layers of compact cumulus cells and ooplasm homogeneity. However, there were no effects of treatment on oocyte complex quality. Data indicated that exercise of pigs is associated with a stress response and can influence ovarian follicle development.

Keywords: exercise, follicular development, stress

1049 The effect of exogenous glucose infusion on early embryonic development in lactating dairy cows.

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The objective of this study was to examine the effect of glucose infusion in late lactation (276 ± 17.3 d in milk) dairy cows on early embryonic development. Estrous cycles were synchronized using a progesterone ovsynch protocol ($n = 12$ cows). On Day 7 after synchronized estrus, cows were randomly assigned to either intravenous glucose infusion (750 g/d; 78 mL/h of 40% glucose, GLUC) or intravenous saline infusion (78 mL/h of 0.9% saline solution, CTRL) for 7 d ($n = 6$/treatment). In vitro produced Day 7 blastocysts (15 per cow) were transferred into all cows on Day 7 of the estrous cycle at the same time as the infusion commenced. Blood samples were collected at 0600 and 1800 every day for glucose, NEFA, BHB and progesterone determination, and transrectal ultrasound was used to measure corpus luteum (CL) volume every second day. All cows were slaughtered on Day 14. Reproductive tracts were recovered and flushed with phosphate-buffered saline containing 5% FCS. The number and dimensions (length and width) of recovered embryos were recorded. Endometrial tissue was dissected and snap frozen for later determination of mRNA abundance of glucose transporters (GRT3, GTR8, SLC2A1, SLC2A3, SLC35A4 and SLC5A1) using qPCR. There was no effect of treatment on milk yield (14.1 ± 1.3 vs. 14.7 ± 1.3 kg/d) or dry matter intake (15.0 ± 1.6 vs. 14.4 ± 0.8 kg/d). Glucose infusion increased mean (± SE) circulating glucose concentration (4.7 vs. 4.15 ± 0.1 mmol/l, $P < 0.001$) and reduced circulating BHB concentration (0.51 vs. 0.70 ± 0.01; $P < 0.001$); plasma NEFA concentrations were not affected (0.13 vs. 0.14 ± 0.01). Mean circulating progesterone concentration (6.8 vs. 6.8 ± 1.0 ng/ml) and CL volume were not affected by treatment. There were no effects of treatment on either uterine lumen fluid glucose concentration or mRNA abundance of glucose transporters. Embryo development was decreased in the GLUC cows compared with CTRL cows (length: 11.5 vs. 18.3 ± 3.05 mm; width: 1.3 vs. 1.7 ± 0.15 mm; area: 15.0 vs. 28.7 ± 3.5 mm^2, all $P < 0.05$). A greater proportion of embryos recovered from CTRL cows had elongated to ≥ 16mm in length compared with GLUC cows (0.16 vs. 0.51 ± 0.12; $P = 0.07$).

These results indicate that increasing circulating glucose concentration during the period of conceptus elongation before maternal recognition of pregnancy had an adverse effect on early embryonic development.

Key Words: embryo development, endometrium, glucose

1050 Influence of cattle temperament on blood serum fatty acid content. T. Gardner[*1], J. F. Legako[1], N. C. Burdick Sanchez[2], P. R. Broadway[2], J. A. Carroll[2], R. C. Vann[3], *[1]Utah State University, Logan, UT, [2]Livestock Issues Research Unit, USDA-ARS, Lubbock, TX, [3]MAFES-Brown Loam, Mississippi State University, Raymond, MS*

Cattle temperament has been reported to influence blood metabolites. Specifically, temperament was related with increased circulation of serum NEFA, decreased blood urea nitrogen, and reduced insulin sensitivity. Metabolic alterations such as these may impact cattle immune function, performance traits, carcass traits, and meat tenderness. Presently, little work has been performed to determine the impacts of temperament on fatty acid content within blood serum. For this study blood and resulting serum was obtained from Angus-cross steers ($n = 31$; 216 ± 6 kg BW), previously assessed to be Temperamental ($n = 15$) or Calm ($n = 16$). Temperament score was calculated as an average of exit velocity and pen score measured at weaning. Serum fatty acid content (mg/mL) was determined via gas chromatography and flame ionization detection. Serum from Temperamental steers contained greater ($P \leq 0.050$) concentrations of linoleic (18:2 n-6; 2.56 mg/mL), α-linolenic (18:3 n-3; 0.34 mg/mL), dihomo-γ-linolenic (20:3 n-6; 0.12 mg/mL), and eicosapentanoic acid (20:5 n-3; 0.26 mg/mL) compared with Calm steers (2.02, 0.25, 0.09, and 0.21 mg/mL, respectively). Furthermore, serum cumulative PUFA of Temperamental steers (4.47 mg/mL) was greater ($P = 0.003$) than Calm steers (3.69 mg/mL). Previous work in other fields of study have used PUFA as markers for stress responsiveness and inflammation in tissues. In agreement with those previous studies, markers of stress and inflammation were related with an increase in overall PUFA concentration in blood in the present study. These findings add to the current body of work regarding cattle temperament and associated alterations of metabolic components. It is not clear if elevated blood PUFA are directly impacting cattle immunity, performance, carcass traits, and/or meat quality among temperamental cattle. However, it is widely known that alteration of fatty acid composition in the final product has numerous organoleptic impacts. Future research is required to determine if circulating lipids in blood ultimately impact overall meat quality.

Key Words: blood metabolites, cattle, fatty acids, PUFA, temperament

1051 Effects of intrammamary LPS infusions on inflammation and reproductive parameters of dairy cows. C. C. Campos[*1], A. C. C. Fernandes[2], I. Hartling[3], M. Kaur[2], R. M. Dos Santos[4], R. L. A. Cerri[3], *[1]FAMEV-UFU, Uberlândia, Brazil, [2]Faculty of Land and Food Systems- University of British Columbia, Vancouver, BC, Canada, [3]Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada, [4]Universidade Federal de Uberlândia, Uberlândia, Brazil*

The objective was to determine the effects of LPS induced mastitis on systemic inflammatory response and early embryo development in lactating Holstein cows. Cows at 35 ± 7 DIM ($n = 20$) were submitted to a modified Double-Ovsynch program (10 d interval between protocols with CIDR and two PGF injections in the second protocol) and timed AI (d0). Cows were randomly assigned (block design) to two treatments: 1) LPS group- cows received an intrammamary infusions (d5 and d10) of 25 μg of LPS (strain 0111:B4) diluted in 10 mL of sterile saline at morning milkings; and 2) Control group- cows received infusion with saline. Blood samples were taken at different time intervals during the study to determine plasmatic concentrations of haptoglobin (Hp), tumoral necrosis factor α (TNF-α) and progesterone (P_4). Milk samples were collected every 2 d for somatic cell count (SCC) and body temperature was recorded using a rumen-reticular bolus logger and summarized for every hour during the period. On Day 15 after AI, uterine flushing for embryo recover and interferon-tau (IFN-τ) measurement, as well as endometrium biopsy were performed. Data were analyzed using the MIXED procedure of SAS. Hp was greater in LPS compared with Control group (0.80 ± 0.06 vs. 0.45 ± 0.07; $P < 0.01$), but TNF-α concentration was similar ($P = 0.72$) between treatments. Milk production from d0 to d15 was greater for Control cows (37.5 ± 1.5 vs. 33.5 ± 1.3 kg/d; $P < 0.01$), whereas SCC was higher in LPS treated cows for about 48 h after each infusion ($P < 0.01$). Likewise, reticular temperature of LPS cows was elevated for 12 h ($P < 0.01$) after each infusion. Progesterone did not differ among treatments at all time collections ($P = 0.72$). However, pregnant cows had greater concentrations of progesterone on d 6, 9, and 10 post-AI ($P < 0.01$). The recovery rate was 55% and the length of recovered embryos (3.6 ± 0.9 vs. 2.4 ± 0.7 cm; $P = 0.56$) and IFN-τ concentration in the luminal uterine flushing ($P = 0.44$) were similar between treatments. In summary, the intrammamary infusion of LPS was able to trigger a systemic inflammatory response during post-AI period, but unable affect conceptus recovery and length, and intraluminal uterine IFN-t concentration.

Key Words: embryo development, inflammation, LPS, mastitis

1052 Relationships of calf vigor at birth with calf size and circulating metabolites in fall-born beef calves. J. M. Larson*[1], B. L. Vander Ley[2], A. M. Meyer[1], [1]*Division of Animal Sciences, University of Missouri, Columbia, MO,* [2]*Department of Veterinary Medicine and Surgery, University of Missouri, Columbia, MO*

To evaluate the relationship of neonatal calf vigor with calf size and circulating metabolites, 66 beef cows and heifers (average age = 4.4 ± 0.5 yr; average BCS = 5.2 ± 0.1; average calving date = September 11, 2015) were monitored during calving. Calf time to stand was determined from the time of birth until the time the calf successfully stood for 5 consecutive seconds (n = 30). Gestation length, birth weight, and body measurements (crown to rump length, shoulder to rump length, heart girth, abdominal girth, and cannon bone circumference) were measured. Jugular blood samples were obtained from 8 bull and 16 heifer calves from this subset at 0, 6, 12, 24, 48, and 72 h postnatally for plasma glucose and serum blood urea nitrogen (BUN), NEFA, albumin, total protein, and globulin analysis. Serum fructose was determined in 0 h samples only. Samples at 0 h were obtained before colostrum intake but after standing. Correlations were determined between time to stand (min) and all neonatal parameters. Birth weight had a moderate positive correlation (P = 0.01) with time to stand. Crown to rump length, shoulder to rump length, abdominal girth, and heart girth tended to have a weak positive correlation ($P \leq 0.11$) with time to stand. Gestation length and cannon bone circumference were not correlated ($P \geq 0.33$) with time to stand, and calf sex did not affect (P = 0.39) calf vigor. Time to stand had a moderate negative correlation with serum NEFA at 24 h (P = 0.04) and 72 h (P = 0.07). Circulating albumin at 0 h tended to have a moderate negative correlation (P = 0.06) with time to stand, and had a moderate or strong negative correlation ($P < 0.02$) with time to stand at the remaining sampling times. Plasma glucose from 12 through 72 h tended to have a weak or moderate positive correlation ($P \leq 0.15$) with time to stand. Time to stand had a moderate or strong positive correlation ($P \leq 0.05$) with BUN at 6 through 48 h. Total protein, globulin, and fructose concentrations were not correlated ($P \geq 0.25$) with time to stand. In conclusion, calf size may play a role in beef calf vigor at birth. Pre-suckling circulating metabolites appear to be poor predictors of vigor, but several neonatal metabolites after colostrum intake were related to vigor in this study.

Key Words: neonates, parturition, vigor

1053 Effect of pregnancy on steroid and eicosanoid metabolizing enzymes in bovine reproductive tissues. M. P. T. Coleson*[1], E. J. Northrop[2], J. J. J. Rich[2], G. A. Perry[2], C. G. Hart[1], K. J. McCarty[1], C. O. Lemley[1], [1]*Mississippi State University, Mississippi State, MS,* [2]*Department of Animal Science, South Dakota State University, Brookings, SD*

The objective was to determine the effects of pregnancy status on steroid and eicosanoid metabolizing enzymes in Angus cross cattle (between 3 and 13 yr) 16 d post-insemination within corpora lutea (**CL**) or endometrial (caruncle; **CAR** and inter-caruncle; **IC**) tissues. Cattle were fixed-time artificially inseminated. Cattle were further classified as either exhibiting or not exhibiting estrus based on estrus activity (confirmed with peripheral concentrations of estradiol). Sixteen d after AI cattle were euthanized and reproductive tracts collected from 18 non-pregnant and 10 pregnant cows (pregnancy determined by presence of an embryo). Activity of cytochrome P450 1A (**CYP1A**) and UDP-glucuronosyltransferase (**UGT**) enzymes were determined using specific luminogenic substrates. Activities were expressed relative to mg of protein or g of tissue. In addition, total activity of the CL was calculated by multiplying activity per g of tissue by CL weight. Data were analyzed using MIXED procedure of SAS and the model statement included pregnancy status, display of estrus, and the respective interaction. In the CL, activity of CYP1A relative to mg of protein, g of tissue, and CL total was not different ($P > 0.19$) between pregnant and non-pregnant cattle, as well as cattle that exhibited or failed to exhibit estrus. In CAR and IC, activity of CYP1A relative to mg of protein and g of tissue was not different ($P > 0.40$) between pregnant and non-pregnant cattle, as well as cattle that exhibited or failed to exhibit estrus. In the CL, activity of UGT relative to mg of protein was not different ($P > 0.14$) between pregnant and non-pregnant cattle, as well as cattle that exhibited or failed to exhibit estrus. However, in CL the activity of UGT relative to g of tissue and CL total decreased ($P < 0.05$) in pregnant vs. non-pregnant cattle which exhibited estrus, while it was not different in pregnant vs. non-pregnant cattle that did not exhibit estrus. In CAR and IC the activity of UGT relative to mg of protein and g of tissue was not different ($P > 0.15$) between pregnant and non-pregnant cattle, as well as cattle that exhibited or failed to exhibit estrus. In conclusion, activity of UGT was decreased in the CL of pregnant vs. non-pregnant cattle that exhibited estrus. This alteration in CL UGT activity could affect steroid and eicosanoid metabolism during early pregnancy.

Key Words: corpus luteum, cytochrome P450, pregnancy

1054 Effect of exogenous β-hydroxybutyrate in the lateral ventricle on circulating serum metabolites and luteinizing hormone in castrated lambs.

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Metabolic dysfunctions are known to have negative impacts on reproduction. It has been well established that during periods of fasting or nutrient restriction, reproduction is inhibited due to the suppression of pulsatile luteinizing hormone (LH) secretion. The manifestation of metabolic dysfunction through elevated β-hydroxybutyrate (BHB) concentrations could be an indication of poor adaptation to negative energy balance (NEB) and modulate reproductive incompetence in livestock. Therefore, the objective of this study was to evaluate the effect of a central injection of exogenous BHB into the lateral ventricle on circulating metabolic markers and LH secretion in lambs. Ten wether lambs were individually housed and fed once a day at a rate of 1.1 kg/d of a 13.5% CP and 72.5% TDN complete feed ration. Before experimental treatments, lambs were fitted with lateral ventricle intracerebroventricular brain cannulas. Lambs were centrally injected with 1 mL into the lateral ventricle with one of two treatments: (1) β-hydroxybutyric acid sodium salt solution (BHB; 12,800 μmol/L) or (2) saline solution (CON). Serum blood samples were collected every 10 min for 60 min before treatment injection and every 10 min for 120 min after infusions. Serum glucose concentrations increased ($P < 0.01$) with BHB injection, indicating stimulation of gluconeogenesis. Infusion of BHB also increased serum non-esterified fatty acid levels ($P < 0.01$). In addition, serum BHB concentrations also increased ($P < 0.01$) in lambs when infusion of BHB in the lateral ventricle occurred. Injection of BHB in the lateral ventricle tended ($P = 0.08$) to inhibit overall LH secretion (mean LH). Number of LH peaks during the 2 h sampling period after injection of treatments did not differ ($P = 0.18$) between lambs injected with BHB or CON. However, lambs injected with BHB had significantly decreased ($P < 0.01$) LH amplitudes. The results of this study suggest that elevated β-hydroxybutyrate in the brain mimics a negative energy signal leading to an increase in the mobilization of glucose and non-esterified fatty acids, while suppressing luteinizing hormone.

Key Words: β-hydroxybutyrate, energy sensing, metabolism, reproduction

1055 WS Comparisons of two short duration estrous synchronization protocols on pregnancy rates to fixed-time AI.

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The objective of the current experiment was to compare pregnancy rate and estrus response between a 5-d or 6-d CO-Synch + CIDR synchronization protocol. Multiparous cows ($n = 238$) were assigned to either a 5-d CO-Synch + CIDR (5-Day) or a PG 6-d CIDR (6-Day) groups based on body weight and body condition score (BCS). Cows assigned to the 5-d protocol were given GnRH (100 μg i.m., Factrel) at the time of insertion of a controlled internal drug releasing device (CIDR; Eazi-Breed CIDR). Five d later CIDR was removed and PGF2α (25 mg i.m., Lutalyse) was given with an additional injection of PGF2α 8 h after CIDR removal. Cows assigned to the 6-d protocol were given an injection of PGF2α and three d later a CIDR was inserted and an injection of GnRH was given. Six d later CIDR were removed and PGF2α was given. Estrus detection aids were applied at CIDR removal. Cows were inseminated by fixed-time AI (FTAI) with conventional semen 72 h after CIDR removal, and GnRH was administered at the time of AI. At insemination, estrus status was categorized as positive (YES), unknown (NR) or negative (NO). Cows were divided into three groups and bulls were introduced 14 d post-insemination at a 1:50 ratio. Bulls were removed 60 d after FTAI and pregnancy was determined by transrectal ultrasound. Pregnancy diagnosis was confirmed by palpation 60 d after the bulls were removed. The AI and final pregnancy rates averaged 62.6% and 95.0%, respectively, and were similar ($P < 0.7$) between 5-Day and 6-Day protocol. There was no difference ($P = 0.11$) in the percentage of cows expressing estrus between the treatments (42.4% and 54.9% for 5-Day and 6-Day, respectively). Expression of estrus before FTAI increased ($P < 0.05$) AI pregnancy rates by 21%; however, it did not increase ($P = 0.32$) final pregnancy rates. There was no interaction ($P = 0.11$) among synchronization protocols and expression of estrus on AI pregnancy rates. In conclusion, expression of estrus increased pregnancy rates; however, there was no difference in pregnancy rates between synchronization protocols.

Key Words: beef cows, estrous synchronization, fixed-time AI

1056 WS Effect of prostaglandin administration after ram exposure on ewe reproductive efficiency.
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A 2-yr experiment was conducted to determine the effect of a single injection of prostaglandin after ram turnout on ewe estrous synchronization. Rambouillet ewes (n = 100; yr 1 = 52; yr 2 = 48) at New Mexico State University West Sheep Unit were stratified by age and BW and assigned to 1 of 3 treatments: untreated (**CON**; n = 33); 12-d CIDR insert (**CIDR**; n = 33); or 1 injection of prostaglandin at d 2.5 (**1PG**; n = 34) after rams were placed with ewes. Ewes were exposed to rams at CIDR insert removal (d 0) for a 35-d breeding season. Ewes were observed twice daily to determine estrus. A greater ($P \leq$ 0.01) number of CIDR ewes were bred in the first 3 d of the breeding season (82%), compared with 1PG (35%) or control (21%) ewes. Moreover, there was an increased ($P \leq 0.01$) number of CIDR ewes bred in the first 4 d (94%) compared to 1PG (50%) ewes, both of which had an increased ($P \leq 0.01$) number of ewes bred compared to control ewes (21%). Both CIDR (94%) and 1PG (73.5) ewes had an increased number ($P \leq 0.01$) of ewes bred in the first 5 d compared to control (33%) ewes. As expected, CIDR-treated ewes had a shorter time (2.2 d) to breeding, than 1PG treat ewes (4.9 d) and control ewes took longer to breed than both CIDR and 1PG ewes (8.1 d) ($P \leq 0.01$). Lambing and weaning data have not yet been collected for yr 2. In yr 1 the number of lambs born per ewe and kg of lamb weaned per ewe was not different ($P \geq$ 0.33) between treatments. Based on these data, utilizing a single injection of PG 2.5 d after ram turnout resulted in similar pregnancy rates at d 5 of the breeding season when compared with CIDR-treated ewes suggesting in a confinement setting the 1PG synchronization protocol could potentially be utilized as a less expensive method of synchronization. Additional information will be collected to determine the effects of synchronization protocol on post-lambing data to determine efficacy of the treatments. Moreover, more research is needed to determine the efficacy of the proposed synchronization protocol in a range production environment.

Key Words: reproduction, sheep, synchronize

1057 The association between Anti-Mullerian Hormone concentrations, antral follicle count and fertility measures in dairy cows.
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The objectives were to (1) characterize variations in plasma concentrations of Anti-Müllerian Hormone (AMH) within a population of dairy cows, and (2) determine associations between AMH categories and AFC, first service conception rate, number of services and days open. Lactating Holstein cows (35 primiparous, 65 multiparous) were subjected to blood sampling (for plasma AMH; AnshLite Bovine AMH CLIA, Ansh Labs, Webster, TX) and transrectal ultrasonography (for AFC; 7.5 MHz linear array transducer; Aloka Co Ltd., Tokyo, Japan) at 75 ± 1 d postpartum (approximately 48 h after the second GnRH of an Ovsynch protocol). Cows were ranked in a descending order based on AMH concentrations and those in the top and bottom thirds were categorized into HIGH- (n = 33) and LOW-AMH (n = 33), respectively. The continuous variables (plasma AMH concentrations, AFC, number of services and days open) were analyzed using MIXED procedure of SAS. The association between AMH and AFC was tested using REG procedure, and the effect of categories of AMH and parity groups on first service conception rate was analyzed using GLIMMIX procedure. Plasma AMH concentrations (pg/mL) ranged from 38.2 to 774.1 (CV 63.4%) with an overall mean (± SEM) of 224.8 ± 14.3. Plasma AMH was greater in the HIGH-AMH than in the LOW-AMH category cows (386.2 ± 14.9 vs. 95.8 ± 15.2 pg/mL; $P < 0.01$). Mean AFC was also significantly greater in HIGH-AMH than those in LOW-AMH category cows (28.1 ± 1.4 vs. 16.7 ± 1.4; $P < 0.01$). Plasma AMH concentrations were linearly associated with AFC (R^2 = 37.5; $P < 0.01$). First service conception rate did not differ between AMH categories (HIGH-AMH vs. LOW-AMH: 35.3 vs. 36.4; $P > 0.05$). However, cows in the HIGH-AMH category tended to have fewer number of services (2.1 ± 0.2 vs. 2.7 ± 0.2; $P = 0.08$) and days open (133.6 ± 11.5 vs. 162.3 ± 11.7 d; $P = 0.09$) than those in LOW-AMH category. Parity did not influence plasma concentrations of AMH, AFC, first service conception rate, number of services or days open ($P >$ 0.05). In summary, plasma AMH concentrations were highly variable and associated with AFC; however, AMH categories did not influence first service conception rates although cows in the HIGH-AMH category had a tendency for fewer days

open and reduced number of services.

Key Words: anti-Müllerian hormone, antral follicle count, fertility

1058 Natural patterns of early postpartum luteal activity and their association with insemination outcomes in dairy cows.

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The objective of this study was to investigate associations between different patterns of luteal activity early postpartum, up to first service, and insemination (AI) outcomes. Milk progesterone (P4) concentrations measured through in-line milk analysis (Herd Navigator, DeLaval Inc) from 785 Holstein cows were assessed from two dairy herds. Progesterone > 5ng/mL was indicative of luteal activity (LA). Milk P4 was determined at set intervals starting 20d postpartum and cows that initiated LA at ≤ 35d and > 35d were considered to have ovulated early (Early-Ov) and late (Late-Ov), respectively. Luteal activity, until first service, lasting 7d to 19d was defined as normal and LA lasting < 7d or > 19d as abnormal. Outcomes of first and second AI were: pregnant (LA > 45d; 1stAI n = 237; 2ndAI n = 133), open (LA ≤ 19d; 1stAI n = 428; 2ndAI n = 337), or pregnancy loss (LA > 20d but ≤ 45d; 1stAI n = 120; 2ndAI n = 62). From calving to 1stAI, luteal phases were classified as at least one normal LA (1NormLA), at least two normal LA (2NormLA), at least one abnormal LA (1AbnLA) and at least two LA whether normal or abnormal (2TotLA). Each of the four categories of luteal phases were analyzed as binomial variables against AI outcomes, Early-Ov or Late-Ov, parity and interactions, using mixed-effects logistic regression (GLMER of R-3.2.3) with herd as random factor. Cows in 1NormLA had increased odds of being pregnant at 1stAI (odds ratio [OR]: 3.21, P = 0.001) and cows in 2NormLA had increased odds of being pregnant at first and 2ndAI (OR: 1.63, P < 0.03). AbnLA1 decreased the probability of pregnancy (OR: 0.66, P = 0.01) and tended to be associated with pregnancy loss at 2ndAI (66%, P = 0.08). Cows having 2TotLA had increased probability of being pregnant at first and 2ndAI (OR: 2.41 and 1.80, respectively, P < 0.01). Cows that were open at 1stAI had twice the odds to suffer pregnancy loss at 2ndAI than cows that suffered pregnancy loss at 1stAI (OR: 1.99, P < 0.03). Primiparous cows were more likely to become pregnant at 1stAI than multiparous cows (OR: 1.56, P < 0.01), while multiparous cows had higher odds of delayed ovulation (32.58%, P = 0.04). Early-Ov cows had higher odds of having 2TotLA (98%, P < 0.001) and lower odds of suffering pregnancy losses at 2ndAI (OR: 0.70, P = 0.05). In summary, an early onset, and an increased frequency of normal luteal activity preceding first AI postpartum benefits insemination outcomes.

Key Words: estrous cycle, fertility, milk progesterone profiles

1059 Circulating LH concentrations after intravaginal instillation of GnRH in lactating dairy cows.

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Our objective was to evaluate circulating LH concentrations after intravaginal (**IVG**) instillation of GnRH in dairy cows. Lactating primiparous (n = 6) and multiparous (n = 27) Holstein cows received two luteolytic doses of PGF2α 12 h apart 7 d after the Ovsynch protocol (GnRH-7d-PGF2α-56h-GnRH). Forty 8 h after the first PGF2α treatment cows were stratified by parity and randomly allocated to five different treatments: 2 mL of saline solution IVG (**SAL-IVG**, n = 6), 100 µg of GnRH i.m. (**G100-im**, n = 5), 100 (**G100-IVG**, n = 7), 500 (**G500-IVG**, n = 8), or 1000 µg of GnRH IVG (**G1000-IVG**, n = 7). For all GnRH treatments Gonadorelin diacetate tetrahydrate (Cystorelin) was used. Blood was collected using indwelling jugular catheters at −1 h, 0 h, every 15 min up to 4 h, and every 30 min from 4 to 6 h after treatment. Data for progesterone, estradiol, and LH concentrations were analyzed by ANOVA with (LH only) or without repeated measures using PROC MIXED of SAS. Concentrations of progesterone and estradiol did not differ (P > 0.10) among groups at time 0. Concentrations of LH were affected by treatment (P < 0.001), time (P < 0.001) and treatment by time interaction (P < 0.001). Cows in G100-im had greater (P < 0.05) mean LH than the IVG treatments from 15 to 195 min after treatment whereas the G1000-IVG group had greater (P < 0.05) mean LH than the SAL-IVG and the other IVG GnRH groups from 45 to 240 min (except at 60, 75, and 90 min) after treatment. Mean LH for SAL-IVG, G100-IVG, and G500-IVG did not differ (P > 0.05) at any time point. The greatest (P < 0.001) area under the curve (**AUC**) was observed for G100-im (1149 ± 51 ng) followed by G1000-IVG (546 ± 108 ng) which had greater AUC than the other IVG treatment groups (242 ± 40, 271 ± 34 and 247 ± 24 ng for SAL-IVG, G100-IVG, and G500-IVG, respectively). Mean LH peak was greater (P < 0.001) for G100-im (6.9 ± 0.4 ng/mL) than G1000-IVG (2.8 ± 0.6 ng/mL) whereas the SAL-IVG, G100-IVG, and G500-IVG groups did not have a discernible LH surge after treatment (maximum LH: 1.2 ± 0.2, 1.3 ± 0.2 and 1.2 ± 0.1 ng/mL for SAL-IVG, G100-IVG and G500-IVG respectively). We conclude that IVG instillation of 1000 µg of GnRH induced more LH release than IVG instillation of saline solution and a 100 or 500 µg dose of GnRH. Also, the amount of LH released after IVG treatment with 1000 µg of GnRH was less than that released after i.m. treatment with 100 µg of GnRH.

Supported by USDA NIFA Hatch project NYC-127434.

Key Words: intravaginal, GnRH, LH

1060 Effect of dose and timing of prostaglandin $F_{2\alpha}$ treatments during a Resynch protocol on luteal regression and fertility to timed artificial insemination in lactating Holstein cows.

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Our objective was to evaluate the effect of a second $PGF_{2\alpha}$ treatment (25 mg dinoprost) or a double dose of $PGF_{2\alpha}$ (50 mg dinoprost) during a Resynch protocol on luteal regression and pregnancies per artificial insemination (P/AI) in dairy cows. Lactating Holstein cows (n = 1438) were randomly assigned at a nonpregnancy diagnosis to receive: 1) Ovsynch (Control: GnRH; 7 d, $PGF_{2\alpha}$; 56 h, GnRH); 2) Ovsynch with a second $PGF_{2\alpha}$ treatment (GPPG: GnRH; 7 d $PGF_{2\alpha}$; 24 h, $PGF_{2\alpha}$; 32 h, GnRH); or 3) Ovsynch with a double dose of $PGF_{2\alpha}$ (GDPG: GnRH; 7 d, 2x$PGF_{2\alpha}$; 56 h, GnRH). All cows received TAI ~16 h after the second GnRH treatment (G2). Pregnancy diagnosis was performed by transrectal palpation 38 ± 3 d after TAI, and pregnancy status was reconfirmed 28 d later. Blood samples were collected at the first $PGF_{2\alpha}$ treatment and at G2 from a subset of cows (n = 546) and assayed for progesterone (P4). Data were analyzed by logistic regression using the GLIMMIX procedure of SAS. At 38 d after TAI, GPPG cows tended to have more (P = 0.12) P/AI than Control cows [37% (181/495) vs. 33% (154/463)], whereas P/AI for GDPG cows [34% (164/480)] did not differ (P = 0.34) from Control cows. Pregnancy loss from 38 to 66 d did not differ (P = 0.46) among treatments and was 8% (38/475). The percentage of cows with complete luteal regression (P4 $\leq$ 0.3 ng/mL at G2) tended to differ (P = 0.06) among treatments and was greater for GPPG cows than for GDPG and Control cows (94% vs. 88% vs. 88%, respectively). Overall, cows with P4 < 1 ng/mL at the first $PGF_{2\alpha}$ treatment had fewer (P < 0.01) P/AI than cows with P4 $\geq$ 1 ng/mL [28% (40/145) vs. 41% (148/365)], whereas cows with P4 > 0.3 ng/mL at G2 had fewer (P < 0.01) P/AI than cows with P4 $\leq$ 0.3 ng/mL [14% (7/51) vs. 39% (167/425)]. We conclude that addition of a second $PGF_{2\alpha}$ treatment during a Resynch protocol tended to increase P/AI to TAI by increasing the percentage of cows with complete luteal regression at G2, whereas doubling the dose of $PGF_{2\alpha}$ did not. *Supported by USDA NIFA Hatch project 1006519*

Key Words: dairy cow, resynchronization, timed AI

1061 Fertility of lactating Holstein cows after synchronization of ovulation and timed artificial insemination versus artificial insemination after detection of estrus at a similar DIM range.

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Our objective was to compare pregnancies per artificial insemination (P/AI) at first service after synchronization of ovulation and timed artificial insemination (TAI) with artificial insemination (AI) after detection of estrus at a similar DIM range. Lactating Holstein cows (n = 408) were randomly assigned to receive their first TAI after a Double-Ovsynch protocol [TAI; Pre-Ovsynch (GnRH; 7 d, $PGF_{2\alpha}$; 3 d, GnRH) followed 7 d later by Breeding-Ovsynch (G1; 7 d $PGF_{2\alpha}$; 24 h, $PGF_{2\alpha}$; 32 h, GnRH; 16 h, TAI)] or to receive first AI after estrus induced using $PGF_{2\alpha}$(Estrus; $PGF_{2\alpha}$; 14 d, $PGF_{2\alpha}$; 24 h, $PGF_{2\alpha}$). Cows were inseminated using frozen-thawed semen from 4 AI sires with proven high fertility (sire conception rate > 0). Overall, 92% (374/408) of cows received their first insemination from 74 to 81 DIM. Estrus cows inseminated > 7 d after the last $PGF_{2\alpha}$ treatment (n = 34) were excluded from the analysis of P/AI but were included in the calculation of insemination rate. Pregnancy status was determined 33 ± 3 d after AI, and pregnancy status was reconfirmed 63 ± 3 d after AI. Data were analyzed by ANOVA and logistic regression using MIXED and GLIMMIX procedures of SAS. DIM at AI did not differ (P = 0.37) between treatments (76.9 ± 0.2 vs. 76.7 ± 0.3 for TAI vs. Estrus cows, respectively). More (P < 0.01) TAI cows received AI within 7 d after the VWP than Estrus cows (100% vs. 83%). At 33 d after AI, primiparous cows had more (P < 0.01) P/AI than multiparous cows [58% (81/139) vs. 37% (87/235)], and TAI cows had 50% more (P < 0.01) P/AI than Estrus cows [51% (109/212) vs. 34% (59/162)]. No parity by treatment interaction was detected (P = 0.20). At 63 d after AI, TAI cows had 39% more (P = 0.02) P/AI than Estrus cows [46% (69/149) vs. 33% (38/116)], and pregnancy loss from 33 to 61 d after AI did not differ (P = 0.16) between treatments [14% (11/81) vs. 5% (2/41) for TAI vs. Estrus cows]. In conclusion, synchronization of ovulation and TAI for first service increased the percentage of cows inseminated within 7 d after the VWP, and TAI cows had greater fertility at first service than Estrus cows at a similar DIM range. *Supported by USDA NIFA Hatch project 1006519 and CEVA Sante Animale*

Key Words: estrus, fertility, timed AI

1062 Increasing estrus expression in lactating dairy cows. J. A. Sauls*, B. E. Voelz, S. L. Hill, J. S. Stevenson, *Kansas State University, Manhattan, KS*

Using an activity monitoring system (AMS) equipped with an accelerometer, 2 experiments were conducted to test the hypotheses that: (1) altering progesterone before inducing luteolysis or (2) exposing cows to estradiol cypionate (ECP) or testosterone propionate (TP) after luteolysis would increase occurrence and intensity of estrus. In experiment 1, cows (n = 154) were fitted with an AMS collar and a pressure-sensitive device (HW) and assigned to 3 treatments: 1) CL only; 2) no CL + progesterone insert (CIDR); or 3) CL + 2 CIDR to achieve different concentrations of progesterone. Progesterone 24 h post-treatment was greatest ($P < 0.01$) in CL + 2 CIDR, followed by CL, and no CL + CIDR cows. Estrus occurred 11 to 12 h earlier ($P < 0.01$) in no CL + CIDR compared with CL-bearing cows. Estrus intensity was greater ($P \leq 0.05$) after CL + 2 CIDR than CL only cows. The AMS and HW determined 68 and 62% of the qualifying cows to be in estrus (estrus was defined: follicle $\geq$ 10 mm at $PGF_{2\alpha}$ and progesterone $\leq$ 0.5 ng/mL 72 h later), respectively. In experiment 2, cows (n = 203) were equipped with an AMS and a friction-activated patch (Estrotect patch; P) and assigned to receive 1 mg ECP, 2 mg TP, or control 24 h after $PGF_{2\alpha}$. Estradiol 24 h post treatment was greater ($P <$ 0.01) in ECP compared with controls. Estrus expression detected by P in all cows tended ($P = 0.10$) to be greater for ECP compared with controls. More ($P < 0.05$) qualifying cows were detected in estrus after ECP compared with controls. Compared with controls and in response to ECP, estrus occurred 17 to 20 h earlier ($P < 0.01$) and was of greater ($P < 0.05$) intensity. The AMS and P determined 71% and 74% to be in estrus, respectively. Of cows exposed to the AMS, HW, or P, 62 to 74% were detected in estrus and more than 94% ovulated. In contrast, of the residual cows not detected in estrus, 60 to 76% ovulated in the absence of detected estrus. Only ECP was successful in inducing more estrus expression, but proportions never exceeded 80%. Given the large proportion of cows ovulating in the absence of estrus, further research is warranted to determine if conception is achievable by inseminating cows not detected in estrus by 72–80 h post-PGF_{2a}.

Key Words: estrus, estradiol, progesterone

1063 The characterization of estradiol concentration before insemination and its effect on fertility in dairy cattle. M. Gobikrushanth*[1], P. A. Dutra[1], C. A. Felton[2], T. C. Bruinjé[1], M. G. Colazo[2], S. Butler[3], D. J. Ambrose[1,2], *[1]Department of Agricultural Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]Livestock Research Branch, Alberta Agriculture and Forestry, Edmonton, AB, Canada, [3]Animal & Grassland Research and Innovation Centre, Teagasc Moorepark, Fermoy, Co. Cork, Ireland*

The objectives of this study were to: (1) characterize variations in plasma concentrations of estradiol (E2) within a population of dairy cows, and (2) determine associations between E2 categories, LH, ovulatory response, first service conception rate, number of services and days open. Lactating Holstein cows (35 primiparous, 65 multiparous) received one injection of $PGF_2\alpha$ (cloprostenol, 500 µg, d 0) followed by GnRH (gonadorelin, 100 µg, d 3; Presynch) and were subjected to an Ovsynch protocol starting on d 10, with timed-AI (TAI) occurring at ~75 d postpartum. Blood samples were collected immediately before (0h) and 2h after the second GnRH of Ovsynch to determine plasma E2 and LH concentrations, respectively. Cows were ranked based on plasma E2 concentrations, from highest to lowest, and those in the top (n = 33) and bottom (n = 33) thirds were classified into HIGH- and LOW-E2 categories. The continuous variables were analyzed using MIXED procedure of SAS and the binomial data were modeled against E2 categories and parity and analyzed using the GLIMMIX procedure of SAS. Plasma E2 concentrations (pg/mL) ranged from 0.1 to 9.2 (CV 78.7%) with an overall mean (± SEM) of 2.0 ± 0.1. The plasma E2 was greater for cows in HIGH-E2 category than those in LOW-E2 category (3.7 ± 0.2 vs. 0.5 ± 0.2 pg/mL; $P < 0.01$). Similarly, cows in the HIGH-E2 category had greater concentrations of plasma LH than cows in the LOW-E2 category (13.5 ± 1.0 vs. 5.9 ± .1.0 ng/mL; $P < 0.01$). The categories of E2 did not influence ovulatory response to the second GnRH of the Ovsynch ($P <$ 0.05). The first service conception rate tended to be greater for cows in HIGH-E2 category than those in LOW-E2 category (44.1 vs. 24.2; $P = 0.10$). Further, cows in the HIGH-E2 category had a tendency for fewer number of services (2.2 ± 0.2 vs. 2.7 ± 0.2; $P = 0.10$) and lesser days open (138.6 ± 11.6 vs. 171.5 ± 11.7 d; $P = 0.06$) than cows in LOW-E2 category. Parity did not influence plasma concentrations of E2 and LH, ovulatory response to the second GnRH of Ovsynch, number of services or days open ($P > 0.05$). However, primiparous cows tended to have greater first service conception rate than multiparous cows (50.0 vs. 25.6%; $P = 0.06$). In summary, plasma E2 concentrations were highly variable in a tested population of dairy cows and cows in the HIGH-E2 category had a tendency for greater first service conception rate and

fewer number of services and lesser days open.

Key Words: estradiol concentration, fertility, variability

1064 Resynchronization of ovulation strategies including or not including GnRH treatment before non-pregnancy diagnosis. R. Wijma*, M. L. Stangaferro, M. Masello, G. E. Granados, J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY*

Our objectives were to evaluate ovarian dynamics and reproductive performance of cows managed with two different resynchronization protocols for second and greater AI services. After each AI, cows were randomly assigned to receive (**G25** group; $n = 649$) or to not receive GnRH (**NoG25**; $n = 656$) 25 ± 3 d after AI and 7 before non-pregnancy diagnosis (**NPD**) by transrectal ultrasonography. Non-pregnant cows in G25 ($n = 353$) and NoG25 ($n = 353$) received the same protocols as follows: cows with a corpus luteum (**CL**) $\geq$ 15 mm received two PGF treatments 24 h apart, GnRH 32 h later, and timed AI (**TAI**) 16 h after GnRH whereas, cows without a CL $\geq$ 15 mm at NPD received the CIDR-Ovsynch protocol (GnRH+CIDR-7d-CIDR-removal+PGF-24h-PGF-32h-GnRH-16h-TAI). Cows in both groups were inseminated to estrus (**AIE**) any time after AI. Circulating concentrations of progesterone (**P4**) were determined and ovarian ultrasonography was performed thrice weekly from 18 ± 3 d after AI until NPD in 44 and 46 cows for G25 and NoG25, respectively. Binomial outcomes were analyzed by logistic regression and continues outcomes using ANOVA. Overall, more cows ovulated ($P < 0.01$) spontaneously or in response to GnRH for G25 (69.9%) than NoG25 (36.4%) from 18 ± 3 d after AI to NPD, the proportion of cows with a CL tended ($P = 0.06$) to be greater for G25 (89.1%) than NoG25 (72.7%), and the proportion of cows with P4 > 1 ng/mL at NPD was similar ($P = 0.14$) for G25 (67.4%) and NoG25 (61.4%). A similar ($P = 0.74$) proportion of cows had an active follicle (**AF**, > 10 mm in the growing or static phase) at NPD (G25 = 91.3% and NoG25 = 95.5%) but size of the AF was greater ($P = 0.02$) for NoG25 (16.5 ± 0.6 mm) than G25 (15.0 ± 0.4 mm). For all cows enrolled, more ($P = 0.04$) non-pregnant cows after AI received AIE in NoG25 (55.8%, 169/353) than G25 (47.9%, 197/353) but more cows had a CL ($P = 0.01$) at NPD for G25 than NoG25 [83.7% (154/184) vs. 72.4% (113/155)]. Pregnancies per AI were similar for G25 and NoG25 for cows AIE [36.5% (51/167) vs. 38.7% (74/191); $P = 0.77$], cows with a CL at NPD [40.0% (58/145) vs. 33.0% (35/106; $P = 0.26$], cows without a CL at NPD [37.9% (11/29) vs. 39.0% (16/41); $P = 0.0.92$] or for all services combined [38.1% (130/341) vs. 36.9% (125/338); $P = 0.69$]. We conclude that despite differences in ovarian function, fertility after TAI and overall P/AI was similar for cows that received or not received GnRH 25 ± 3 d after AI.

Key Words: dairy cow, resynchronization, timed AI

1065 Effects of modification of proestrus length and duration of progesterone exposure on automated measurements of estrous expression in lactating Holstein cows. B. F. Silper*, T. A. Burnett, P. F. M. P. Souto, M. S. Baylao, A. P. O. Santos, R. L. A. Cerri, *Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, BC, Canada*

Objectives were to investigate if longer proestrus, via longer exposure to pre-ovulatory estradiol concentrations, would induce behavioral estrus of greater intensity, and to investigate if longer exposure to progesterone would offset possible effects of shorter proestrus on estrous behavior. Three treatments consisting of different intervals between GnRH-PGF (5 or 7 d) and PGF-ECP (1 or 3 d) on a Heatsynch program were applied to lactating Holstein cows ($n = 48$). All cows were fitted with three activity monitors (Heatime, SmartDairy, and AfiActII) and enrolled into pre-synchronization at 40 ± 3 DIM, followed by random allocation to treatments at 57 ± 3 DIM. Treatments were 5d3d (GnRH-5d-PGF-3d-ECP), 5d1d (GnRH-5d-PGF-1d-ECP), and 7d1d (GnRH-7d-PGF-1d-ECP). The AI was performed at a fixed time 48 h after ECP, except for those detected in high activity before timed-AI. Ovarian ultrasonography and blood samples were performed at injection days, day of AI, and 2, 5, and 7 d after timed-AI. Rates of estrous detection, ovulation (until 84 h after ECP) and presence of CL 7 d after timed-AI were not different among treatments ($P > 0.05$). Although the goal of 5d3d was to increase proestrus length, 6 of the 10 cows that showed high activity in this treatment did so before or at the day of ECP. Consequently, proestrus length was not different among treatments (3.0 ± 0.2, 3.2 ± 0.2, and 2.7 ± 0.2 d, for 5d1d, 5d3d, and 7d1d, respectively; $P > 0.05$). Pre-ovulatory follicle diameter was not significantly different among treatments and was 20.9 ± 0.7 mm (multiparous) and 19.2 ± 0.9 mm (primiparous). Odds of estrous expression were not influenced by parity, BCS, or progesterone concentration and follicle diameter at the PGF injection. Parity and BCS were the factors most frequently associated with measurements of estrus. Cows in 5d1d had estrus of greater duration (Heatime) than 7d1d (13.9 ± 0.9 vs. 11.1 ± 0.9 h; $P = 0.04$), whereas intensity of estrus (AfiActII) was greater for 5d3d cows (377.3 ± 43.0; $P = 0.04$) and tended to be greater for 7d1d (350.8 ± 41.3; $P = 0.09$), both in comparison with 5d1d (243.3 ± 45.8). Although estrous detection rate and proestrus length were not different among treatments, the use of a Heatsynch program with different GnRH-PGF or PGF-ECP intervals was capable of altering duration and intensity of estrus, likely due to changes in the endocrine profile during the estrous cycle.

Key Words: automated estrous detection, estradiol, proestrus

1066 Effect of GnRH removal at CIDR insertion in the 5 d CO-Synch + CIDR ovulation synchronization protocol on ovarian function in beef cows.

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The objective of this experiment was to evaluate the effects of GnRH removal at controlled internal drug release (CIDR) insertion in the 5-d CO-Synch + CIDR protocol (5dCO) on ovarian follicle growth and circulating steroid hormone concentrations. Non-pregnant, non-lactating beef cows (n = 15) were used in a 3 × 3 Latin square design and assigned to treatment by age and BCS to receive either: 1) standard 5dCO hormone administration including 100 μL of GnRH at CIDR insert and 2 concurrent 25-mg doses of $PGF_{2\alpha}$ (PG) delivered at CIDR removal (G2PG), 2) no GnRH at CIDR insert and 2 concurrent, 25-mg doses of PG at CIDR removal (NoG2PG), or 3) no GnRH at CIDR insert and a single, 25-mg dose of PG at CIDR removal (NoG1PG). All cows were monitored for estrous for 72 h after CIDR removal at which time 100 μL of GnRH was administered. Cows underwent transrectal ultrasonography to record ovarian structures and blood samples were taken for progesterone and estradiol analyses at CIDR insertion, CIDR removal, final GnRH administration, and d 5 and 10 post PG administration. An additional blood sample was collected on cows that displayed estrus between PG and GnRH. Data were analyzed using the MIXED and GLIMMIX procedures of SAS for the continuous and binary response variables, respectively. Dominant follicle diameter did not differ between treatments at CIDR removal or final GnRH ($P \geq 0.61$). Percentage of animals that regressed their corpus luteum (CL) in response to PG, estrus detection aid score, and CL volume 10 d following PG administration did not differ between treatments ($P \geq 0.18$). Post ovulation plasma progesterone did not differ between treatments ($P \geq 0.29$), and plasma estradiol was not different at CIDR removal or final GnRH administration ($P \geq 0.59$). However, peak plasma estradiol concentrations were greater ($P = 0.01$) in NoG2PG than NoG1PG (5.85 and 2.93 ± 0.55 pg/mL, respectively), with G2PG intermediate (3.31 ± 0.55 pg/mL). In conclusion, follicle and CL growth as well as subsequent progesterone concentrations were not negatively affected by removal of the initial GnRH in the 5-d CO-Synch + CIDR protocol; however fluctuations in estradiol concentrations merit implementation of a field trial to elucidate protocol impacts on fertility.

Keywords: 5-d CO-Synch, GnRH, Synchronization

1067 Effect of eCG and P4 level in timed AI programs in bos indicus and bos indicus x bos taurus heifers.

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This study evaluates the effects of P4 level and eCG treatment in timed-AI in Bos indicus (Nellore) and Bos indicus x Bos taurus (crossbred) heifers. Heifers used in the study (n = 1989) included Nellore (n = 992) and Crossbred (n = 997) that were 14–24 mo of age (BCS: 3.08 ± 0.01, BW: 329.09 ± 0.66 kg). Ovarian ultrasonography was performed twice (7 d apart) in all heifers at start of the study to identify heifers with a CL. Heifers with a CL were submitted to estrous synchronization and timed AI. Heifers without a CL in either ultrasonography were submitted to a puberty induction protocol (Rodrigues et al., 2014). Heifers with a detectable CL 12 d after puberty induction remained in the study. Timed-AI program was as follows: D0– Insertion of an intravaginal P4 device (CIDR 1.9 g; Zoetis, Sao Paulo, Brazil) and 2 mg of estradiol benzoate (Gonadiol; Zoetis); D7– 12.5 mg of dinoprost tromethamine (Lutalyse; Zoetis); D9– CIDR withdrawal and 0.5 mg of ECP (ECP; Zoetis). At D9 heifers were randomly assigned to receive either 0 (Control; 994) or 200 IU (eCG; 995) of eCG (Novormon; Zoetis); D11– timed AI was performed. On Days 9 and 11, a subgroup of heifers were evaluated by ultrasonography to record the largest follicular diameter. Continuous variables were analyzed using the PROC MIXED and binomial variables using the PROC GLIMMIX, both from SAS. Included in the models were effects of breed, group, eCG and serum P4 level (determined by ROC curve). Significance set when $P < 0.05$. Follicle diameter at D9 was greater for crossbred heifers (10.1 ± 0.01 mm) than Nellore heifers (9.5 ± 0.01) and in LowP4 (10.0 ± 0.01) compared to HighP4 (9.5 ± 0.01). Follicle diameter at D11 were not affected by tested variables. Ovulation rate was greater for eCG compared to Control (92.3% vs. 87.5%, respectively). Crossbred heifers had greater conception rate (63.7% vs. 56.3%) and greater pregnancy rate than Nellore (58.2% vs. 50.7%). eCG treatment (62.3%) tended to have greater conception than Control (55.3%). LowP4 heifers have greater conception and pregnancy rate than HighP4 (64.8, 59.6% and 55.3, 49.4%, respectively). Differences between Crossbred and Nellore heifers synchronized with the same timed AI program were observed, regardless of breed low P4 environments resulting in increased pregnancy rates. Acknowledgment: FAPESP process n° 2014/05270–9.

Keywords: bos indicus, bos taurus x bos indicus, timed-AI

1068 Gonadal and extra-gonadal sperm characteristics of rabbit bucks fed raw or fermented cottonseed cake– cased diets supplemented with ginger (Zingiber officinale Roscoe). A. A. Olajide*, *Ladoke Akintola University of Technology (Lautech), Ogbomoso, Nigeria*

The potential of cottonseed cake (CSC) as a veritable source of protein, energy and fiber for farm animals has been demonstrated. However, its use is limited to ruminant feeding due to the presence of gossypol, a polyphenolic compound of significant physiological implications. Fermentation is one of the biotechnological options for detoxifying a variety of feed ingredients. This study was conducted to investigate the effect of raw or fermented CSC– based diets (with or without ginger supplementation) on gonadal and extra-gonadal sperm characteristics of rabbit bucks. Thirty (30) cross-bred (New Zealand White X Chinchilla) rabbit bucks, 6 −7 wk old and averagely weighing 768.54 g, were randomly assigned to five dietary treatments (n = 6 per treatment) in a 2 × 2 factorial within a completely randomized design (CRD). The CSC replaced soyabean meal (SBM) at 0% (control) and 100% (Raw or Fermented) with or without ginger supplementation (30mg/kg feed). Animals were fed for 12 wk after which they were slaughtered; and their reproductive organs removed and processed for sperm evaluation. Raw CSC without ginger supplementation resulted in lower ($p < 0.05$) sperm count, Gonadal Sperm Reserve (GSR), Daily Sperm Production (DSP); and higher ($p < 0.05$) dead sperm than other treatments. The sperm count (69.33×10^6), motile sperm (79.97%), GSR (66.44×10^6) and extra-gonadal sperm reserve (109.98×10^6) were highest for bucks that were fed with fermented CSC with ginger supplementation. This study shows that total replacement of SBM with raw CSC reduced sperm quality in rabbit bucks. This adverse effect was corrected by a combination of fermentation and ginger supplementation.

Key Words: Rabbit bucks, Cottonseed cake, Sperm characteristics

1069 Supplementation with a Lactobacillus acidophilus fermentation product alters the metabolic response following a lipopolysaccharide challenge in weaned pigs. N. C. Burdick Sanchez*[1], J. A. Carroll[1], P. R. Broadway[1], B. E. Bass[2], J. W. Frank[2], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Diamond V, Cedar Rapids, IA*

This study was designed to determine if feeding a *Lactobacillus acidophilus* fermentation product to weaned pigs would alter the metabolic response following a lipopolysaccharide (LPS) challenge. Pigs (n = 30; 6.4 ± 0.1 kg BW) were housed individually with ad libitum access to feed and water. Pigs were weighed on arrival, assigned to 1 of 3 groups (n = 10/treatment), and fed for 18 d: 1) Control, fed a non-medicated starter diet; 2) Control + *Lactobacillus acidophilus* fermentation product at 1 kg/MT (SGX1; Diamond V SynGenX, Cedar Rapids, IA), and 3) Control +*Lactobacillus acidophilus* fermentation product at 2 kg/MT (SGX2). Pigs were anesthetized on d 7 and 14 for insertion of an i.p. temperature device and jugular catheter, respectively. On d 15, pigs were challenged i.v. with LPS (25 μg/kg BW LPS from *E. coli* O111:B4). Blood samples were collected at 0.5 h intervals from −2 to 8 h and at 24 h relative to LPS administration at 0 h and serum isolated for glucose, NEFA, and blood urea nitrogen (BUN) analysis. There was a treatment x time interaction ($P < 0.001$) for serum glucose; Control pigs had greater glucose than SGX1 and/or SGX2 pigs at 0.5, 1.5, 2.5, 4, 5, and 6.5h post-LPS ($P \leq 0.04$), while SGX2 had greater glucose than SGX1 at 3.5 h ($P = 0.02$). Baseline (−2 to 0h) NEFA was affected by treatment ($P < 0.001$) such that SGX1 pigs had the greatest (0.12 ± 0.01mmol/L) followed by Control (0.10 ± 0.01 mmol/L) and SGX2 pigs (0.08 ± 0.01 mmol/L). Thus, NEFA were analyzed as the change relative to baseline values. There were treatment ($P = 0.006$) and time ($P < 0.001$) effects for the change in NEFA; Control (0.23 ± 0.02 mmol/L) and SGX2 (0.27 ± 0.02 mmol/L) pigs had a greater change in NEFA than SGX1 pigs (0.15 ± 0.02 mmol/L). Baseline serum BUN was affected by treatment ($P < 0.001$); Control (12.62 ± 0.41 mg/dL) and SGX2 (13.26 ± 0.35 mg/dL) pigs had greater BUN than SGX1 pigs (10.86 ± 0.40 mg/dL); thus serum BUN were analyzed as the change relative to baseline values. There was a treatment x time interaction ($P = 0.004$) for the change in BUN; SGX1 pigs had greater BUN than Control and/or SGX2 at 0.5, 4, 5 to 6, 7, 7.5, and 24 h post-LPS challenge. These data demonstrate that feeding a *Lactobacillus acidophilus*fermentation product to weaned pigs may alter the redistribution of energy stores in response to an immune challenge which may expedite recovery.

Key Words: *Lactobacillus acidophilus* fermentation product, lipopolysaccharide, metabolism

1070 Non-targeted metabolomic evaluation of the uterine milieu during the transitional period of embryo elongation in the pig. J. R. Miles*[1], E. C. Wright-Johnson[1], T. D. Laughlin[2], C. D. Broeckling[3], L. A. Rempel[1], A. K. Pannier[2], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]Department of Biological Systems Engineering, University of Nebraska, Lincoln, NE, [3]Proteomics & Metabolomics Facility, Colorado State University, Fort Collins, CO*

Alterations in the signaling of critical molecular factors within the uterine milieu lead to deficiencies in embryo elongation. The objective of this study was to identify metabolites within the uterine environment that are present as porcine embryos transition between spherical, ovoid, and tubular embryos at Day 9, 10, and 11 of gestation, respectively. White crossbred

gilts (n = 9) were bred at standing estrus (designated d 0) and again 24 h later and randomly assigned to collection group. At Day 9, 10, or 11 of gestation (n = 3 per day), reproductive tracts were collected immediately following harvest and flushed with 40 mL of RPMI-1640 media. Embryo morphologies were assessed for each pregnancy to ensure gilts were assigned to the correct gestation day treatment group (i.e., Day 9 contained only spherical conceptuses, Day 10 contained only ovoid conceptuses, and Day 11 contained a mixture of ovoid and tubular conceptuses). Subsequent uterine flushings were submitted for non-targeted profiling by GC–MS and UPLC-MS techniques. Raw spectral data was processed using XCMS package in R and features were clustered using RAMclustR. Unsupervised multivariate principal component analysis (PCA) was performed in R using pcamethods package and univariate ANOVA was performed in R with a Benjamini-Hochburg false discovery rate (FDR) adjustment. Multivariate analysis of both the GC–MS and UPLC-MS spectral data demonstrated sample grouping that reflected the day of gestation. Maximum separation for the GC–MS data over time was observed with PC1 vs. PC2 accounting for 90% of the variance and PC2 identified several significant (P = 0.03) putative metabolites that changed over time. For the UPLC-MS data, separation over time was not as obvious but PC2 vs. PC6 did account for 28% of the variance and PC2 identified some significant (P = 0.04) metabolites that changed with time. After FDR adjustment of the GC–MS and UPLC-MS data, only C553, an unknown compound, was significantly (P = 0.02) greater in Day 11 uterine flushings compared to Day 9 and 10. However, several annotated compounds were trending toward differences, including aminomalonic acid which tended to be increased (P = 0.07) in Day 11 uterine flushings compared to Day 9 and 10. In conclusion, these data illustrate putative metabolites that change within the uterine milieu as porcine embryos transition between spherical, ovoid, and tubular embryos. USDA is an equal opportunity provider and employer.

Key Words: embryo elongation, metabolome, uterine milieu

1071 Effect of neuromedin u on pig immune regulation.

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Neuromedin U (NMU) is a conserved mammalian neuropeptide discovered in the 1980s, and found in two forms, NMU-25 and NMU-8. Wide distribution of NMU in animal organs suggests that NMU is involved in multiple physiological functions, including immue regulation. However, the role of NMU in pig immune regulation is still largely unknown. To study the effect of NMU on pig immune regulation, we cloned and detected the expression of NMU and its receptors in pig lymphatic organs and immune cells. We also investigated the effect of NMU on cytokine secretion after injection of (0, 5, 15, 45 nmol) NMU via intracerebral ventricle (i.c.v) into 16 pigs (n = 4 within each group), and the effect of (0.1 × 1000 nM) NMU on cytokine secretion in cultured dendritic cells and natural kill (NK) cells using ELISA and RIA methods. The results were as follows: 1. NMU and its receptors are expressed in lymphatic organs, cultured dendritic cells and NK cells. 2. Compared with the control group, NMU stimulated (P < 0.05) IL-1β, IL-6, IL-8, TNF-α and IL-10 secretion post-injection in a time- and dose-dependent manner. 3. NMU increased IL-8, IL-6 and IL-13 secretion and reduced IL-10 secretion (P < 0.05) in cultured dendritic cells. 4. NMU enhanced the killing activity of cultured NK cells, stimulated IFN-γ secretion and inhibited IL-10 secretion (P < 0.05) in NK cells in a time- and dose-dependent manner. Results from this study suggest that NMU has a role in pig immune regulation through its effect on cytokine secretion and increasing killing activity of NK cells.

Key Words: cytokine, immune regulation, NMU

1072 Evaluation of immune function of circulating leukocytes during the transition period in dairy cows.

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The aims of the study were to determine immune function circulating leukocytes using an ex vivowhole blood stimulation assay (WBA) with lipopolysaccharide (LPS) and assess gene expression profiles by RNA sequencing in the transition period of dairy cows. The WBA was performed on whole blood of 6 Holstein multiparous cows at −20, −3, 3, 7 d from parturition (DFP) using 0, 0.01 and 5 μg LPS/mL. The plasma collected after stimulation was used to analyze IL-1β and IL-6 concentration via ELISA. The data were analyzed as a factorial design with repeated measures, using PROC MIXED in SAS. At the same day of the WBA test, RNA was isolated from whole blood and sequenced on a Hiseq1000 (Illumina, USA). Differential gene expression analysis was conducted with the edgeR package, and a general linear model was applied considering −20 DFP as the baseline. A threshold of 1.5-fold change and P < 0.05 were used to define differentially expressed genes (DEG), which were subsequently analyzed through the Dynamic Impact Approach (DIA) using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database. The IL-1b and IL-6 released after LPS stimulation was higher at −3 DFP (P < 0.05) in comparison with −20 DFP. After calving, the response of IL-1β to stimulation of LPS decreased markedly, while the IL-6 response was unchanged up to 3 DFP (P < 0.01 vs. -20 DFP) and then declined at 7 DFP. The most-impacted and activated KEGG pathways highlighted by the DIA

analysis at −3 vs. −20 DFP were: PPAR signaling, adipocytokine signaling, hematopoietic cell lineage, ECM-receptor interaction and phagosome. After calving (3 and 7 DFP) the impact and activation of the above listed pathways was strongly increased, but there also was a strong inhibition of arachidonic acid metabolism (in particular enzymes regulating leukotrienes synthesis) as well as glycine, serine and threonine metabolism. Overall, the WBA and transcriptomic data confirmed changes in immune-competence of the circulating leukocytes around calving and, in particular, indicate mainly an increase of their activity and function. These data support the idea that the dairy cow's immune system is dysfunctional but not immunosuppressed around calving.

Key Words: Immune system, transition period dairy cows, transcriptomics, whole blood stimulation assay

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1073 Branched-chain amino acids (BCAA) in serum and skeletal muscle and mRNA expression of BCAA catabolizing enzymes in muscle of dairy cows around parturition.

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The BCAA (Leu, Ile, and Val), besides being substrates for protein synthesis or generation of energy, also act as signaling molecules and modulate overall AA and protein metabolism. The BCAA are mainly catabolized in skeletal muscle by transamination, followed by an irreversible oxidative decarboxylation by the action of branched-chain α-keto acid dehydrogenase complex (BCKDH). In view of the substantial mobilization of muscle protein during the transition period and the specific requirements of BCAA for milk protein synthesis and for supporting immune functions, our objective was to investigate the changes in the expression of BCAA catabolizing enzymes in conjunct with BCAA profiles during late gestation and the subsequent lactation in dairy cows. Biopsies from *M. semitendinosus* and blood were collected from 11 multiparous German Holstein cows on d −21, 1, 21, and 70 relative to calving. The BCAA profiles in muscle and serum were determined by LC-MS/MS profiling through targeted metabolomics using the Biocrates Absolute IDQ p180 Kit. The mRNA abundance of BCKDHA and BCKDHB was quantified by qPCR. Data were analyzed using the MIXED procedure of SAS. The concentrations of Leu, Ile, and Val in muscle increased from d −21 to d 1 ($P < 0.001$), remained unchanged until d 21 and then declined (except in case of Val) on d 70 ($P < 0.001$). In serum, the concentrations of Val and Ile changed over time ($P < 0.01$ and 0.06, respectively), whereas Leu remained stable. The mRNA abundance of BCKDHA decreased ($P = 0.03$) from d −21 to d 1, followed by a 1.9-fold increase ($P < 0.01$) on d 21 and then again declined thereafter ($P < 0.01$). The abundance of BCKDHB mRNA decreased 1.7-fold from d −21 to d 1 ($P < 0.01$), remained at this level on d 21, and then increased ($P < 0.01$) to nearly prepartum values on d 70. Negative correlations ($P < 0.01$) between BCKDHB mRNA abundance and muscle concentrations of Leu, Ile, and total BCAA ($r = −0.48$, −0.53, and −0.44, respectively) were observed across all time-points. Reduced abundance of BCKDHA and BCKDHB mRNA coincided with greater muscle concentrations of BCAA, suggesting an attenuation of BCAA oxidation in skeletal muscle shortly after parturition. This would favor sparing of BCAA for milk protein synthesis and other metabolic processes.

Key Words: branched chain amino acids, dairy cow, skeletal muscle

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1074 Incidence and risk factors related to anovulation in dairy cows.

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This study evaluated incidence and risk factors associated with anovulation in lactating dairy cows. Primiparous ($n = 357$) and multiparous ($n = 585$) Holsteins (43.6 ± 11.0 kg/d of milk and body condition score at 35 ± 3 days in milk [DIM] of 2.9 ± 0.3 [mean ± sd) had ovaries scanned at 35 ± 3 and 49 ± 3 DIM at PGF2α treatments of the Presynch to determine presence of corpus luteum and diameter of the largest follicle. Cows without corpus luteum at both examinations were considered anovular and classified in phenotypes according to follicle diameter: 4 to 8 mm; 9 to 14 mm; 15 to 24 mm; and ≥ 25 mm. The following information was collected until 49 ± 3 DIM. Dry period, incidence of retained placenta, metritis, ketosis, mastitis, lameness, respiratory and digestive problems. Cows detected in estrus until 5 d after the second PGF2α of the Presynch were inseminated, and the other cows were subjected to a fixed-time artificial insemination (FTAI) protocol. Categorical data were analyzed by logistic regression using the GLIMMIX procedure of SAS, and continuous data were analyzed using of the MIXED procedure ($P < 0.05$). The incidence of anovulation was 28.5% (268/942), and the distribution of phenotypes was 4.1% (11/268), 27.6% (74/268), 59.7% (160/268), and 8.6% (23/268) for 4 to 8 mm, 9 to 14 mm, 15 to 24 mm, and ≥ 25 mm, respectively. There was

a positive linear effect of dry period, and a negative linear effect of BCS on the incidence of anovulation. Milk production level was not associated with anovulation. Less healthy cows were anovular as compared to cows with history of one or multiple diseases (17.9%[c] [61/341], 29.8%[b] [94/315], and 39.5%[a] [113/286], respectively). All evaluated diseases were associated with increased incidence of anovulation when analyzed separately. A lower proportion of anovular cows was inseminated by estrus detection (27.1% [49/181] vs. 63.5% [344/542]) and, regardless of AI type, anovular cows were inseminated later (73.0 vs. 62.0 DIM) than cyclic cows. There was no difference in pregnancy per AI (P/AI) on d 60 of cows inseminated after estrus detection between anovular and cyclic cows (16.7% [8/48] vs. 18.1% [62/342], respectively). Nevertheless, when inseminated by FTAI, anovular cows had lower P/AI on d 60 than cyclic cows (16.3% [22/135] vs. 25.6 [50/195]). In conclusion, peri-parturient diseases were highly associated with increased anovular condition. Additionally, anovular cows had delayed first postpartum AI and lower P/AI when submitted to FTAI.

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Key Words: disease, estrus, fertility.

1075 Increasing fatty acid oxidation improves insulin sensitivity in primary differentiated bovine adipocytes. J. E. Rico*, F. Seck, M. V. Pinti, J. W. McFadden, *West Virginia University, Morgantown, WV*

Dairy cows develop insulin resistance during the transition from gestation to lactation. Because insulin is an anti-lipolytic hormone, insulin resistance promotes adipose tissue lipolysis. Increasing fatty acid oxidation (FAox) is a means to improve insulin sensitivity in monogastrics. Therefore, our objective was to evaluate the effects of a pharmacological stimulator of FAox on insulin sensitivity in bovine adipocytes. To test our objective, we utilized subcutaneous adipose tissue collected from Angus steers. Stromal-vascular cells were grown from explants in DMEM/F12 growth medium containing 17.5 mM glucose and 10% fetal bovine serum (FBS). Cells were harvested by trypsinization and replated. Once confluent, cells were differentiated using DMEM/F12 medium containing 17.5 mM glucose, 5 mM acetate, 1 mM octanoate, 5% FBS, 1.72 mM insulin, 0.25 mM dexamethasone, 0.5 mM isobutylmethylxanthine, and 2 mM rosiglitazone. Following d 8 of differentiation, cells were cultured in DMEM/F12 treatment medium containing 5 mM glucose, 1 mM acetate, 1% FBS, and 1.2 nM insulin. Differentiated adipocytes were treated with C75 (stimulator of carnitine palmitoyltranserase 1 and FAox; 0 to 100 μM) or palmitic acid (C16:0; 0 to 800 μM) complexed with bovine serum albumin for 3 to 18 h. Control cells did not receive C75 or C16:0 treatment. A minimum of two independent experiments with three replicates per experiment were performed. The statistical model included the fixed effects of treatment, experiment, and their interaction. Replicate within experiment was the random effect. Triacylglycerol (TAG) accumulation and cell viability were determined using colorimetric and fluorescence assays, respectively. Measurement of FAox and insulin sensitivity were measured using radiolabeled 2-deoxyglucose (2DOG) and C16:0. Relative to undifferentiated adipocytes, TAG accumulation was 736% greater in differentiated adipocytes ($P < 0.01$). Following differentiation, treatment with C16:0 or C75 for 18 h did not impair cell viability. Interestingly, 100 μM C75 improved cell viability by 40%, relative to control ($P < 0.01$). Treatment of adipocytes with 100 μM C75 for 3 h increased FAox, as demonstrated by a 122% increase in the recovery of radiolabeled acid-soluble products as well as a 30% increase in radiolabeled CO_2 ($P < 0.05$). Although C16:0 did not modify insulin 2DOG uptake following an 18 h treatment, treating adipocytes with 100 μM C75 for 18 h increased 2DOG uptake by 141%, relative to control ($P < 0.01$). We conclude that the stimulation of FAox enhances insulin-stimulated glucose uptake in primary differentiated bovine adipocytes.

Key Words: C75, fatty acid oxidation, insulin sensitivity

1076 Global gene expression in the endometrium of primiparous dairy cows during the early-luteal phase of the estrous cycle. A. L. Astessiano Dickson*[1], F. Peñagaricano[2], A. Meikle[3], and M. Carriquiry[1], *[1]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay, [2]University of Florida, Gainesville, [3]Facultad de Veterinaria, Montevideo, Uruguay.*

The uterine endometrium plays a central role in early conceptus-maternal communication for the establishment and maintenance of pregnancy. Primiparous Holstein dairy cows were used in a randomized block design to evaluate gene expression changes in the endometrium during the early-luteal phase of the estrous cycle induced by two different feeding strategies: total mixed ration (TMR) vs. pasture + TMR applied during early lactation. In particular, during the first 65 d of lactation, cows were fed either [i] TMR ad libitum (17 kgDM/d offered; 70% forage, 30% concentrate; T1) or [ii] grazing of alfalfa (*Medicago sativa*; 6-h am grazing in 3-d strips; pasture allowance = 20 kgDM/d) plus TMR (70% of ad libitum TMR; 12 kgDM/d offered; T2). At 45 ± 1 d, cows were synchronized and at d 7 of the estrous cycle (d 0 = estrous) endometrial biopsies were obtained. A total of 10 endometrium samples (5 cows per treatment) were analyzed using RNA sequencing. Sequence reads were mapped to the bovine reference genome (bosTau7) using Tophat and the resulting alignments were used to reconstruct transcript models using Cufflinks. Gene expression differences were tested using edgeR package. From the 14,753 genes detected

in the transcriptome, 102 genes were differentially expressed (FDR = 0.10; fold change $\geq$ 2) between T1 vs. T2. Specifically, 20 genes were significantly upregulated in T1 while 82 genes were upregulated in T2. Many of these genes are involved in biological processes such as regulating enzymatic activity (e.g., phospholamban, secretoglobin family 1A member 1), protein binding (e.g., caveolin 3, α-2-HS-glycoprotein), and immune response (e.g., immunoglobulin heavy constant epsilon, major histocompatibility complex class II DQ β, myelin protein P0-like). Functional enrichment analysis, using both Gene Ontology and KEGG databases, revealed significant terms associated with cell and tissue development, cell adhesion, endopeptidases, calcium ion transport, calcium signaling, tryptophan metabolism, among others, with most of the genes being upregulated in T2 compared to T1. Overall, this study characterized genes and pathways expressed in the endometrium of dairy cows at Day 7 of the estrous cycle, and evidenced a differential endometrial environment according with a nutritional management during early lactation in which most of the genes differentially expressed were upregulated in grazing cows.

Key Words: dairy cows, nutrition, transcriptome

1077 Influence of reproductive indicators and genetic parameters on lactation curves.

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Low levels of reproduction indicators in dairy farms are linked to low net returns associated with low milk production and replacement levels and high breeding and veterinary costs. The objectives of this study were to assess the association between lactation curve and reproductive efficiency and to evaluate the genetic variability. A novel reproductive indicator that combines pregnancy status after first (Prg first AI) and second artificial insemination (Prg second AI) and subsequent pregnancy loss after first (Non-Prg first AI) and second artificial insemination (Non-Preg second AI) was developed. The lactation curve was described using Wilmink's and Wood's functions that were incorporated into nonlinear mixed effects models that included the effect of sire, contemporary group, lactation number, the novel reproductive indicator, months open after calving, and cyclicity status at Day 35 after calving. Data on more than 50,000 test-day milk records from more than 6000 U.S. Holstein cows were considered. Cyclicity status was not associated with any lactation curve parameter. Higher months open was associated with higher persistency in milk yield. Estimates from the Wilmink function indicated that cows positive for Prg first AI and negative for Non-Prg first AI and cows negative for Prg first AI, positive for Prg second AI, and negative for Non-Prg second AI had significantly higher levels of milk yield during lactation, higher milk yield at peak production, and lower persistency than cows positive for Non-Prg first and 2ndAI. The Wood's parameter estimates confirmed the higher milk yield immediately after calving, higher incline in milk yield after calving, and higher persistency of the former relative to the latter reproductive groups. The ratio of sire to residual variance estimates was 0.4 and was consistent across models. The novel reproductive indicator that integrates reproduction-related variables intrinsic to the cow combined information on pregnancy and pregnancy loss at the first two AI events and together with genetic parameter estimates offers insights into the factors influencing the lactation curve. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: lactation curves, nonlinear mixed models, reproductive efficiency

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1078 Hematocrit, milk yield, and production related parameters comparisons between slick and wild-type-haired Puerto Rican Holstein cows.

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Previous research has suggested the presence of a slick hair coat as well as greater hematocrit values (HCT) as adaptations resulting in the thermoregulatory superiority of *Bos indicus* in comparison with *Bos Taurus* cattle. However, although it is well established that wild-type-haired (WT) Holstein cows have inferior thermoregulatory capacity than their slick-haired (SLICK) counterparts, there has been no research comparing both phenotypes in terms of HCT values in the Puerto Rican dairy cattle population. Therefore, the present study compared the HCT values (recorded in triplicate) from 29 SLICK and 35 WT lactating Puerto Rican Holstein cows. The SLICK and WT classifications were previously confirmed in a genotyping experiment. Additionally, to determine the uniformity of the evaluated groups the body weight (BW), days in milk (DIM), number of lactations, and production (averaged from the week

before the sampling) were compared between phenotypes. Data, averaged by cow, were analyzed using the GLIMMIX procedure of SAS. No differences were found in BW (538.25 ± 11.77 vs. 570.31 ± 15.61kg; $P = 0.5098$), DIM (187.57 ± 16.25 vs. 186.90 ± 18.17; $P = 0.9992$), and lactation number (1.94 ± 0.25 vs. 2.17 ± 0.22; $P = 0.9984$) between WT and SLICK cows, respectively. However, WT cows exhibited lower milk production values than their SLICK counterparts (17.11 ± 0.63 vs. 20.26 ± 1.28 kg/d; $P = 0.0288$, respectively). Nevertheless, there were no differences ($P = 0.4040$) in HCT values between the WT and SLICK cows (29.30 ± 0.46 vs. 29.79 ± 0.49, respectively). Although there was a difference in milk production, our results suggest that greater HCT values are not part of the adaptations to hot environments present in the Puerto Rican slick-haired Holstein cattle.

Key Words: heat stress, hematocrit, milk yield, slick-haired

1079 Effect of milk yield genotype on hepatic metabolic gene expression and repeated lipopolysaccharide (LPS) administration. G. T. Cousillas[*1], W. J. Weber[1], B. Walcheck[1], R. Chebel[1], D. E. Kerr[2], T. H. Elsasser[3], and B. A. Crooker[1], *[1]University of Minnesota, Saint Paul, [2]University of Vermont, Burlington, [3]USDA, Agricultural Research Service, Beltsville, MD.*

Objectives were to determine effects of milk yield genotype on hepatic expression of genes related to the somatotropic axis and glucose and lipid metabolism during an LPS challenge. Multiparous cows ($n = 12$/genotype) from unselected (stable milk yield since 1964, UH) and contemporary (CH) Holsteins that differed by more than 4500 kg milk/305-d were housed together and fed the same diet ad libitum for more than 4 mo before being blocked (2/genotype) by DIM and randomly assigned within genotype to receive saline or 0.25 μg/kg BW of LPS (*Escherichia coli* 055:B5). Cows were synchronized to be at Day 8 of their estrous cycle for the first challenge (C1) at 70–84 DIM. Liver biopsies were collected at 0, 4, and 24 h relative to treatment. A second identical challenge (C2) and sampling was conducted 4 d later. RNA was extracted and expression of 23 genes associated with metabolism were determined by digital multiplexed analysis (nanoString nCounter). Expression was normalized to the positive control and the geometric mean of 4 internal control genes. Data were transformed (square root) and analyzed by repeated measures using PROC MIXED (SAS) with time as the repeated effect. Means differed when $P < 0.05$. Sixteen genes presented a time by treatment interaction due to changes in expression after LPS. Expression of INSR, INSR-b, and IGFBP2 was greater and GHR-1A was less in CH than UH, expression of these genes decreased in response to LPS in both challenges, but the response did not differ between genotypes. There was a time by challenge interaction for IGFBP2 as it was decreased at 24 h in C1 but not in C2. There were challenge effects for IGF1 and GHR-1A due to greater expression in C1 than in C2 but the response did not differ between genotypes. There were time by treatment interactions for PC1, PCK1, PPARa, and PPARd. In response to LPS expression of PC1 and PPARd increased, and PCK1 and PPARa decreased at 4 h in both challenges, but the response did not differ between genotypes. Results indicate that LPS administration altered hepatic expression of genes related to the somatotropic axis, glucose, and lipid metabolism and that these responses were similar for the low and high milk yield genotypes.

Key Words: bovine genotype, gene expression, lipopolysaccharide, metabolism

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1080 Milk yield genotype impacts expression of hepatic innate immune genes during the transition period in Holsteins. *G. T. Cousillas[*1], W. J. Weber[1], B. Walcheck[1], D. E. Kerr[2], T. H. Elsasser[3], and B. A. Crooker[1], [1]University of Minnesota, Saint Paul, [2]University of Vermont, Burlington, [3]USDA, Agricultural Research Service, Beltsville, MD.*

Objectives were to determine effects of milk yield genotype on hepatic expression of genes related to innate immunity. Multiparous cows from unselected (stable milk yield since 1964; UH; $n = 10$) and contemporary (CH; $n = 10$) Holsteins that differed in milk yield by more than 4500 kg milk/305-d were housed together, fed the same diet ad libitum, and milked 2X/d. Liver biopsies were collected at −14, 3, 14, and 42 d in milk (DIM). RNA was extracted and expression of 44 genes was determined by digital multiplexed analysis (nanoString nCounter). Expression was normalized to the positive control and the geometric mean of 4 internal control genes. Data were transformed (square root) and analyzed by repeated measures using PROC MIXED (SAS) with DIM as the repeated effect. Means differed when $P < 0.05$. Expression of 19 genes was altered by DIM. Expression of 9 genes was greater and 9 genes was less in CH than UH. There were genotype by DIM interactions for CD14 and C/EBPd. Expression of CD14 was lower in CH than UH. In both genotypes, expression of CD14 decreased at 3 DIM, but remained lower in CH through 42 DIM, while CD14 expression recovered at 14 DIM in UH. C/EBPd expression was greater in CH than UH. In CH expression of C/EBPd increased at 3 DIM and returned to prepartum values at 42 DIM. Expression of C/EBPd in UH did not decrease until 42 DIM. LBP and XBP1 were greater in CH than UH, increased at 3 DIM and recovered by 14 DIM. TLR4 decreased at 3 DIM and although it was increasing, remained less than prepartum expression through 42 DIM for both genotypes. TLR2 and ICAM1 were less in UH than CH, decreased at 3 DIM and remained decreased by 42 DIM. XDH was greater in CH than UH, increased at 14 DIM and remained increased by 42 DIM. IL-1b was greater in UH than CH, but its receptor (IL1bR1) was less in UH than CH

and there was no effect of DIM. Results indicate expression of genes involved with cytokine production, inflammation, cell differentiation and activation were altered in both genotypes during the transition period and that there was a less robust response in the contemporary cow.

Key Words: gene expression, Holstein genotype, innate immunity

1081 Effect of milk yield genotype on hepatic metabolic gene expression during the transition period.

G. T. Cousillas*[1], W. J. Weber[1], B. Walcheck[1], D. E. Kerr[2], T. H. Elsasser[3], B. and A. Crooker[1], *[1]University of Minnesota, Saint Paul, [2]University of Vermont, Burlington, [3]USDA, Agricultural Research Service, Beltsville, MD.*

Objectives were to determine effects of milk yield genotype on hepatic expression of genes related to the somatotropic axis and carbohydrate and lipid metabolism. Multiparous cows from unselected (stable milk yield since 1964; UH; $n = 10$) and contemporary (CH; $n = 10$) Holsteins that differed in milk yield by more than 4500 kg milk/305-d were housed together, fed the same diet ad libitum, and milked 2X/d. Liver biopsies were collected at −14, 3, 14, and 42 d in milk (DIM). RNA was extracted and expression of 23 genes was determined by digital multiplexed analysis (nanoString nCounter). Expression was normalized to the positive control and the geometric mean of 4 internal control genes. Data were transformed (square root) and analyzed by repeated measures using PROC MIXED (SAS) with DIM as the repeated effect. Means differed when $P < 0.05$. Expression of 17 genes was altered by DIM. Liver expression of 8 genes was greater and 5 genes was less in CH than UH. There was a genotype by DIM interaction for STAT5A as it decreased at 3 DIM and recovered by 42 DIM in CH but did not change in UH. GHR-1A and IGF-1 were less and STAT3 greater in CH than UH but expression of JAK2 and STAT5B did not differ. There was a genotype by DIM interaction for PC1 as it increased at 3 DIM in both genotypes and remained increased by 42 DIM in CH; in UH PC1 returned to prepartum values at 42 DIM. INSR, PCK1, and PPARGC1A were greater in CH than UH, increased at 3 DIM and remained increased by 42 DIM. PPARa did not differ between genotypes, decreased at 3 DIM and returned to pre-partum values by 14 DIM. PPARd did not differ between genotypes or DIM. Results are consistent with postpartum reduction in hepatic sensitivity to somatotropin which lasted longer in CH cows. During the postpartum interval, expression of INSR and genes for enzymes related to gluconeogenesis were greater in CH than UH which is consistent with their greater need for lactose synthesis in the contemporary cow.

Key Words: gene expression, milk genotype, transition

1082 Gene expression and secretion of chemerin in bovine mammary epithelial cells.

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A variety of cytokines are secreted in a paracrine manner within the bovine mammary gland to maintain the microenvironment of the tissue. Our previous study showed that treatment with chemerin induced the expression of genes related to lactogenesis in immortalized bovine mammary epithelial cells (MAC-T cells). This suggested that chemerin is a secreted protein with chemotactic ability to antigen presenting cells has a regulatory effect on the function of mammary gland. However, what type of cell in mammary glands expresses chemerin and what kind of factor regulates its expression are not clear. In this study, we investigated the chemerin protein expression in bovine mammary tissues, milk, and cultured MAC-T cells. Mammary tissues were sampled from Holstein dairy cows in the lactation and dry-off periods, and chemerin protein expression was determined immunohistochemically. Chemerin protein was also detected in fresh milk and cell lysate of MAC-T cells by western blotting. Further, the effect of TNF-α on chemerin mRNA expression was investigated in MAC-T cells. MAC-T cells were grown until confluence and then treated with TNF-α (0.1, 1, and 10 nM) for 24 h. Chemerin gene expression was analyzed by Q-RT-PCR. Statistical analysis was performed using Tukey's HSD test. The results showed that chemerin protein was expressed in epithelial cells and stromal cells of bovine mammary gland from Holstein dairy cows and in cultured MAC-T cells. In addition, secreted chemerin protein was also detected in fresh milk. TNF-α significantly induced chemerin mRNA expression in MAC-T cells ($p < 0.05$). These results indicate that chemerin is secreted within the mammary gland in an auto/paracrine manner and that chemerin expression is upregulated by inflammatory cytokine. This study suggests the roles of chemerin as a chemoattractant that might attract immune cells to eliminate infectious bacteria or apoptotic cells in the mammary gland, as well as its role in lactogenesis.

Key Words: chemerin, inflammatory cytokine, mammary epithelial cells

1083 Proteomic analysis reveals increased Nrf2-mediated oxidative stress response in adipose tissue of late pregnant dairy cows during summer heat stress. M. Zachut[*1], G. Kra[1], G. Friedlander[2], and Y. Levin[3], *[1]Institute of Animal Science, Volcani Center, Bet Dagan, Israel, [2]The Ilana and Pascal Mantoux Institute for Bioinformatics, Weizmann Institute of Science, Rehovot, Israel, [3]The Nancy and Stephen Grand Israel National Center for Personalized Medicine, Weizmann Institute of Science, Rehovot, Israel.*

Nuclear factor erythroid 2-related factor 2 (Nrf2) is a critical regulator of key aspects of the antioxidant defense pathway under chronic stress. Oxidative stress and Nrf2 affect adipose tissue (AT) function. Heat stress at late pregnancy affects the physiology and performance in subsequent lactation. We investigated the effects of seasonal heat load on the proteome of adipose tissue in late pregnant dairy cows. Adipose tissue biopsies were obtained from 18 multiparous late pregnant dry cows at 14 d before expected calving during summer (S, n = 10) or winter (W, n = 8). Cows were also divided retrospectively according to BW loss during the first month postpartum to HWL–high weight loss (n = 9), and LWL–low weight loss (n = 9). Blood samples were collected twice a week for oxidative stress marker malondialdehyde (MDA) and cortisol concentrations. Proteins were analyzed by intensity based, label-free quantitative shotgun proteomics at Weizmann Institute of Science (Rehovot, Israel). Proteins were extracted and subjected to in-solution tryptic digestion, followed by nanoflow liquid chromatography coupled to high-resolution tandem mass spectrometry (nanoLC-MS/MS). Quantitative data were extracted using Genedata Expressionist data analysis package and proteins identified using Mascot search engine. Proteomics data, after logarithmic transformation, were analyzed by two-way ANOVA for effects of season (S vs. W), subgroup (HWL vs. LWL), and their interaction. Both pre- and postpartum, S cows had higher plasma MDA and cortisol concentrations compared with W (P < 0.005). Proteomic analysis quantified 1496 proteins in AT, from which the abundance of 132 (8.8%) proteins was differential in S vs. W [Fold change (FC) ± 1.5 and P < 0.05]. One of the top canonical pathways affected by season was Nrf2-mediated oxidative stress response (Ingenuity Pathway Analysis, Qiagen); the abundance of ubiquitin-conjugating enzyme E2 K (P < 0.006) and stress-induced-phosphoprotein 1 (P < 0.001) was elevated, while mitogen-activated protein kinase kinase 1 (P < 0.02), ferritin (P < 0.02), glutathione S-transferase Mu 1 (P < 0.04) and microsomal glutathione S-transferase 1 (P < 0.02) decreased in S vs. W adipose. These findings imply that Nrf2-mediated oxidative stress response plays a main role in the reaction of AT to counterbalance the increased oxidative stress under heat stress conditions in late pregnant dairy cows.

Key Words: adipose, heat stress, proteomics, transition

1084 Cholesterol deficiency associated APOB mutation affects lipid metabolism in Holstein cattle. J. J. Gross[*1], A. C. Schwinn[1], F. Schmitz-Hsu[2], F. Menzi[3], C. Drögemüller[3], C. Albrecht[4], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland, [2]Swissgenetics, Zollikofen, Switzerland, [3]Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, Switzerland, [4]Institute of Biochemistry and Molecular Medicine, University of Bern, Bern, Switzerland.*

During the last months, the number of reports on Holstein calves suffering from incurable idiopathic diarrhea dramatically increased. Affected calves showed severe hypocholesterolemia, and mostly died within days up to a few months after birth. This new autosomal monogenic recessive inherited fat metabolism disorder termed cholesterol deficiency (CD) is caused by a loss of function mutation of the bovine *APOB* gene. The objective of the present study was to investigate specific components of the lipid metabolism in 6 CD affected homozygous for the *APOB* mutation (CDS) and six normal Holstein calves with different *APOB* genotypes. Independent of sex, CD affected calves (CDS) had significantly lower plasma concentrations of total cholesterol (TC), free-cholesterol (FC), high density lipoprotein-cholesterol (HDL-C), low density lipoprotein-cholesterol (LDL-C), very low density lipoprotein-cholesterol (VLDL-C), triacylglycerides (TAG), and phospholipids (PL) compared to homozygous wild-type calves (P < 0.05). Furthermore, we studied the effect of the *APOB* genotype on cholesterol metabolism in adult Holstein breeding bulls of Swissgenetics. Among a total of 254 adult males the homozygous mutant genotype was absent, 36 bulls were heterozygous carriers (CDC), and 218 homozygous wild-type (CDF). In CDC bulls, plasma concentrations of TC, FC, HDL-C, LDL-C, VLDL-C, TAG, and PL were lower compared to CDF bulls (P < 0.05). The ratios of FC:cholesteryl esters (CE), and FC:TC were higher in CDC compared to CDF bulls, whereas the ratio of CE:TC was lower in CDC compared to CDF bulls (P < 0.01). In conclusion, the cholesterol deficiency associated *APOB* mutation was shown to affect lipid metabolism in affected Holstein calves and adult breeding bulls. Besides cholesterol also the concentrations of PL, TAG, and lipoproteins were distinctly reduced in homozygous and heterozygous carriers of the *APOB* mutation. Beyond malabsorption of dietary lipids, deleterious effects of apoB deficiency on hepatic lipid metabolism, steroid biosynthesis, and cell membrane function can be expected, which may result in unspecific symptoms of reduced fertility, growth, and health.

Key Words: cholesterol deficiency, hypobetalipoproteinemia, hypocholesterolemia

1085 Characterization of changes in temporal concentrations of fibroblast growth factor 21 (FGF21) before and after parturition in multiparous beef cows. L. Prezotto*[1], J. F. Thorson[1], J. Dafoe[1], M. R. Herrygers[2], and J. G. Berardinelli[2], *[1]Montana State University, Havre, [2]Montana State University, Bozeman.*

The objectives of this experiment were to characterize the secretion of Fibroblast Growth Factor 21 (FGF21) in beef cows during the last month of gestation, parturition, and early lactation and correlate these concentrations with metabolites. Pregnant, multiparous cows (n = 30) fed a TMR to meet or exceed NRC requirements were weighed and blood samples collected on days −14, −7, 0, 14, 28, and 60 relative to parturition. Samples were assayed for concentrations of FGF21, glucose, BUN, and NEFA. Individual average daily gain (ADG) was calculated for the experimental period. As previously shown in dairy cows, concentrations of FGF21 increased as parturition neared with concentrations of FGF21 increasing (P = 0.003) from day −14 (447 ± 120 pg/ml; mean ± SE) to 0 (790 ± 87 pg/ml). After parturition, concentrations of FGF21 decreased (P < 0.0001) by Day 14 (299 ± 88 pg/ml) to concentrations no different than day −14. Concentrations of FGF21 were maintained (P = 0.85) after parturition to Day 28 (288 ± 88 pg/ml). At Day 60, concentrations of FGF21 tended (P = 0.08; 391 ± 87 pg/ml) to increase compared to concentrations on Day 28. Concentrations of FGF21 and ADG tended (P = 0.09) to be negatively correlated on Day 56. Concentrations of glucose increased (P = 0.002) between day −14 and 0 and then decreased (P = 0.04) between Day 0 and 14. Concentrations of BUN increased (P = 0.0006) from day −14 to 0, decreased (P = 0.03) between Day 0 and 14, then continued to decrease (P < 0.0001) from Day 28 to 60. Finally, concentrations of NEFA decreased (P < 0.0001) from day −14 to 0 then increased (P = 0.04) by Day 14 to concentrations maintained (P = 0.94) to Day 28. There was no correlation (P ≥ 0.42) between metabolites and FGF21 on Day 0. However, on Day 60 concentrations of FGF21 tended (P = 0.09) to be negatively correlated with concentrations of glucose, positively correlated with concentrations of BUN (P = 0.0004), and not correlated with concentrations of NEFA (P = 0.30). These data indicate that FGF21 can be used as a biomarker to indicate reproductive and nutritional status in the beef cow.

Key Words: metabolites, parturition, performance

1086 Effect of investigational kisspeptin/metastin analog, TAK-683, on luteinizing hormone secretion at different stages of the luteal phase in goats. L. P. Rahayu*[1,2], M. E. Behiry[3], N. Endo[1,2], and T. Tanaka[1,2], *[1]Tokyo University of Agriculture and Technology, Tokyo, Japan, [2]United Graduate School of Veterinary Sciences, Gifu University, Gifu, Japan, [3]Visiting Research Scientist from Egypt, Tokyo University of Agriculture and Technology, Tokyo, Japan.*

Our previous study showed differential changes in luteinizing hormone (LH) secretion after administration of an investigational kisspeptin/metastin analog, TAK-683, between the endocrine conditions of the follicular and luteal phases in goats (Anim. Reprod. Sci. 2015). The present study aimed to examine the response of LH secretion to TAK-683 treatment and its association with ovarian changes during different stages of the luteal phase in goats. Nine cycling Shiba goats (4.4 ± 2.3 yr old) were assigned into 3 groups: early luteal phase (ELP, n = 4), mid-luteal phase (MLP, n = 4), and a control (n = 5) group. The ELP and MLP groups were administered 50 µg of TAK-683 intravenously on the 5 d after ovulation and on Days 7–14 after ovulation, respectively. The control group received vehicle on Days 7–14 after ovulation. Blood samples were collected at 10-min (hours 2–6) or 2 h (hours 6–24) intervals, and at 48 h after treatment for analysis of endocrine profiles. Ovarian ultrasonographic images and estrous behavior were assessed daily or every other day until the subsequent ovulation for analysis of effects on follicular and luteal dynamics and the length of the estrous cycle. LH concentration increased with a relatively small amplitude within 6 h of treatment with a mean peak value of 1.9 ± 0.6 ng/ml in the MLP group. Meanwhile, in the ELP group, TAK-683 treatment initially induced a sustained rise in the LH concentration with a relatively small amplitude, and then a surge-like release of LH with the highest values of 18.4 and 12.8 ng/ml, and with a peak time at 12 h and 14 h after treatment, respectively, in 2 goats. There is no significant difference in the progesterone concentration between pre- and post-treatment periods in all groups. Ovulation was detected within 2 d of the administration of TAK-683 in 2 goats showing a surge-like release of LH. Time-course of the LH response to TAK-683 treatment in the 2 goats showing a surge-like release of LH in the ELP group support our previous study that initial secretory response of LH to TAK-683 treatment is characterized as a small amplitude increase, and the secretion pattern of LH subsequently changes to a robust increase. It is suggested that responses of pulsatile and surge mode secretions of LH to the treatment of a kisspeptin analog depend on the stage of luteal phase in cycling goats.

Key Words: kisspeptin, luteal phase, luteinizing hormone

1087 MAC-T cell as in vitro evaluation system for casein gene expression involving glucose level.
H. Y. Jeong*[1], Y. T. Heo[2], H. S. Kang[1], E. T. Kim[1], and H. Song[2], *[1]Dairy Science Division, National Institute of Animal Science, RDA, Cheonan-si, Korea, [2]Konkuk University, Seoul, Korea.*

Glucose is essential fuel in energy metabolism and synthesis pathways of all mammalian cells. In lactating animals, glucose is the major precursor for lactose and is a substrate for the synthesis of milk proteins and fat in mammary secretory (alveolar) epithelial cells. However, clear utilization level of glucose in mammary cell during lactogenesis is still unknown due to lack of in vitro analyzing model. Therefore, objective of this study is to test reliability of mammary alveolar (MAC-T) cell as in vitro study model for glucose metabolism and lactating system. Undifferentiated MAC-T cells were cultured in three types (Non-glucose: 0 g/L, low glucose: 1 g/L, and High glucose: 4.5 g/L) of DMEM for 8 days, and then differentiation was induced. Cell proliferation and expression levels of apoptotic genes, IGF1 receptor, Oxytocin receptor, αS1, αS2, and β casein genes were analyzed at 1, 2, 4, and 8 d after differentiation. Proliferation of MAC-T cells with high glucose treatment was significantly higher. Expression of apoptotic genes was not affected by any groups. However, expression levels of mammary development related gene IFG1 r and lactating related gene Oxytocin r were significantly higher in low glucose group. Expressions of αS1-casein, αS2-casein, and β-casein were also higher in low glucose treated group compared with none and high glucose groups. Results demonstrated that although high glucose environment to MAC-T cells increase cell proliferation, low glucose treatment to MAC-T cells induce higher expression of casein genes. Our results may suggest that MAC-T cell can be in vitro model to analyze mammary cell development and lactation connect with precise biological effects.

Key Words: casein, glucose, IGF1, mammary alveolar (MAC-T) cell, oxytocin

1088 mRNA abundance of steroid hormone metabolizing enzymes (17β-HSD isoforms and CYP19) in adipose tissue of dairy cows during the periparturient period.
A. Alizadeh[1,2,3], H. Sadri[1], J. Rehage[4], S. Dänicke[5], and H. Sauerwein*[1], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Bonn, Germany, [2]Department of Animal Science, Saveh Branch, Islamic Azad University, Saveh, Iran, [3]Department of Embryology, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran, [4]University for Veterinary Medicine, Foundation, Hannover, Germany, [5]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Braunschweig, Germany.*

Besides being a storage organ for lipophilic compounds such as steroids, adipose tissue (AT) is now recognized in humans as being also capable of synthesizing and interconverting steroid hormones. In view of the comprehensive changes in body fat content of dairy cows during the lactation cycle, effects on steroid metabolism and release and potentially on fertility are conceivable. With this background, our research objectives were (1) to assess the mRNA expression of 17β-hydroxysteroid dehydrogenases (17β-HSD), i.e., the enzymes catalyzing the interconversion between the active and inactive forms of specific steroid hormones (focusing on subtypes 17β-HSD-1, −3 and −12), and of P450-aromatase (CYP19), converting androgens to estrogens, in bovine AT, (2) to characterize the time course of their mRNA abundance during late pregnancy and early lactation and (3) to compare this time course in a subcutaneous versus a visceral fat depot. From 20 Holstein cows, biopsies were collected from the subcutaneous (sc) and the retroperitoneal fat depot (rpAT) on d −42 and d 1, 21, and 100 relative to calving. The mRNA abundance of the target genes was assessed in the tissue samples by qPCR and normalized by using the 4 most stable reference genes. Data were analyzed using the MIXED procedure of SAS. Among the 4 target genes studied, only 17β-HSD-12 mRNA was detectable with the protocol used herein (suitability of the protocols was confirmed using ovary as positive control). The mRNA abundance of 17β-HSD-12 in scAT was highest on d −42, followed by a substantial decline on d 1 and 21 (7.5- and sixfold, respectively), and an increase on d 100 ($P < 0.001$). In rpAT, the peripartal changes of 17β-HSD-12 mRNA abundance were largely analogous to the ones observed in scAT; i.e., the values on d −42 and 100 were greater than on d 1 and 21 ($P < 0.001$). Our results indicate that aromatization of androgens to estrogens via CYP19 is not taking place in bovine AT, but estradiol-17β might be formed in AT by 17β-HSD-12 from estrone taken up from the circulation.

Key Words: 17β-HSD, adipose tissue, dairy cows

1089 Mitochondrial biogenesis and DNA content in metabolically tissues of lactating cows with divergent milk production. R. Weikard* and C. Kühn, *Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany.*

An appropriate metabolic adaptation of key tissues important for bioenergetic homeostasis and lactogenesis is required in cows to adjust for changes in energy demands and physiological conditions during the lactation period. Mitochondria are recognized to be central for meeting energy demands and maintaining metabolic homeostasis, and mitochondrial DNA (mtDNA) content reflects the capacity of cells for energy generation. The focus of our study was to elucidate, if mtDNA content and mitochondrial biogenesis were associated with lactation performance of cows characterized by a divergent genetic background regarding milk production. Therefore, we took advantage of cows from a resource population with a combined genetic dairy and beef background (Charolais x German Holstein cross, CHxGH) and compared them to purebred German Holstein (GH) dairy cows regarding mtDNA content and mRNA expression of important nuclear encoded genes controlling mitochondrial biogenesis in in two metabolically active tissues, liver and mammary gland. Genomic DNA and total RNA were isolated from tissue samples of 30 cows separated into three experimental groups based on their milk production during the week before slaughtering (each $n = 10$). Analysis of expression of genes involved in mitochondrial biogenesis, replication/transcription and translation of mtDNA and determination of mtDNA content were performed using quantitative real-time PCR. The study revealed a tissue-specific variation of mtDNA content that is higher in liver than in mammary gland, which agrees to the higher hepatic metabolic activity. When comparing high-lactating GH cows to cows with medium lactation performance (CHxGH-M), the mtDNA content was similar in liver but clearly reduced in mammary gland in GH cows. Unexpectedly, the mtDNA levels in mammary gland of GH cows resembled those of low-lactating cows (CHxGH-L). Gene expression analysis revealed lower transcript levels of genes involved in mitochondrial biogenesis, replication/transcription and translation in the liver of GH cows compared to CHxGH-M cows. In the mammary gland of GH cows, the gene expression levels pointed to a reduced mitochondrial biogenesis and mtDNA translation compared to CHxGH-M cows, whereas transcript levels related to mtDNA transcription/replication did not differ between both cow groups. The results suggest that the hepatic and mammary mitochondrial biogenesis processes are differentially modulated in high-lactating dairy cows and lactating cows from a CHxGH cross population indicating toward impaired mitochondrial biogenesis during high lactation and obviously reflecting genetic differences in coping with metabolic and physiological changes during lactation.

Key Words: gene expression, lactation, liver, mammary gland, mitochondrial DNA, mitochondrial biogenesis

1090 Lipopolysaccharide exposure in swine alters ovarian toll-like receptor 4 expression. K. L. Bidne*, M. J. Dickson, S. K. Kvidera, L. H. Baumgard, J. W. Ross, and A. F. Keating, *Iowa State University, Ames.*

Heat stress (HS) is associated with decreased fertility and endotoxemia as evidenced by increased systemic lipopolysaccharide (LPS) arising from decreased intestinal integrity. Across multiple species, LPS is associated with reduced female fecundity; phenotypic responses similar to HS-induced infertility, including spontaneous abortion and increased wean-to-estrus interval length. LPS binds to toll-like receptor 4 (TLR4), a membrane bound receptor, to initiate a signaling cascade culminating in the phosphorylation of nuclear factor kappa-B (pNFκB) and pro-inflammatory cytokine production. Acyloxyacyl hydrolase (AOAH) participates in LPS detoxification by cleaving the lipid A moiety, rendering the deacylated LPS unable to effectively bind TLR4. We hypothesized that endotoxemia could impact ovarian function in swine. Postpubertal gilts were synchronized to the follicular phase of their estrous cycle using Matrix® administered orally for 14 d. Immediately following Matrix® removal, gilts were treated with vehicle control (CT; 3 mL sterile saline; $n = 6$) or LPS (0.1 μg/kg BW; *E. coli* 055:B5; $n = 6$) via jugular catheter four times daily (0000, 0600, 1200, 1800 h) for 5 d during the follicular phase preceding estrus. Six hours after the final LPS infusion, animals were euthanized and ovaries collected. Whole ovarian protein homogenates were prepared and western blotting performed to quantify abundance of TLR4 and AOAH protein. Relative to CT, ovaries from LPS treated gilts had reduced ($P < 0.05$) abundance of TLR4 protein. No effect ($P > 0.05$) of LPS infusion on AOAH abundance was observed. These data demonstrate that the ovary to be responsive to chronic, low-level LPS exposure, and that endotoxemia potentially contributes to seasonal infertility in swine. Funded by the Global Food Security Consortium.

Key Words: endotoxemia, heat stress, ovary

1091 Milk yield genotype affects hepatic expression of innate immune genes when challenged with lipopolysaccharide (LPS).

1092 WS Mycobacterium avium subspecies paratuberculosis serum lipid profile analysis through Fourier transform ion cyclotron resonance mass spectrometry. A. L. Salazar*[1], J. M. Jarvis[1], N. M. Sudasinghe[1], S. Kumar[1], M. Song[1], J. Stabel[2], T. Thacker[2], S. L. Ivey[1], and T. Schaub[1], *[1]New Mexico State University, Las Cruces, [2]USDA-ARS, Ames, IA.*

Mycobacterium avium subspecies paratuberculosis (MAP) is responsible for Johne's disease (paratuberculosis; paraTB) in bovine which elicits serve enteritis in the lower intestinal tract; similar to Crohn's disease in humans. The objective of our study was to observe lipid changes in serum extracts of cattle infected with MAP using ultra-high resolution mass spectrometry. We hypothesized through the use of Fourier transform ion cyclotron resonance mass spectrometry (FT-ICR MS) the identification of unique lipid biomarkers induced by MAP infection will be observed. Field samples from cattle infected with MAP (INF; $n = 10$) were provided by the National Animal Disease Center (NADC). Uninfected serum (SC2012 and SC2015) from cattle with no history of paraTB came from two sources provided by the NADC. Negative controls used to test cross reactivity, with no MAP infection or previous exposure, included serum extracts from cattle challenged with lipopolysaccharide (LPS) and cattle infected with *Mycobacterium bovis* (bTB). Spectral differences were observed in the INF treatment compared to all other samples. Heteroatom class distribution, in positive ion mode, showed higher relative lipid abundance in the INF treatment in O_5Na_1, O_3, O_9Na_1, $O_{10}Na_1$, O_8Na_1, N_1, O_7Na_1, and N_1O_1 compounds whereas $N_1O_8P_1$ and $N_1O_7P_1$, were higher abundance in both control treatment groups. In negative-ion mode, O_3compounds were greater relative abundance in the INF treatment and both control treatments had higher relative abundance of $N_1O_{11}P_1$ and $O_{13}S_1$compounds. Assigned elemental compositions were searched in the Lipidomic Gateway Databased to identify relative abundance of lipid classes. The majority of compounds classified in the glycerophospholipid, polyketide, or sterol class. Bioinformatics showed forty-five unique compounds ($P < 0.05$), twenty-six in positive-ion mode, and nineteen in negative-ion mode, purely present in MAP infected cattle; no cross reactivity observed. The shift in heteroatom class distribution provides specific lipids may be present only in paraTB infected cattle, which is confirmed by the compounds identified solely in MAP infected cattle.

Key Words: Johne's disease, lipidomics, *Mycobacterium avium* subspecies *paratuberculosis*, paratuberculosis, ultra-high resoltuion mass spectrometry

1093 WS Insulin-associated and insulin-independent impacts of β adrenergic agonists and pro-inflammatory cytokines on glucose metabolism in primary rat soleus muscle. C. N. Cadaret*, K. A. Beede, H. E. Riley, and D. T. Yates, *University of Nebraska-Lincoln, Lincoln.*

Recent studies show that catecholamines and pro-inflammatory cytokines may help regulate skeletal muscle growth and metabolism even at sub-stress levels. The objective of this study was to determine the acute effects of β1 and β2-specific adrenergic agonists as well as TNFα and IL-6 on muscle glucose uptake and oxidation under basal and insulin-stimulated conditions. Primary soleus muscle was collected from adult Sprague-Dawley rats, separated tendon-to-tendon into 25–45 mg strips, and incubated in KHB spiked with or without insulin, and/or ractopamine HCl (β1 agonist), zilpaterol HCl (β2 agonist), TNFα, and IL-6. Glucose uptake was determined from cellular content of [^{3}H]-2-deoxyglucose after 20 min. Glucose oxidation of [^{14}C-U] glucose was determined after 2 h. Phospho-Akt/total Akt (p-Akt/Akt) was determined from protein isolated after 1 h. Compared to muscle incubated in un-spiked (basal) media, incubation with insulin increased ($P < 0.05$) glucose uptake by ~47%, glucose oxidation by ~32%, and p-Akt/Akt by ~238%. Muscle incubated with β2 agonist exhibited ~20% less ($P < 0.05$) glucose uptake but ~32% greater ($P < 0.05$) glucose oxidation than basal. Moreover, incubation with β2 agonist+insulin increased ($P < 0.05$) glucose oxidation and p-Akt/Akt over insulin alone. Muscle incubated with β1 agonist did not differ from basal for any output. Likewise, β1 agonist+insulin incubations did not differ from insulin alone. Glucose oxidation was ~23% and ~33% greater ($P < 0.05$), respectively, in muscle incubated with TNFα and IL-6 compared to basal, yet glucose uptake and p-Akt/Akt did not differ. Glucose uptake, glucose oxidation, and p-Akt/Akt were similar among muscle incubated with TNFα+insulin, IL-6+insulin, and insulin alone. In addition, glucose oxidation in muscle incubated with TNFα+insulin and IL-6+insulin did not differ from TNFα alone or IL-6 alone. These results show that acute β2 stimulation had opposite effects on glucose uptake and glucose oxidation in muscle, and that acute β1 stimulation had no evident impact on muscle metabolism. Moreover, β2 stimulation was synergistic with insulin, as glucose oxidation and Akt phosphorylation were greater with the two products together than with either individually. Lastly, acute stimulation with TNFα or IL-6 increased glucose oxidation rates independently of insulin or Akt phosphorylation. Together, our findings demonstrate that adrenergic and inflammatory mediators can have insulin-associated or insulin-independent effects on glucose metabolism and that these

effects may differ for glucose uptake and oxidation.

Key Words: β-agonist, glucose metabolism, stress hormones

1094 WS Relationship between current temperament measures and physiological responses to handling of feedlot cattle. A. F. Williams*[1], J. A. Boles[1], M. R. Herrygers[1], J. G. Berardinelli[1], M. C. Meyers[2], and J. M. Thomson[1], *[1]Montana State University, Bozeman, [2]Idaho State University, Pocatella.*

Interest in beef cattle temperament has increased due to growing consumer awareness of animal welfare. Researchers have defined temperament as behavioral responses to a perceived stressor. Subjective chute scoring has been used by many researchers for temperament, however, the subjectivity and associated variability among observers has been questioned. The most practical objective method of assessing temperament is exit velocity. Corresponding chute side measures to physiological markers are important. Faster exit velocities have been related to both increased cortisol and increased plasma lactate. The objectives of this study were to compare temperament differences between feedlot steers and heifers and to confirm chute side measures relationship to physiological responses to stress. Body temperature, serum and plasma lactate, serum glucose, salivary and serum cortisol concentrations were measured on mixed breed and sex feedlot cattle (n = 197). Fast, medium, and slow classifications were developed from exit velocities. Plasma lactate was significantly different between all classes. Sex had a significant effect on exit velocity and physiological measures. Heifers had higher exit velocities (P = 0.003), plasma lactate concentrations (P = 0.03), and cortisol concentrations (P = 0.001). Simple correlations among these variables indicated body temperature (heifers r = 0.44, P < 0.0001; steers 0.45 P < 0.0001), plasma lactate (heifers r = 0.52 P < 0.0001; steers r = 0.63 P < 0.0001), serum lactate (heifers r = 0.53 P < 0.001; steers r = 0.59 P < 0.001) and glucose (heifers r = 0.54 P < 0.001; steers r = 0.32 P < 0.003) were all correlated to exit velocity in both steers and heifers. Cortisol measures were not correlated to exit velocity in steers but were in heifers. Linear models constructed and evaluated using Akaike information criterion indicated that plasma lactate in combination with body temperature were strong candidates to predict exit velocity. Using the discriminate function analysis, the model categorized fast and slow classifications 69.23% and 61.54% respectively, indicating that in combination with exit velocity simple objective chute side measures of body temperature and plasma lactate can potentially increase accuracy of temperament identification.

Key Words: cortisol, lactate, temperament

1095 Cardiovascular performance of modern swine does not comply with allometric scaling laws. G. van Essen*, *University Medical Center Rotterdam, Rotterdam, Netherlands.*

In view of long-standing concerns about possible consequences regarding the cardiovascular capacity and adaptability of modern pigs we investigated the proportionality and performance of porcine hearts over a wide range of body weights (25– 225 kg), according to allometric scaling laws. Specifically, we tested the hypothesis that both heart mass (HM) and cardiac output (CO) scale with body mass (M) to the power of 0.75 (HM or CO = a.M0.75), stroke volume (SV), and left ventricular end-diastolic volume (LVEDV) to the power of 1.00. For this purpose, 21 Yorkshire x Landrace pigs were instrumented under anesthesia to measure CO and SV and LVEDV. Subsequently, animals were sacrificed and hearts were excised and weighed and tissue samples of the LV anterior myocardial wall analyzed for collagen content. Using a linear mixed model, the scaling coefficients of the relations between M and CO, SV, HM, and LVEDLV were determined. The 95% confidence intervals of the power-coefficient b for HM were 0.67– 0.88, encompassing the predicted value of 0.75, indicating that HM increased proportionally to M. In contrast, the 95% confidence intervals of power-coefficient b for CO amounted 0.40–0.65, thus failing to encompass the predicted value of 0.75. This was principally due to the lack of proper scaling of SV as the confidence interval of 0.52–0.83 failed to encompass the predicted value of 1.0, which in turn appeared to be due to a lack of scaling of LVEDV as its confidence interval of b values amounted 0.57–0.99, thus failing to encompass the predicted value of 1.0. The increase of HM without a proportional increase of LV volume, was accompanied by a doubling of collagen content in the LV of swine > 150 kg compared to swine < 75 kg (p < 0.05). In conclusion, cardiac geometry and function of modern swine fail to obey allometric scaling laws, likely due to an increased extracellular matrix deposition preventing physiological remodeling during growth.

Key Words: allometric scaling laws, cardiovascular system, swine

1096 DL-methionine increases glutathione concentration and alleviates inflammatory responses in primary bovine hepatocytes. Q. Zhang*[1], D. N. Luchini[2], and H. M. White[1], *[1]University of Wisconsin-Madison, Madison, [2]Adisseo S.A.S., Alpharetta, GA.*

Supplementation of rumen-protected methionine (Met) to dairy cows during the peripartal period improves postpartal performance and may decrease oxidative stress. The aim of the present study was to determine the effects of increasing concentrations of DL-Met on hepatic inflammatory responses and oxidative status. Hepatocytes isolated from 4 calves less

than 7 d old were maintained as monolayer cultures for 24 h before addition of treatments. Treatments included 0, 10, or 40 μM DL-Met added to Met-free media containing 100 μM Lys (0MET100LYS, 10MET100LYS, or 40MET100LYS), and 10 μM DL-Met added to Met-free media containing 25 μM Lys (10MET25LYS). Both 40MET100LYS and 10MET25LYS had a Met:Lys of 1:2.5. Cells were exposed to each treatment in triplicate for 16 h and then challenged with either 0 or 100 ng/mL lipopolysaccharide (LPS) for 8 h. Cell lysates were collected for quantification of glutathione (GSH) by fluorometic assay and quantification of gene expression by quantitative PCR. Abundance of mRNA was normalized to the mean of 3 reference genes. Cell media was collected for quantification of reactive oxygen species (ROS) by fluorometric assay. Data were analyzed using PROC MIXED of SAS 9.3. The model included treatment, LPS, their interaction, and random effect of calf. Data are reported as LSMEANS ± SE. There was an interaction ($P < 0.05$) of treatment and LPS on GSH concentration which increased ($P < 0.01$) as Met concentration increased (107.5, 114. 5 vs. 131. 5 ± 23.5 μM) without LPS challenge, and 40MET100LYS had greater ($P < 0.01$) GSH than 10MET-25LYS (131. 5 vs. 97.5 ± 23.5 μM). With LPS challenge, GSH concentration was not different ($P > 0.10$) among treatments. Hepatocytes challenged by LPS showed an inflammatory response with increased ($P < 0.001$) expression of tumor necrosis factor (1.425 vs. 2.257 ± 0.344 arbitrary unit (AU)) independent of treatment. However, there was an interaction ($P < 0.01$) of treatment and LPS on interleukin *(IL)-6* expression, which was increased by LPS in cells receiving 10MET-100LYS (1.086 vs. 3.851 ± 0.643 AU) and 10MET25LYS (0.918 vs. 2.296 ± 0.643 AU), but was not increased by LPS in cells receiving 40MET100LYS (0.912 vs. 1.770 ± 0.643 AU). Cell culture media ROS concentration was not different ($P > 0.10$) among treatments with or without LPS. The data suggest that a stress model can be established using primary bovine hepatocytes with LPS challenge. Increasing Met concentration enhances intracellular antioxidant production and alleviates inflammatory responses, although ROS released from the cells was not affected. The treatment effects were attributed to increase in Met concentration, not the Met:Lys.

Key Words: glutathione, interleukin, lipopolysaccharide

1097 Elevated hepatic lipid peroxidation and oxidative stress in underperforming piglets. *T. G. Ramsay*, M. J. Stoll, L. A. Blomberg, and T. J. Caperna, USDA, ARS, BARC, Beltsville, MD.*

The present study was designed to determine if normal weight pigs that grow poorly during the pre-weaning period have altered hepatic metabolism, as previously reported for intrauterine growth retarded pigs relative to littermates with normal growth rates. Eight pairs of average birth weight pigs (1.57 ± 0.05 kg) were identified that diverged in weight by a minimum of 50 g/day until 21 d of age. At 21 d, slow growing (SG) pigs weighed 5.47 ± 0.22 kg while control littermates weight 6.98 ± 0.28 kg ($P < 0.001$). Livers were collected for analysis at Day 21 for analysis of enzyme activity, glycogen content, and gene expression. Metabolomic analysis of the liver tissue was performed by Metabolon (Durham, NC). No changes with growth rate were detected in liver enzyme activity per mg tissue protein for enzymes in glycolysis, lipogenesis, or the pentose phosphate shunt ($P > 0.05$). Liver glycogen content (mg/gm liver protein) was similar between SG piglets and control littermates ($P = 0.908$). The mRNA abundance for the two genes regulating peroxisomal fatty acid oxidation: acyl CoA oxidase 1 (ACOX1; $P < 0.001$) and peroxisome proliferator-activated receptor α (PPARα; $P < = 0.003$), superoxide dismutase 2 ($P = 0.021$), lactate dehydrogenase ($P = 0.016$), insulin-like growth factor 2 (IGF2; $P = 0.002$), IGF binding protein 2 (IGFBP2; $P = 0.004$), and IGFBP3 ($P = 0.015$) were increased in the liver of the SG piglet relative to liver of piglets experiencing normal growth, as measured by real-time quantitative PCR. The increases in PPARα and ACOX1 mRNA abundance suggest that the liver of the SG piglet has the capacity to oxidize an increased proportion of long chain fatty acids relative to the control piglet through peroxisomal β-oxidation. The parallel increase in SOD2 mRNA abundance suggests that SOD2 may function to reduce the oxidative stress caused by an increase in peroxisomal β-oxidation. Metabolomic analysis of the liver from these SG piglets confirmed an increase in mono- and dihydroxy-fatty acids indicative of increased lipid peroxidation and oxidative stress relative to liver from control littermates ($p < 0.05$). These data indicate that the SG piglet utilizes alternative pathways for fatty acid oxidation during the preweaning period which may be a predictor for poor postnatal growth or a target for treatment to improve growth.

Key Words: growth, lipid peroxidation, liver, oxidative stress, pig,

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1098 Yeast supplementation altered the metabolic response to a combined viral-bacterial challenge in feedlot heifers. A. B. Word[*1], P. R. Broadway[2], N. C. Burdick Sanchez[2], K. P. Sharon[3], S. L. Roberts[4], J. T. Richeson[4], P. J. Defoor[5], M. D. Cravey[6], J. R. Corley[7], M. A. Ballou[1], and J. A. Carroll[2], *[1]Texas Tech University, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Department of Animal and Food Sciences, Texas Tech University, Lubbock, [4]Department of Agricultural Sciences, West Texas A&M University, Canyon, [5]Cactus Feeders, Canyon, TX, [6]Phileo Lesaffre Animal Care, Milwaukee, WI, [7]Phileo Lesaffre Animal Care, Cedar Rapids, IA.*

Two treatments were evaluated in feedlot heifers to determine the effects of feeding a yeast supplement on metabolic responses to a combined viral-bacterial respiratory disease

challenge. Thirty-two beef heifers (325 ± 19.2 kg) were selected and randomly assigned to one of two treatments: 1) Control (CON), receiving a standard feedlot ration with no yeast supplement, or 2) yeast, (YEAST) control ration plus a combination live yeast (2.5 $g \cdot hd^{-1} \cdot d^{-1}$) and yeast cell wall (2.5 $g \cdot hd^{-1} \cdot d^{-1}$) supplement (Phileo-Lesaffre Animal Care, Milwaukee, WI). Cattle were maintained on treatments for 31 d. On d −3 all cattle were challenged intra-nasally with 1 x 10^8 PFU of bovine herpesvirus-1 (BHV-1) and then allowed to rest in outdoor pens for 3 d. On d 0, each heifer was challenged intra-tracheally with approximately $3x10^7$ CFU of *Mannheimia haemolytica*, was fitted with an indwelling jugular catheter and indwelling vaginal temperature recording device, and was moved into individual stanchions in an environmentally-controlled barn. Whole blood samples were collected at the time of BHV-1 challenge, at 1-h (serum) or 2-h (complete blood cell counts) intervals from 0 to 8 h, and at 12, 24, 36, 48, 60, and 72 h following the *M. haemolytica* challenge. Data were analyzed using the mixed procedure of SAS specific for repeated measures with fixed effects of treatment, time, and their interaction. Cattle in the YEAST group had a greater glucose concentration following *M. haemolytica* challenge (121.38 ± 2.91 vs. 109.86 ± 2.90 mg/dL, respectively; $P < 0.01$) and decreased serum concentrations of blood urea nitrogen compared to CON (11.82 ± 0.53 vs. 10.12 ± 0.53 mg/dL, respectively; $P = 0.03$). There was no difference in serum NEFA concentration between YEAST (0.14 ± 0.01 mg/dL) and CON (0.15 ± 0.01mg/dL; $P = 0.37$). These data indicate that feeding a combination live yeast and yeast cell wall product may modulate energy stores by reducing muscle catabolism to provide energy for the activated immune system in response to a respiratory disease challenge. The reduction in catabolism has the potential to improve live animal performance when an animal is exposed to respiratory diseases.

Key Words: feedlot health, respiratory disease challenge, yeast

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1099 In vivo production, quality and pregnancy of bovine embryos from cows with high or low intake of dry matter or energy. R. Sartori*[1], R. S. Surjus[2], A. B. Prata[2], P. L. J. Monteiro Jr.[1], M. C. C. Mattos[3], F. C. Mattos[4], G. B. Mourao[5], and F. A. P. Santos[6], *[1]University of São Paulo-ESALQ/USP, Piracicaba, Brazil, [2]ESALQ/USP, Piracicaba, Brazil, [3]CEVA Animal Health, Paulinea, Brazil, [4]Ourofino Animal Health, Cravinhos, Brazil, [5]Department of Animal Science, University of São Paulo/ESALQ, Piracicaba, Brazil, [6]University of São Paulo, Piracicaba, Brazil.*

This study evaluated the influence of dry matter (DM) or energy intake on in vivo embryo production and quality. Non-lactating Nelore cows ($n = 32$, 4 to 10 y old) weighing 489.5 ± 11.3 kg and with BCS of 3.3 (1 to 5) were used. After 15 d on a maintenance diet [1.2% of DM per kg of body weight (BW)], cows were randomly divided into four groups. Maintenance (M), 0.7M, and 1.5M received the equivalent of 70, 100, and 150% of the M diet, respectively. The fourth group (Energy; E) received a diet with DM similar to the M group, but with an energy level equivalent to the 1.5M group. Cows were fed individually and offered all diets in a Latin-square arrangement every 42 d. Cows were submitted to a conventional superovulation protocol. Superovulatory response was assessed by ultrasonography and embryo quality was evaluated according to the IETS guidelines, as well as by pregnancy per fixed-time transfer (P/ET) of 274 vitrified embryos to Nelore recipients. Pre-prandial blood plasma insulin was performed by RIA at the onset of superovulation. Data were analyzed by PROC GLIMMIX of SAS ($P < 0.05$). Circulating insulin was greater in the E group (8.7 ± 0.9 μIU/mL) compared with groups 0.7 M (4.6 ± 0.9) and M (5.3 ± 0.85), not differing from group 1.5M (6.6 ± 0.9). Superovulation (CL number) was lower in donors fed high energy (9.7 ± 1.2) compared with cows receiving the standard diet [0.7M (13.0 ± 1.3), M (14.2 ± 1.2) or 1.5M (13.9 ± 1.2)] due to the negative correlation between circulating insulin and CL number ($r = -0.32$). Nevertheless, there was no difference between groups for number of ova/embryos (~6), viable (~3), or freezable embryos (~2.7). Regardless of treatment, circulating insulin was negatively correlated with the number of viable embryos ($r = -0.22$). There was lower P/ET at 60 d in the 97 cows receiving embryos from donors fed high energy (E; 29.4%) compared with the 177 cows receiving embryos from donors fed the standard diet (0.7M, M or 1.5M; 43.3%). Moreover, probability of P/ET at 60 d evaluated by logistic regression decreased as circulating insulin of donor cows increased from 0.64 to 25.0 μIU/mL. In conclusion, there was effect of diet on the superovulatory response and P/ET. Additionally, high circulating insulin of the donors was associated with lower superovulatory response, less viable embryos and less P/ET at 60 d. Financial support from FAPESP and CNPq. We also thank InVitro Brasil and Hildergard Pritzelwitz Experimental Station.

Key Words: cattle, fertility, insulin, nutrition

1100 Body condition score affects milk yield and energy balance of dairy cows after a short or no dry period. A. van Knegsel* and B. Kemp, *Adaptation Physiology Group, Wageningen University, Wageningen, Netherlands.*

Shortening or omitting the dry period of dairy cows is of interest because it limits the negative energy balance in early lactation, mainly due to a reduction in milk yield postpartum. Moreover, there are indications that individual cow characteristics, like parity or genotype, affect the response of dairy cows to a short or no dry period. The objective of this study was to evaluate the effects of prepartum BCS on the response of cows in milk yield, energy balance (EB), and plasma metabolites to a short or no dry period, compared with

a conventional dry period. Holstein-Friesian dairy cows (n = 167) were assigned randomly to three dry period lengths: 0 (no), 30 (short), or 60 d (conventional). Across treatments, cows were classified on prepartum BCS as lean (BCS < 3.0; n = 64), normal (3.0 ≤ BCS < 3.5; n = 60) or fat (BCS ≥ 3.5; n = 43). Feed intake and milk yield were recorded daily from week −8 till 14 relative to calving and averaged per week. Energy balance was calculated weekly. Blood was sampled weekly. Repeated measures ANOVA was performed to analyze the data. Data are expressed as LSMEANS ± SEM. Postcalving, milk production, EB, plasma free-fatty acids, and β-hydroxybutyrate concentration were affected by BCS-class*dry period length interaction (P < 0.05). More specifically, in fat cows milk yield and EB were similar between dry period lengths (milk: 39.9 ± 0.8 kg/d; EB: −113 ± 15 kJ/kg$^{0.75}$*d). In lean cows, however, shortening or omitting the dry period reduced milk yield (short: 38.5 ± 1.0 kg/d; no: 31.1 ± 1.1 kg/d) and improved the EB (short: −56 ± 19 kJ/kg$^{0.75}$*d; no: 89 ± 20 kJ/kg$^{0.75}$*d) compared with a conventional dry period. In normal cows, shortening or omitting the dry period reduced milk yield (short: 38.9 ± 1.2 kg/d; no: 30.1 ± 1.1 kg/d), compared with a conventional dry period. Between lean and normal cows, there were no differences in milk yield reduction or EB improvement due to dry period length. Results for plasma metabolites were in line with results for EB. In conclusion, prepartum BCS affects milk yield and EB of dairy cows after a short or no dry period. This might imply that the optimal dry period length for dairy cows depends on prepartum BCS. Currently, studies are ongoing to develop a decision support tool for dry period length based on individual cow characteristics, like parity and BCS, to optimize milk yield and cow health.

Key Words: energy balance, individual variation, metabolic status

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1101 The effect of stocking rate and cow breed on resumption of cyclicity, blood indicators of energy status, uterine health and reproductive parameters in pasture-based dairy systems.

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Identifying the optimum stocking rate (SR) and cow breed for pasture-based systems is essential to maximize output/ha without compromising reproductive performance. The objective of this study was to compare the performance of two different breeds (Holstein Friesian, HF, and Jersey crossbreds, JEX; n = 69 per breed) on one of three different SR (Low: 2.5 cows/ha; Medium: 2.9 cows/ha; and High: 3.3 cows/ha; n = 46 per treatment). The study was performed over 3 consecutive years. Milk samples were collected three times per week from parturition until week 5 post AI for progesterone analysis. Ten blood samples/cow/year were collected (weeks −2, 1, 2, 3, 4, 6, 8, 10, 14, and 18 relative to parturition) to determine circulating concentrations of glucose, non-esterified fatty acids (NEFA), β-hydroxybutyrate (β-HBA) and insulin-like growth factor-1 (IGF1). Uterine cytology samples were collected on Week 6 after parturition from 252 cows during Years 2 and 3 of the study to determine the proportion of cows with sub-clinical endometritis. The fertility performance of each herd was monitored during a 12-wk breeding season across 3 yr of the study. Days to resumption of cyclicity was not affected by SR or breed (25.2, 24.5, and 25.1 ± 1.2 d for Low, Med, and High SR; 24.7, vs. 25.2 ± 1.7 d for HF vs. JEX, respectively, P > 0.05). Mean plasma glucose (72.9, 71.9, and 72.4 ± 0.9 mg/dl), BHBA (0.61 ± , 0.61, and 0.62 ± 0.01, mmol/l), NEFA (0.46, 0.48, and 0.47 ± 0.01 mmol/l), and IGF1 (93.7, 92.9, and 98.9 ± 4.3, mmol/l) concentrations were not affected by SR (Low, Med, and High, respectively; P > 0.05). Mean glucose concentrations were greater in JEX than HF (73.5 ± 0.7 vs. 71.3 ± 0.8, mg/dl; P < 0.05, respectively), but concentrations of NEFA, β-HBA, and IGF1 were not affected by breed (P > 0.05). Neither SR nor breed affected the proportion of cows with sub-clinical endometritis at Week 6 postpartum (SR: 0.15, 0.14, and 0.27 of cows for low, medium and high SR, respectively; Breed: 0.18 and 0.18 of HF and JEX cows, respectively) or 42d pregnancy rate and final in-calf rate (all P > 0.05). In conclusion, under the conditions of this study, there was no major effect of increased SR or cow breed on reproductive performance. It is important that farm SR allows nutritional requirements to be met and that cows are genetically suited to seasonal-calving pasture based systems.

Key Words: breed, fertility, stocking rate

1102 Implications of acute or chronic pasture restriction on indicators of metabolic status in grass-based dairy cows.

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Annual variation in pasture growth rate has a major effect on grass availability for grazing dairy cows, especially at the onset of lactation in early spring. The objective was to determine the effect of imposing acute (2 wk) or chronic (6 wk) periods of varying levels of pasture restriction on indicators of metabolic health and hepatic gene expression in early lactation dairy cows. Holstein Friesian and Jersey crossbred cows (n = 96) were randomly assigned to one of four daily herbage allowances (DHA: 60, 80, 100, and 120% of intake capacity) for either two or 6 wk (12 cows per treatment) during early

lactation for 2 consecutive years. During the experimental period no supplemental concentrates were fed. Milk samples were collected three times per week for progesterone analysis to determine effects on estrous cyclicity. Blood was collected once weekly during the study to determine circulating concentrations of glucose, non-esterified fatty acids (NEFA), and β-hydroxybutyrate (β-HBA). In Year 2 of the study, liver biopsies were collected from a subset of cows assigned to the 60% DHA for 2 wk, 60% DHA for 6 wk, and the 100% DHA for 6 wk treatments at experimental weeks 0, 2, and 6. Reverse-transcription quantitative PCR (RT-qPCR) analysis was used to determine the mRNA abundance of 24 target genes related to energy metabolism. Data were analyzed using PROC MIXED of SAS. The DHA treatments had no effect on resumption of cyclicity, mean plasma glucose, or NEFA concentrations. Mean plasma β-HBA concentrations during the treatment periods were increased in cows on the restricted DHA treatments for 2 wk (1.25 ± 0.09, 1.08 ± 0.1, 1.03 ± 0.1, 0.9 ± 0.09 mmol/l; $P < 0.05$; 60%, 80%, 100%, and 120%, respectively) and 6 wk (1.43 ± 0.09, 1.32 ± 0.1, 1.06 ± 0.1, 1.04 ± 0.09 mmol/l; $P < 0.05$; 60%, 80%, 100% and 120%, respectively). At week six, 60% DHA increased mean expression of *glucose-6-phosphatase, pyruvate carboxylase, carnitine palmitoyltransferase 1A, acyl-CoA synthetase long-chain 1* and decreased mean expression of *fatty acid synthase and acetyl-CoA-carboxylase.* DHA had no effect on mRNA abundance of *IGF-1*, but 60% DHA for 6 wk increased expression of *insulin-like growth factor binding protein-2*. We conclude that imposing acute periods of restricted DHA had only modest effects on metabolic health in early lactation dairy cows.

Key Words: gene expression, metabolites, restriction

1103 The effects of ketosis, feed restriction, and an endotoxin challenge on circulating serotonin (5-HT) in lactating dairy cows. E. A. Horst*[1], S. K. Kvidera[1], M. Abuajamieh[1], E. J. Mayorga[1], M. A. Al-Qaisi[1], H. B. Green[2], K. M. Schoenberg[2], W. E. Trout[3], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Elanco Animal Health, Indianapolis, IN, [3]Elanco Animal Health, Greenfield, IN.*

Circulating serotonin (5-HT) is thought to be associated with various metabolic disorders and hypocalcemia during the transition period. Objectives were to evaluate the effect of ketosis, feed restriction, or endotoxin challenge (models where energetic and calcium metabolism is markedly altered) in lactating cows on circulating 5-HT. Blood samples were obtained from three separate experiments and circulating BHBA, NEFA, and glucose were measured in all three experiments while ionized calcium was only measured in the endotoxin challenge. Data were analyzed using PROC MIXED and PROC CORR of SAS 9.4. In the ketosis study, blood samples from cows clinically diagnosed with ketosis ($n = 10$) or classified as healthy ($n = 9$) were obtained from a commercial dairy farm at d −7, 3, and 7 relative to calving (Abuajamieh et al., 2015 JDS. 98[2]:876). There was no effect of health status on circulating 5-HT. Circulating 5-HT was negatively correlated with NEFA ($r = -0.47$, $P = 0.04$); however, no other relationships existed between 5-HT and the other metabolites. In the feed restriction experiment (Stoakes et al., 2015 JDS. 98[2]:274), mid-lactation cows were either fed ad libitum ($n = 3$) or restricted to 20% of their ad libitum intake ($n = 5$). There were no effects of feed restriction on circulating 5-HT, and energetic metabolites were not correlated with circulating 5-HT. In a model of endotoxemia (Stoakes et al., 2015 JDS. 98[2]:509), mid-lactation cows were either challenged with lipopolysaccharide (LPS; 1.5 μg/kg BW; $n = 6$) or sterile saline (CON; $n = 6$). LPS decreased blood ionized Ca^{2+} (56%; $P < 0.05$), but had no effect on circulating 5-HT. No relationships existed between circulating 5-HT and energetic metabolites or ionized Ca^{2+}. In summary, ketosis, feed restriction, nor endotoxemia affected circulating 5-HT. Circulating 5-HT was moderately correlated with NEFA in the transition cow experiment, but no other relationships existed between 5-HT and energetic metabolites and calcium in these experimental conditions.

Key Words: feed restriction, ketosis, lipopolysaccharide, serotonin

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1104 Transcriptome analysis reveals fundamental differences between liver of neonatal calves and transition dairy cows. F. Batistel*, M. Vailati Riboni, A. Agrawal, and J. J. Loor, *University of Illinois, Urbana.*

Primary hepatocytes isolated from neonatal calf liver have been used to infer aspects of liver metabolism of dairy cows, with the assumption that physiological responses of neonatal hepatocytes mimic those of cows. To evaluate more directly the usefulness of calf hepatocytes as model to study cow responses, in particular during the early postpartal period, liver RNA from 7 Holstein cows (20 d in milk) and 7 Holstein calves (4-d old) was used for transcriptome analysis. Individual samples were used to determine expression of 7 key metabolic genes via quantitative RT-PCR. Data were $\log_2$ normalized and subjected to ANOVA using the Proc MIXED procedure of SAS. Compared with calves, the expression of genes related with lipoprotein synthesis (*APOB,* $P = 0.01$; *MTTP,* $P = 0.01$), gluconeogenesis (*FBP1*, $P = 0.07$), fatty acid oxidation (*CPT1A,* $P = 0.01$), and methionine metabolism (*MAT1A,* $P = 0.03$; *BHMT,* $P = 0.07$) was lower in calves than cows. Samples were pooled by type (calves or cows) and co-hybrized onto the 44K-Agilent bovine (V2) gene expression microarray chips (Agilent Technologies Inc.). This allowed for a direct comparison of transcriptomes in calves and cows. Out of 14,772 unique annotated genes detected by the array, 354 (2.39%) differentially expressed genes with expression ratio ≥ (calf specific) or ≤ (cow specific) than mean

± 2 SD were considered highly-expressed in calves or cows and used for pathway analysis using the Dynamic Impact Approach (DIA) with the KEGG database. Within this set, 221 (1.49%) had at least 40-fold greater expression in cows (e.g., *ACSL6, APOBEC3A, IGF2BP1, PFKFB3, SLC11A1, VLDLR*) or calves (e.g., *AOX1, CYP1A1, CYP7A1, SLC27A2*). Instead, expression of 73 genes was equal among cows and calves. The 25 most-impacted pathways from the DIA analysis indicated that critical metabolic processes involving amino acid, lipid, carbohydrate, and vitamin metabolism (e.g., branched-chain amino acid degradation; primary bile acid biosynthesis; fatty acid elongation in mitochondria; and glycolysis/gluconeogenesis) were biologically more important and highly-activated in calves than cows. In contrast, signaling pathways related to immunity (e.g., NOD-like receptor, Toll-like receptor, and chemokine), as well as cofactor metabolism (e.g., folate, pantothenate, and CoA biosynthesis) were highly-activated in cows than calves. Overall, results indicate that liver of calves and cows have unique transcriptome profiles, hence, hepatocytes isolated from calves might not be a suitable model to study hepatic function/metabolic responses of cows.

Key Words: calf, dairy cow, liver transcriptome

1105 ADSA®-EAAP speaker exchange presentation: Effect of rumen content exchange on gene expression in rumen epithelium of lactating cows.

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The ruminal epithelium may adapt to changes in diet either by adjusting the absorptive capacity and surface area of papillae or through acute cellular functional adaptations. To test this hypothesis, an experiment involving total rumen content exchange between 3 pairs of lactating cows fed the same diet was performed to investigate the influence of variation in rumen contents and microbial populations therein on gene expression in rumen papillae. Papillae samples were taken during and 1 wk after digesta exchange from the ventral sites of rumen. Sequencing libraries were prepared according to Illumina TruSeq® Stranded mRNA and TruSeq® Small RNA sample preparation. Paired-end sequencing with Illumina HiSeq3000 with 2 × 150 bp read length was used for mRNA (average 50.6 M reads per sample) and single-read sequencing with 1 × 50 bp read length for miRNA (average 2.5 M reads per sample). From mRNA 67.8% of reads were mapped, of which 53.5% were located to known genes, the remaining reads mapping to unannotated regions of the bovine genome. Each animal was analyzed for differential gene expression (DE) between the two time points using edgeR. The *p*-values of DE genes were used for hierarchical clustering to identify groups with different responses. Using this approach experimental animals ($n = 6$) formed two clusters. DE analysis within the clusters revealed 170 genes differentially expressed at FDR < 0.1 in cluster 1 and two genes differentially expressed in cluster 2. The gene set was analyzed with Ingenuity®Pathway analysis (Qiagen). The top five affected canonical pathways were Acyl-CoA hydrolysis, xenobiotic metabolism signaling, dermatan sulfate biosynthesis, chrondroitin sulfate biosynthesis, and IGF-1 signaling. Twelve phenotypes were significantly different between the two clusters before exchange (ANOVA, $p < 0.1$ by permutation test), with cows in cluster 1 having higher milk protein content, lower total tract N digestibility, greater fecal N excretion, and higher molar acetate and lower valerate proportions in rumen VFA. From miRNA libraries 36.3% of reads were uniquely mapped. From 811 annotated miRNAs, 382 miRNAs were expressed. Analyses of miRNA expression between the two clusters revealed miRNAs with large differences before and after the exchange, five of which have been recently reported to be correlated with N efficiency in cows fed low quality forage diets. To conclude, the transfer of digesta contents was associated with alterations in the expression of key genes and gene networks in rumen epithelium.

Key Words: dairy cow, rumen epithelium, transcriptomics

1106 Identification of effects of different forage source on metabolism and function of liver from dairy cows using systematic approaches.

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Liver occupies a unique role in nutritional physiology of lactating dairy cows, but the effects of forage source on its metabolism and function have not been well examined. This study was conducted to investigate the effects of different forage source on liver metabolites and key gene functions in dairy cows using gas chromatography–time of flight/mass spectrometry (GC-TOF/MS) based metabolomics and RNA-seq analysis. A total of 12 multiparous Holstein dairy cows were fed 2 diets with different forage source: Alfalfa hay (AH, $n = 6$) and corn stover (CS, $n = 6$). The multivariate statistical analysis (PCA, PLS-DA, and OPLS-DA) showed a clear separation of metabolomics profiles between AH and CS groups. A total of 270 metabolites were identified in the liver with 28 of them significantly different between the 2 diets (VIP > 1&$P < 0.05$). In AH, 71 up-regulated metabolites ($\log_2$(z-score) > 1 & $P < 0.05$) were associated with gluconeogenesis, vitamin and mineral metabolism, amino acid metabolism, propanoate metabolism, cell death and survival, carbohydrate metabolism, and energy production. In CS, 64 up-regulated metabolites were involved in cellular growth and proliferation, organismal development, cell-to-cell signaling and interaction, molecular transport and lipid metabolism. Three

metabolites, leucine, cystine, and hippuric acid were further identified as biomarkers based on the analysis (AUC value, predicted class probabilities, and predicted accuracy) of different combinations of significantly different metabolites. In addition, expression of 11,781 genes was detected (more than 50% of samples with CPM > 1) in the liver. One gene module containing 122 genes had a significantly strong positive correlation ($R = 0.82$, $P = 0.001$) with cystine abundance by weighted gene co-expression network analysis (WGCNA). The main functions represented by these genes were gluconeogenesis, pyruvate metabolic process, monosaccharide biosynthetic process, carbohydrate homeostasis, glucose homeostasis, hexose biosynthetic process, chemical homeostasis, and vitamin-related metabolic process which were all up-regulated in the AH group. Our results suggest that various metabolites, pathways, and gene functions were significant changed in response to forage source. These can be used for further characterization of the regulatory mechanisms of forage-related milk performance in dairy cows.

Key Words: dairy cow, gene function, liver metabolomics

1107 Early postpartum administration of sodium salicylate to multiparous dairy cattle is associated with alterations in feeding behavior up to 120 d in milk.

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Previous research has indicated that the use of non-steroidal anti-inflammatory drugs such as sodium salicylate following calving can alter milk yield later in lactation. In the current experiment, sodium salicylate was administered following calving, and cattle were observed through 120 d in milk (DIM). Cows in their second parity and greater were blocked by parity and alternately enrolled into 1 of 2 treatments following calving, receiving either drenches of water (CON) or drenches of 125 g of sodium salicylate dissolved in a similar volume of water (SAL) at approximately 24, 48, and 72 h postpartum. A total of 28 animals per treatment were enrolled in this experiment, and 42 of these animals ($n = 21$ cows/treatment) were included in feeding behavior measurements. Of these, 16 cows were in their third parity and greater, and 26 were in their second parity. Feeding behavior was measured by feed bunks suspended from load cells that continuously monitored bunk weight. For all feeding behavior responses, variables (meal weight, meal length, number of meals/d, and intermeal interval) were averaged by day, and daily responses were averaged by week for statistical analysis. No differences were detected due to treatment for milk yield, energy-corrected milk (ECM), or DMI; however, a significant parity by treatment interaction was observed ($P = 0.03$), where SAL decreased intake in second parity cows but not cows in their third parity and greater. This resulted in a tendency for a treatment by parity interaction for milk yield:DMI ($P = 0.08$) and a significant interaction between treatment and parity on ECM:DMI ($P = 0.02$). Similarly, a significant interaction between parity and treatment was observed for average meal weight ($P = 0.04$), with no difference between treatments in second parity animals but increased average meal weight for older cows receiving SAL. Treatment with SAL was associated with fewer daily meals and greater average meal length ($P = 0.03$). A tendency for an interaction between treatment and week was also observed for intermeal interval ($P = 0.06$). For all feeding behavior variables measured, responses to treatment were delayed by at least 5 wk following administration. In conclusion, despite a failure to detect differences due to treatment in milk production or intake, postpartum treatment with sodium salicylate resulted in subtle and prolonged differences in feeding behavior in multiparous cows.

Key Words: feeding behavior, inflammation, sodium salicylate

1108 Proteomic analysis reveals increased abundance of inflammation-related proteins in adipose tissues from postpartum dairy cows treated with sodium salicylate.

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The objective was to investigate the effects of sodium salicylate (SS) on the proteome of adipose tissue in early lactating dairy cows. Holstein cows in parity 3+ were assigned alternately at time of calving to either control or SS treatments. CON treatment received a molasses carrier in drinking water while the SS received 2.5 g/L SS with the molasses carrier in drinking water for 7 d after parturition. Adipose tissue biopsies were obtained from control cows ($n = 5$) and cows treated with SS ($n = 5$) at 7 DIM. Proteins were analyzed by intensity based, label-free quantitative shotgun proteomics at Weizmann Institute of Science (Rehovot, Israel). Proteins were extracted and subjected to in-solution tryptic digestion, followed by nanoflow liquid chromatography coupled to high-resolution tandem mass spectrometry (nanoLC-MS/MS). Quantitative data were extracted using Genedata Expressionist data analysis package and proteins identified using Mascot search engine. PCA analysis revealed two distinctive clusters, therefore proteomics data, after logarithmic transformation, were analyzed by two-way ANOVA for effects of treatment (control vs. SS), cluster (1 vs. 2) and their interaction. Only proteins that were different at $P < 0.05$ for effect of treatment and $P > 0.05$ for effect of interaction, as well as having a fold change (FC) of ± 1.5 were further considered. Proteomic analysis quantified 1422 proteins in adipose tissue, from which the abundance of 80 (5.6%) proteins differed in SS vs. control.

The top canonical pathways affected by SS treatment (IPA, Ingenuity) were the complement system, IL-10 signaling and acute phase response signaling. The abundance of several proteins related to these pathways was altered; for example, complement C1q subcomponent subunit B (C1QB, FC = 360, $P < 0.002$), complement component 1-r subcomponent (C1R, FC = 1.6, $P < 0.04$), flavin reductase (NADPH; BLVRB, FC = 1.6, $P < 0.05$) and lipopolysaccharide-binding protein (LBP, FC = 2.3, $P < 0.004$) were increased in SS adipose compared to controls. These findings imply that SS treatment up-regulates some inflammation-related proteins in adipose tissue, perhaps to maintain the desired inflammatory tone during the subacute inflammation in postpartum cows.

Key Words: adipose, immune, proteomics, sodium salicylate

1109 WS Effect of delayed insemination of non-estrual beef heifers following a 7-d-CO-Synch plus controlled internal drug release (CIDR) insert timed artificial insemination protocol.

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Synchronizing estrus before AI is an effective way to shorten the calving season, and increasing the number of pregnancies per AI may lead to greater use and acceptance of synchronization protocols among beef producers. Our objective was to determine if pregnancy rates to fixed-time AI (FTAI) would be improved by delaying insemination in heifers not expressing estrus before FTAI in a 7-d CO-Synch + controlled internal drug release (CIDR) estrous synchronization protocol. Four hundred sixty-five yearling beef heifers across three locations of commercial and purebred herds were given 100 μg of GnRH (Cystorelin; Merial) i.m. and a CIDR insert (Zoetis; 1.38 g of progesterone) on d 0. On d 7 CIDR inserts were removed and all heifers received 25 mg of $PGF_{2\alpha}$ i.m. (Lutalyse; Zoetis) and were fitted with an estrous detection patch (Estrotect; Rockway, Inc.). Heifers were placed in one of three treatment groups based on estrous detection patch color at 48 h after $PGF_{2\alpha}$: 1. Estrus-Red 48 h (n = 180)—heifers displayed estrus as indicated by red estrous detection patch and were given GnRH (100 μg i.m. Cystorelin) and inseminated at 48 h after $PGF_{2\alpha}$, 2. Non-Estrus-Gray 48 h (n = 137)—heifers did not display estrus by 48 h after $PGF_{2\alpha}$ and were given GnRH (100 μg i.m. Cystorelin) and inseminated at 48 h after $PGF_{2\alpha}$, and 3. Non-Estrus Delayed-Gray 56 h (n = 148)—heifers did not display estrus by 48 h after $PGF_{2\alpha}$ and were given GnRH (100 μg i.m. Cystorelin) at 48 h and inseminated at 56 h after $PGF_{2\alpha}$. Pregnancy data were analyzed using SAS PROC GLIMMIX with treatment as a fixed effect, herd as a random variable, and heifer as the experimental unit. By 48 h after $PGF_{2\alpha}$, 38.7% of all heifers were in estrus (as indicated by a red estrous detection patch). Pregnancy rate to AI was greatest for Estrus-Red 48 h heifers (67.8%; $P < 0.0001$) as compared to heifers in the Non-Estrus-Gray 48 h (39.4%) and Non-Estrus Delayed-Gray 56 h (42.6%) groups. Among heifers not expressing estrus before FTAI, delayed insemination achieved a similar (P = 0.83) percent of pregnancies (Non-Estrus Delayed-Gray 56 h; 42.6%) as compared to Non-Estrus-Gray 48 h heifers (39.4%). Delaying insemination by 8 h in heifers not displaying estrus by 48 h after $PGF_{2\alpha}$ did not improve pregnancy rates to AI.

Key Words: beef heifers

1110 GnRH increased pregnancy risk in suckled beef cows that did not display estrus when subjected to a split-time artificial insemination program.

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We hypothesized GnRH would induce ovulation in a split-time AI program by increasing pregnancy risk (PR) when estrus was not detected. A total of 1236 suckled beef cows at 12 locations in 3 states (CO, KS, and ND) were enrolled. Before applying the fixed-time AI program, BCS was assessed. Cows were treated on d −7 with a CIDR insert concurrent with 100 μg GnRH and on d 0 with 25 mg $PGF_{2\alpha}$ plus removal of the insert. Estrotect patches were affixed to cows at CIDR insert removal. Estrus was defined to have occurred when an estrus-detection patch was > 50% colored (activated). Cows in estrus by 65 h (n = 758; 61.3% of all cows) were allocated randomly to 2 treatments: 1) GnRH and early AI at 65 h (E+G; n = 373), or 2) AI only at 65 h (E–G; n = 385). Remaining cows were allocated randomly to 2 treatments: 1) GnRH injection at 65 h and late AI at 84 h (L+G; n = 252), or 2) AI only at 84 h (L–G; n = 226). Pregnancy was determined 35 d after AI via transrectal ultrasound. Pregnancy risk did not differ (P = 0.68) between E+G and E–G cows (61.9 vs. 60.4%), respectively. Conversely, for cows inseminated at 84 h, PR was greater (P = 0.01) in cows that received GnRH at 65 h compared with their herd mates not receiving GnRH (41.7 vs. 30.8%), respectively. Of those cows not in estrus by 65 h, 57.7% displayed estrus by 84 h for a total expression of estrus by all cows of 77.6%. Pregnancy risk was greater ($P < 0.01$) in cows not detected in estrus by 84 h when treated with GnRH at 65 h compared with no GnRH (+G = 33.4% [n = 146] vs.–G = 15.0% [n = 128]), whereas no difference in PR was detected for cows detected in estrus (+G = 65.3% [n = 103] vs.–G = 61.7% [n = 97]). Neither estrus expression by 65 or 84 h nor pregnancy risk was influenced by BCS, parity, or days postpartum at AI. Cows had greater PR when they displayed estrus before AI and cows

that did not display estrus by 65 h benefited from an injection of GnRH at 65 h before insemination occurred at 84 h.

Key Words: beef cows, GnRH, split-time AI

1111 Comparison of long- versus short-term CIDR-based protocols to synchronize estrus before fixed-time AI in primiparous 2-yr-old beef cows.

J. M. Abel*, B. E. Bishop, J. M. Thomas, M. R. Ellersieck, S. E. Poock, M. F. Smith, and D. J. Patterson, *University of Missouri, Columbia.*

This experiment was designed to compare the 14-d CIDR-PG (14-d) and 7-d CO-Synch + CIDR (7-d) protocols on the basis of estrous response, pregnancy rates resulting from fixed-time AI (FTAI), and final pregnancy rates at the end of the breeding season in primiparous 2-yr-old beef cows. Cows assigned to the 14-d treatment (n = 355) received a CIDR insert on d 0 with removal on d 14. Cows assigned to the 7-d treatment (n = 349) received GnRH and CIDR inserts on d 23. On d 30 CIDRs were removed from cows assigned to the 7-d treatment and $PGF_{2\alpha}$ was administered to cows in both treatments. On d 33 GnRH was administered concurrent with FTAI at 66 and 72 h after $PGF_{2\alpha}$ for 7-d and 14-d treated cows, respectively. Estrus response at FTAI was higher for 7-d compared to 14-d treated cows (7-d = 74%; 14-d = 43%; $P < 0.0001$); however, pregnancy rates resulting from FTAI were similar between treatments (7-d = 64%; 14-d = 63%; $P = 0.52$). Furthermore, 87% and 88% of 14-d and 7-d treated cows conceived within the first 30 d of the breeding season, and final pregnancy rates at the end of the breeding season did not differ between treatments (7-d = 96%; 14-d = 95%; $P = 0.93$). To understand similarities between treatments in pregnancy rates resulting from FTAI, despite differences in estrous response rates before FTAI, ovaries were mapped and serum estradiol-17-β (E_2) concentrations were evaluated among a subset of cows in each treatment. The 14-d treated cows had smaller diameter dominant follicles at $PGF_{2\alpha}$ ($P = 0.04$) and FTAI ($P = 0.002$) compared to 7-d treated cows (10.9 ± 0.3; 13.0 ± 0.3; vs. 11.9 ± 0.4; 14.5 ± 0.3); however, serum E_2 concentrations at $PGF_{2\alpha}$ ($P = 0.06$) and FTAI ($P = 0.001$) were greater for 14-d vs. 7-d treated cows (3.7 ± 0.4; 8.0 ± 0.7 vs. 2.5 ± 0.4; 4.2 ± 0.8). These differences suggest that dominant follicles of 14-d treated cows remain in an active growth stage at the time FTAI is performed compared to 7-d treated cows in which growth of dominant follicles may have plateaued. This theory is supported from previous studies that report decreased aromatase activity in granulosa cells when growth of dominant follicles plateau compared to actively growing follicles. In summary, these data suggest that the 14-d CIDR-PG and 7-d CO-Synch + CIDR protocols may be used to effectively synchronize estrus before FTAI in primiparous 2-yr-old beef cows.

Key Words: artificial insemination, estrus synchronization, primiparous 2-yr-old beef cow

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1112 Comparing split-time AI pregnancy rates among non-estrous heifers based on administration of GnRH at AI.

B. E. Bishop*, J. M. Thomas, J. M. Abel, M. F. Smith, M. R. Ellersieck, S. E. Poock, and D. J. Patterson, *University of Missouri, Columbia.*

This experiment was designed to evaluate split-time artificial insemination (STAI) in beef heifers following administration of the 14-d (d) controlled internal drug release (CIDR)-prostaglandin $F_{2\alpha}$ (PG) protocol and to compare pregnancy rates among non-estrous heifers based on administration of GnRH at AI. Estrus was synchronized for 1138 heifers across six locations. Heifers received a CIDR insert (1.38 g progesterone) on Day 0 with removal on Day 14. Estrus detection aids (Estrotect) were applied at PG (25 mg) 16 d after CIDR removal on Day 30. Treatments were balanced across locations for heifers using reproductive tract score and weight. Split-time AI was performed at 66 and 90 h after PG, and estrus was recorded at these times. Heifers in both treatments that exhibited estrus by 66 h were inseminated at that time and did not receive GnRH, whereas AI was delayed 24 h until 90 h after PG for heifers that failed to exhibit estrus by 66 h. For heifers in treatment 1 that were inseminated at 90 h, GnRH (100 μg) was administered concurrent with AI at 90 h. Heifers in treatment 2 that were inseminated at 90 h did not receive GnRH. Estrous response did not differ between treatments at 66 h after PG (1 = 70%; 2 = 71%; $P = 0.58$) or during the 24 h delay period (1 = 59%; 2 = 52%; $P = 0.21$). There was no effect of treatment on total AI pregnancy rate (1 = 54%; 2 = 56%; $P = 0.60$) or on AI pregnancy rate for heifers inseminated at 66 h (1 = 58%; 2 = 62%; $P = 0.86$) or 90 h (1 = 44%; 2 = 39%; $P = 0.50$) after PG. Ovulation was confirmed via ultrasonography for a subset of heifers that failed to exhibit estrus before 90 h after PG. For heifers that failed to exhibit estrus by 90 h, ovulation rate did not differ between treatments (1 = 52%; 2 = 50%; $P = 0.64$) nor did AI pregnancy rate (1 = 24%; 2 = 15%; $P = 0.97$). In summary, when split-time AI was used in conjunction with the 14-d CIDR-PG protocol in heifers, comparable pregnancy rates were achieved without administering GnRH.

Key Words: beef heifer, gonadotropin-releasing hormone, split-time artificial insemination

1113 Comparing fixed-time artificial insemination to split-time artificial insemination with delayed administration of GnRH in postpartum beef cows. B. E. Bishop*, J. M. Abel, J. M. Thomas, M. F. Smith, S. E. Poock, M. R. Ellersieck, and D. J. Patterson, *University of Missouri, Columbia.*

This experiment was designed to compare pregnancy rates in postpartum beef cows following split-time (STAI) or fixed-time (FTAI) artificial insemination. Estrus was synchronized for 671 cows at seven locations following administration of the 7-d CO-Synch + CIDR protocol (100 μg GnRH + CIDR insert [1.38 g progesterone] on d 0; 25 mg prostaglandin $F_{2\alpha}$ [PG] at CIDR removal on d 7). Cows were assigned to treatments that were balanced across locations based on age, body condition score, and days postpartum at the time treatments were initiated. All cows in treatment 1 (n = 333; FTAI) were inseminated at 66 h after PG and GnRH was administered concurrent with insemination regardless of estrus expression. For cows in treatment 2 (n = 338), STAI was performed at 66 and 90 h after PG, and estrus was recorded at these times. Cows in the STAI treatment that exhibited estrus by 66 h were inseminated at that time and did not receive GnRH, whereas AI was delayed 24 h until 90 h after PG for cows that failed to exhibit estrus by 66 h. Gonadotropin-releasing hormone (100 μg) was administered concurrent with AI at 90 h only to cows failing to exhibit estrus. Estrus expression that occurred during the 24 delay period among cows assigned to the STAI treatment increased the total proportion of cows that expressed estrus before insemination (1 = 60%; 2 = 86%; P < 0.001). Pregnancy rates for cows inseminated at 66 h that exhibited estrus did not differ between treatments (1 = 58%; 2 = 58%; P = 0.93); however, pregnancy rates among non-estrous cows at 66 h was improved (1 = 35%; 2 = 51%; P = 0.01) among cows assigned to the STAI treatment when insemination was postponed by 24 h. Consequently, total AI pregnancy rate tended to be higher for cows that received STAI (1 = 49%; 2 = 56%; P = 0.06). In summary, following administration of the 7-d CO-Synch + CIDR protocol, total estrous response increased and pregnancy rates resulting from AI tended to be higher among cows assigned to STAI versus FTAI treatments.

Key Words: beef cow, fixed-time artificial insemination, split-time artificial insemination

1114 Split-time artificial insemination following synchronization of estrus with the 14-d CIDR-PG protocol in primiparous 2-yr-old beef cows. J. M. Abel*, B. E. Bishop, J. M. Thomas, M. R. Ellersieck, S. E. Poock, M. F. Smith, and D. J. Patterson, *University of Missouri, Columbia.*

This experiment was designed to test the hypothesis that estrous response and pregnancy rate following synchronization of estrus with the 14-d CIDR-PG protocol in primiparous 2-yr-old beef cows would be improved using split-time AI (STAI) compared to fixed-time AI (FTAI). Estrus was synchronized for 523 primiparous, postpartum beef cows at five locations. Cows received a CIDR insert (1.38 g progesterone) on d 0 with removal on d 14. On d 30, 16 d after CIDR removal, cows were administered $PGF_{2\alpha}$ (25 mg) and estrus detection aids (Estrotect) were applied. All cows were administered GnRH (100 μg) on d 33, 72 h after $PGF_{2\alpha}$ administration. Treatments were equally represented across locations, and cows within each location were assigned to one of two treatments based on days postpartum and body condition score. Cows assigned to the FTAI treatment (n = 266) were inseminated at a fixed-time concurrent with GnRH administration at 72 h after $PGF_{2\alpha}$ regardless of estrus expression, while cows assigned to the STAI treatment (n = 257) were inseminated based on estrus expression observed at 72 h. Cows assigned to STAI that expressed estrus by 72 h were inseminated; however, AI was delayed 24 h until 96 h after $PGF_{2\alpha}$ for cows that failed to express estrus before the standard fixed time. Estrus detection aids remained attached following GnRH at 72 h for all non-estrous cows assigned to the STAI treatment, and estrus expression during the delayed time period was recorded. Estrous response at 72 h did not differ between treatments (FTAI = 42%; STAI = 40%; P = 0.33). Delayed insemination to 96 h after $PGF_{2\alpha}$ of STAI treated cows that failed to exhibit estrus before the standard FTAI at 72 h increased total estrous response (FTAI = 42%; STAI = 64%; P < 0.0001); however, pregnancy rates resulting from AI were similar between treatments (FTAI = 56%; STAI = 55%; P = 0.60). In summary, estrus expression was increased when STAI was used following synchronization of estrus with the 14-d CIDR-PG protocol in primiparous 2-yr-old beef cows; however, this strategy did not result in significant improvements in AI pregnancy rates compared to FTAI.

Key Words: artificial insemination, estrus synchronization, primiparous 2-yr-old beef cow

1115 The 9-d CIDR-PG protocol: Incorporation of prostaglandin pretreatment into a long-term, CIDR-based estrus synchronization protocol improves timed AI pregnancy rates in postpartum suckled beef cows. *J.* M. Thomas*, B. E. Bishop, J. M. Abel, J. W. Locke, S. E. Poock, M. F. Smith, and D. J. Patterson, *University of Missouri, Columbia.*

An experiment was designed to test the hypothesis that pregnancy rates after fixed-time artificial insemination (FTAI) among postpartum suckled beef cows would be improved by incorporating pretreatment with prostaglandin $F_{2\alpha}$ (PG) into a long-term, CIDR-based estrus synchronization protocol. The 9-d CIDR-PG protocol, a modified protocol in which PG is used to facilitate a decreased length of progestin treatment, was compared to the 14-d CIDR-PG protocol. Protocols were compared on the basis of initial estrus response following

CIDR removal, final estrus response following the administration of PG, and pregnancy rate resulting from FTAI. Estrus was synchronized for 321 cows across three locations. Treatments were represented across locations, and cows within each location were randomly assigned to one of the two protocols based on age and body condition score (BCS). Cows assigned to the 14-d CIDR-PG treatment received a CIDR insert (1.38 g progesterone) on d 0 with removal of CIDR on d 14; 25 mg PG 16 d after CIDR removal on d 30; and 100 μg GnRH on d 33, 72 h after PG. Cows assigned the 9-d CIDR-PG treatment received 25 mg PG and a CIDR insert (1.38 g progesterone) on d 5; 25 mg PG and removal of CIDR on d 14; 25 mg PG 16 d after CIDR removal on d 30; and 100 μg GnRH on d 33, 72 h after PG. Estrus response following CIDR removal on d 14 did not differ between treatments (87% versus 85%, $P = 0.71$), and there was no difference in final estrus response following the administration of PG on d 30 (53% versus 50%, $P = 0.69$). A significant effect of treatment was found on pregnancy rate resulting from FTAI, with cows assigned to the 9-d CIDR-PG protocol achieving greater FTAI pregnancy rates than cows assigned to the 14-d CIDR-PG protocol (63% versus 53%, $P < 0.05$). Across treatments, greater pregnancy rates ($P = 0.06$) tended to be achieved by cows that expressed estrus before FTAI (69% for 9-d CIDR-PG, 57% for 14-d CIDR-PG) than were achieved by cows that failed to express estrus (57% for 9-d CIDR-PG, 48% for 14-d CIDR-PG). In summary, when using a long-term, CIDR-based estrus synchronization protocol among mature, suckled beef cows, FTAI pregnancy rates are improved through use of the 9-d CIDR-PG protocol.

Key Words: artificial insemination, beef cow, estrus synchronization

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1116 Requirement of GnRH administration at the onset of the 5 d CO-Synch + CIDR protocol in suckled beef cows.

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The objective of this experiment was to evaluate the requirement of GnRH administration at controlled internal drug release (CIDR) insertion in the 5-d CO-Synch + CIDR protocol (5dCO). Postpartum, suckled beef cows ($n = 2159$) from 11 herds at 5 universities were assigned by age, BCS, and days postpartum to receive either: 1) standard 5dCO hormone administration including 100 μL of GnRH at CIDR insert and 2 concurrent 25-mg doses of $PGF_{2\alpha}$ (PG) at CIDR removal (G2PG), 2) no GnRH at CIDR insert and 2 concurrent, 25-mg doses of PG at CIDR removal (NoG2PG), or 3) no GnRH at CIDR insert and a single, 25-mg dose of PG at CIDR removal (NoG1PG). Estrous response between PG and timed-AI (TAI) was determined using estrous detection aids. All cows were TAI 72 h after CIDR removal, concurrent with administration of 100 μL of GnRH. Estrous cyclicity before synchronization was determined using a combination of 2 blood samples collected 10 d apart and estrus detection aids administered approximately 24 d before CIDR insert. Transrectal ultrasonography was used on a subset of cows at both CIDR insert and removal to record all ovarian structures as well as to detect pregnancy 31 to 42 d after TAI. Data were analyzed using the MIXED and GLIMMIX procedures of SAS for continuous and binary response variables, respectively. Herd nested within university was included as a random effect. Number of total follicles and size of the largest 2 follicles at CIDR insertion were not different ($P \geq 0.34$). However, the largest follicle at CIDR removal was greater ($P = 0.02$) in NoG2PG than G2PG and NoG1PG (13.2, 11.5, and 12.1 ± 0.5 mm, respectively). Though estrus response was not different ($P = 0.99$) before TAI, detection aid activation was more advanced ($P = 0.01$) in NoG1PG than G2PG and NoG2PG. However, pregnancy to TAI did not differ ($P = 0.66$) among G2PG (55.4%), NoG2PG (52.8%), and NoG1PG (50.5%) treatments. Cows exhibiting estrus before TAI had greater ($P < 0.001$) TAI pregnancy rates (58.1%) than those not exhibiting estrus (39.3%) and cows determined to be cyclic at synchronization initiation had greater ($P < 0.001$) TAI pregnancy rates (53.6%) than non-cyclic cows (37.1%). In conclusion, TAI pregnancy rates were not negatively affected by removal of initial GnRH in the 5-d CO-Synch + CIDR protocol.

Key Words: 5-d CO-Synch, GnRH, synchronization

1117 Comparison of follicular dynamics and subsequent progesterone profiles in Brahman cows with either two or three ovarian follicular waves.

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The objective of this study was to identify differences in follicular dynamics in a *Bos indicus* bovine estrous cycle with 2 or 3 follicular waves (2FW or 3FW) and the subsequent progesterone profiles. Daily ultrasonography was performed on 15 multiparous Brahman cows through a complete estrous

cycle. Blood samples were collected daily from the coccygeal vein throughout the subsequent estrous cycle to determine serum progesterone concentrations by RIA. The ultrasound images were collected using a SonoSite M-Turbo ultrasound with a 7.5 MHz L52X transducer. Follicular data were analyzed using Proc Mixed procedures and serum progesterone data were analyzed using Proc Mixed procedures specific for repeated measures using SAS v9.3. The first FW from cows with 2 or 3 FW estrous cycles were compared and the ovulatory FW were compared. Size and day (d) of the dominant and largest subordinate follicle did not differ between 2 or 3 FW estrous cycles during either the first or ovulatory FW. As expected the length of the FW differed ($P < 0.01$) during the first (2FW = 11.90 ± 0.73; 3FW = 7.00 ± 1.03) and ovulatory FW (2FW = 10.80 ± 0.90; 3FW = 6.00 ± 1.27) between groups, respectively. The d the largest follicle appeared differed ($P < 0.01$) in the first (2FW = 9.5 ± 0.48; 3FW = 5.6 ± 0.67) and ovulatory FW (2FW = 9.8 ± 1.05; 3FW = 5.6 ± 1.47). The greatest number of antral follicles found differed during the first (2FW = 14.20 ± 1.60; 3FW = 6.00 ± 2.25) ($P < 0.01$) and ovulatory FW (2FW = 21.0 ± 2.00; 3FW = 12.5 ± 2.83) ($P = 0.025$). The serum progesterone profile of the following estrous cycle was normalized by analyzing the first 10 d after estrus (CL growth phase) and the 10 d before the succeeding estrus (CL regression phase). There was a tendency ($P = 0.08$) for an interaction between day and number of FW for the CL regression phase of the estrous cycle. The 3FW cows tended to have greater progesterone concentrations during the last 7d of the regression phase compared with the 2FW. These results suggest that cows with 2FW have greater a number of antral follicles within the first and ovulatory FW and the 3FW cows had increased serum progesterone concentrations during the CL regression phase of the subsequent estrous cycle.

Key Words: Brahman cows, follicular dynamics, serum progesterone.

1118 Effect of a progesterone-based estrous synchronization program for timed AI (TAI) on reproductive performance in a seasonal pasture-based dairy production system.

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The aim of this study was to investigate the effect of progesterone-based TAI programs on fertility in seasonal-calving pasture-based dairy herds. At 10 d before the mating start date (MSD), 840 lactating dairy cows on 3 seasonal-calving farms were blocked based on days in milk (DIM) and parity and randomly allocated to one of three treatments: (i) Control: no treatment, inseminated at detected estrus; (ii) P4-Ovsynch: cows received a 7-d progesterone-releasing intravaginal device (PRID®Delta) with 100 mg of GnRH analog (Ovarelin®) at PRID insertion, 25 mg injection of PGF2α (Enzaprost®) at PRID removal, GnRH at 56 h after device removal and TAI 16 h later; (iii)P4-Ovsynch+eCG: same as P4-Ovsynch, but cows received 500 IU equine chorionic gonadotropin (eCG; Syncrostim®) at PRID removal. At trial initiation all cows that were $\geq$ 30 DIM were ultrasound scanned to assess presence/absence of a corpus luteum (CL) and Body Condition Score (BCS) was also recorded. Pregnancy diagnosis was performed by transrectal ultrasonography 30–35d after insemination. Binary data were analyzed using the GLIMMIX procedure of SAS, and time-dependent data were analyzed using survival analysis. Overall, conception rate was not different between groups (51.0%, 52.0%, and 51.8% for Control, P4-Ovsynch, and P4-Ovsynch+eCG, respectively; $P = 0.9$), but the 21-d pregnancy rate was increased by the synchronization protocols (38.6%, 58.6%, and 53.6%; $P < 0.0001$). Supplementation with eCG at PRID removal did not affect pregnancy rate (53.3 vs. 52.5, P4-Ovsynch vs. P4-Ovsynch+eCG, respectively; $P = 0.9$). Compared to the Control group, synchronization treatments significantly reduced the interval from MSD to conception (36.7, 24.0, and 27.1 d, respectively; $P < 0.001$), and consequently reduced the average days open (87.0, 75.0, and 78.0 d, respectively; $P < 0.001$). Across all treatment groups, DIM at start of synchronization had a significant effect on conception rate (44.3%, 51.1%, and 59.5% for < 60, 60–80, and > 80 DIM, respectively; $P < 0.05$), but parity (49.7%, 51.5%, and 53.9% for parity 1, 2, and $\geq$ 3, respectively; $P = 0.7$), BCS (44.9%, 51.6%, and 58.6% for $\leq$ 2.50, 2.75–3.25, and $\geq$ 3.50, respectively; $P = 0.2$) and presence of a CL (51.7% vs. 51.7%; $P = 0.9$) did not have significant effects on the likelihood of pregnancy per AI. Additionally, there were no two-way interactions detected ($P > 0.05$) between treatment and DIM, parity, BCS, or CL status category. In conclusion, the use of TAI accelerated pregnancy establishment of cows in a pasture-based system by reducing days open, but eCG supplementation at PRID removal did not affect pregnancy rate.

Key Words: eCG, progesterone, synchronization, timed AI

1119 Hepatic gluconeogenic enzymes are differentially altered by methyl-donors choline and methionine in bovine primary hepatocytes. T. L. Chandler*[1], S. J. Bertics[1], B. A. Barton[2], and H. M. White[1], [1]*Department of Dairy Science University of Wisconsin, Madison,* [2]*Balchem Corporation, New Hampton, NY.*

Tricarboxylic acid cycle (TCA) and gluconeogenic carbon flux are controlled by balances of pyruvate carboxylase (*PC*) and phosphoenolpyruvate carboxykinase (*PEPCK*). The lipotropic action of choline and methionine may alter fatty acid (FA) oxidation and gluoneogenic carbon availability. The objective of this experiment was to examine regulation of genes controlling gluconeogenesis in response to increasing concentrations of choline chloride (CC), DL-methionine (DLM), and added FA. Primary hepatocytes isolated from 4 Holstein calves were maintained as monolayer cultures for 24 h in media containing optimal concentrations of essential amino acids and 1.25 m*M* pyruvic acid. Treatments of physiologically relevant concentrations of CC (33, 100, 2000, 4500 μ*M*) and DLM (16, 30, 100, 300 μ*M*), with or without a 1 m*M* FA cocktail, were added to a methionine-free media in a factorial design. After 24 h of treatment, cells were harvested for RNA isolation, cDNA generation, and quantification of gene expression by quantitative PCR. Abundance of mRNA was normalized to the geometric mean of three reference genes. Data were analyzed using PROC MIXED of SAS 9.4 with linear and quadratic contrasts in a model accounting for fixed effect of treatment and random effect of calf and reported as least squares means ± SE. Expression of *PC* tended to be linearly increased ($P = 0.06$) by CC (1.28, 1.42, 1.43, 1.50 ± 0.21 arbitrary units (AU)) and was unaffected ($P > 0.15$) by DLM (1.39, 1.51, 1.38, 1.35 ± 0.21 AU). Although, *mitochondrial PEPCK* (*PEPCKm*) expression was unaffected ($P \geq 0.15$) by CC (1.64, 1.58, 1.60, 1.59 ± 0.5 AU) or DLM (1.49, 1.57, 1.65, 1.69 ± AU), *cytosolic PEPCK* (*PEPCKc*) tended to be linearly increased ($P = 0.11$) by CC (1.03, 1.19, 1.30, 1.57 ± 0.32 AU) and decreased ($P = 0.08$) by DLM (1.60, 1.31, 1.21, 0.97 ± 0.32). Expression of *glucose 6-phosphatase* (*G6P*) was quadratically affected ($P = 0.009$) by CC (1.14, 1.42, 0.99, 1.13 ± 0.30) and unaffected ($P > 0.15$) by DLM (1.14, 1.17, 1.19, 1.17 ± 0.30). Treatment with FA increased ($P < 0.001$) expression of *PC* (1.11 vs. 1.70 ± 0.20 AU), *PEPCKc* (0.55 vs. 2.0 ± 0.27 AU), *PEPCKm* (1.36 vs. 1.84 ± 0.48 AU), and *G6P* (0.93 vs. 1.41 ± 0.29 AU). Coordinated increases in *PC* and *PEPCKc* with increasing CC suggests increased capacity for gluconeogenesis. Conversely, decreased *PEPCKc* without altered *PC* may indicate that DLM may increase TCA capacity but not gluconeogenic capacity. Choline and methionine appear to differentially regulate TCA cycle and gluconeogenesis.

Key Words: gluconeogenesis, methyl-donors, primary hepatocytes

1120 Expression of the putative gonadotropin-inhibitory hormone receptor, NPFFR1, in the anterior pituitary gland of the gilt is affected by age and sexual maturation. C. A. Lents*, J. F. Thorson, and D. J. Nonneman, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Gonadotropin-inhibitory hormone (GnIH) purportedly suppresses secretion of luteinizing hormone (LH) by acting through a G protein coupled receptor (NPFFR1) in the anterior pituitary gland and hypothalamus. The objective of these studies was to determine if expression of mRNA for NPFFR1 in the reproductive neurosecretory axis of gilts differed with age or sexual maturation. In Exp. 1, the anterior pituitary gland was collected from gilts at 24 (weaning), 60, 100, and 140 d of age ($n = 14$ to 16 per age). In Exp. 2, the anterior pituitary gland and medial basal hypothalamus were collected from gilts at 240 d of age. Gilts were classified ($n = 12$ to 14 per classification) as prepubertal, peripubertal, or cyclic (midluteal phase) based on estrus records and ovarian morphology at slaughter. Relative abundance of LHβ, FSHβ, CGA, GnRHR1, and NPFFR1 mRNA in pituitary glands from Exp. 1 and 2 and NPFFR1, GnRH1, NPY, POMC, and RFRP in hypothalami from Exp. 2 was measured with qPCR. Data were analyzed by ANOVA with age or reproductive classification as fixed effects. In Exp. 1, age did not affect expression of GnRHR1 or CGA. Expression of FSHβ at weaning was not different from 60 d of age but was greater ($P < 0.05$) than expression at 100 and 140 d of age. Compared to weaning, expression of LHβ was less ($P < 0.05$) at 60 d of age and greater ($P < 0.05$) at 100 d of age, but not different at 140 d of age. Pituitary expression of NPFFR1 was greater ($P < 0.05$) at 100 d of age compared with all other ages. In Exp. 2, prepubertal gilts had less pituitary expression of LHβ ($P < 0.02$) and greater pituitary expression of FSHβ ($P < 0.04$), CGA ($P < 0.001$), GnRHR1 ($P < 0.01$), and NPFFR1 ($P < 0.001$) than cyclic gilts. Expression of LHβ and GnRHR1 was intermediate in peripubertal gilts. Expression of FSHβ, CGA, and NPFFR1 in the pituitary did not differ between peripubertal and cyclic gilts. Expression of NPFFR1 in the hypothalamus of peripubertal gilts was less ($P < 0.05$) than in cyclic gilts. Reproductive classification did not affect hypothalamic expression of GnRH1, NPY, POMC, or RFRP. Increased expression of NPFFR1 in prepubertal gilts indicates an increased sensitivity to GnIH inhibition of LH secretion. Support: NIFA AFRI 2011–67015. USDA is an equal opportunity provider and employer.

Key Words: gene expression, pig, pubertal development,

1121 Role of focal adhesion molecules in maternal recognition of pregnancy in the mare.
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The mechanism responsible for maternal recognition of pregnancy (MRP) in the mare remains unknown. During early pregnancy the equine conceptus and endometrium communicate to attenuate prostaglandin $F2_{\alpha}$(PGF) secretion thus sparing the corpus luteum and maintaining progesterone production. Based on previous experiments we identified focal adhesion molecules (FAM) as potentially playing a key role in this process. We hypothesize that contact of an embryo with equine endometrium causes (i) a change in FAM transcription and (ii) decrease PGF secretion. We designed an in vitro experiment to test this hypothesis. Endometrial biopsies were obtained from mares in a crossover design, with each mare providing samples from a pregnant and non-pregnant (non-mated) control cycle (n = 3/sample day) on d 9 and 11 post-ovulation, a critical time immediately before and during MRP. Pregnancy was confirmed by ultrasonography and presence of an embryo following uterine lavage. Mares were matched by day and embryos collected were used in co-culture experiment. Endometrial samples were divided and placed in culture with or without contact by an equine embryo for 24 h. Total RNA from endometrial biopsies was evaluated by qPCR using primers designed to detect 22 equine-specific FAM transcripts and ELISA was used to assay PGF content in medium. All comparisons were made within day between groups and pregnancy status. Differential expression of 4 and 6 FAM were noted in samples collected on d 9 ($P \leq 0.02$) and 11 ($P \leq 0.05$), respectively, when compared by pregnancy status alone. No changes were detected in FAM expression in samples collected from pregnant mares due to the presence or absence of an embryo, while 1 and 4 FAM differed when embryos were co-cultured with endometrial samples from non-mated mares at d 9 (P = 0.04) and 11 ($P \leq 0.04$), respectively. Secretion of PGF was not attenuated with embryo contact on d 9 regardless of pregnancy status. Embryo contact resulted in dramatic decreases (P < 0.003) in PGF secretion in samples collected from both pregnant and non-pregnant mares 11 d post-ovulation. These data support our hypothesis that FAM expression is altered with the presence of an embryo and implicates FAM in the modulation of PGF secretion. Together these provide new insight into a potential mechanism for MRP in mares.

Key Words: embryo, endometrium, equine, focal adhesion molecule, maternal recognition of pregnancy

1122 Modification of embryonic resistance to heat shock in cattle by melatonin and genetic variation in HSPA1L.
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Seeking for new methods to reduce the effect of heat stress on fertility we examined 1) whether melatonin blocks inhibition of embryonic development caused by heat shock and 2) whether frequency of a thermoprotective allele for *HSPA1L* is increased in blastocysts formed from heat-shocked zygotes as compared to blastocysts from control zygotes. It was hypothesized that melatonin prevents effects of heat shock on development by reducing accumulation of reactive oxygen species (ROS). Effects of 1 μM melatonin on ROS were determined in Exp. 1 and 2. Zygotes were cultured at 38.5 or 40°C for 3 h in the presence of CellROX® reagent. Culture was in a low [5% (v/v)] oxygen (Exp. 1) or low or high [21% (v/v)] oxygen environment (Exp. 2). Heat shock and high oxygen increased ROS; melatonin decreased ROS. In Exp. 1, for example, fluorescent intensity at 38.5°C was 346 ± 54 and 451 ± 51 and 769 ± 47 and 361 ± 50 at 40°C for control and melatonin-treated embryos (interaction, $P < 0.0001$). Development was assessed in Exp. 3–5. In Exp. 3 and 4, zygotes were cultured in low oxygen + 1 μM melatonin and exposed to 38.5 or 40°C for 12 (Exp. 1) or 24 h (Exp. 2) beginning 8 h after fertilization. Melatonin was not thermoprotective in either experiment. Exp. 5 was performed similarly except that temperature treatments (38.5 or 40°C, 24 h) were performed in a low or high oxygen environment (2 x 2 x 2 factorial design with temperature, melatonin, and oxygen concentration as main effects). Heat shock decreased (P = 0.003) percent of zygotes developing to the blastocyst stage (26 ± 1.5 vs. 20 ± 1.5%) independent of melatonin or oxygen concentration. For Exp. 5, blastocysts were genotyped for a deletion (D) mutation (C®D) in the promoter region of *HSPA1L* associated with thermotolerance. Genotype was affected by temperature (P = 0.002). The percent of blastocysts CC, CD, or DD was 43.3, 28.5, and 28.2% for blastocysts from control zygotes and 32.4, 36.0, and 31.6% for blastocysts from heat-shocked zygotes. It was concluded that 1) lack of effect of melatonin or oxygen concentration on embryonic development means that the negative effects of heat shock on the zygote are not mediated by ROS, 2) previously reported effect of melatonin on fertility of heat-stressed cows might involve actions independent of the antioxidant properties of melatonin, and 3) the deletion mutation in the promoter of *HSPA1L* confers protection to the zygote from heat shock. Perhaps, embryonic survival during heat stress could be improved by selecting for thermotolerant genotypes (Support: BARD US-4719–14).

Key Words: heat shock, melatonin, reactive oxygen species, *HSPA1L*

1123 Transgenerational paternal influence on temperament and growth performance of crossbred beef calves. R. C. Vann[*1], B. P. Littlejohn[2], C. R. Long[3], T. H. Welsh, Jr.[2], and R. D. Randel[4], *[1]MAFES-Brown Loam Experiment Station, Mississippi State University, Raymond, [2]Texas A&M AgriLife Research and Department of Animal Science, College Station, [3]Texas A&M AgriLife Research, Overton, [4]Texas A&M AgriLife Research, Texas A&M University System, Overton.*

The objective was to evaluate the transgenerational paternal influence on temperament characteristics and growth performance in a group of crossbred calves sired by bulls that did or did not experience prenatal stress (PNS). These sires were derived from a purebred Brahman population in which dams were assigned to receive 1 of 2 treatments, control (CTRL; $n = 42$) or PNS ($n = 43$). Cows in the PNS group were subjected to 2 h of transportation at 60, 80, 100, 120, and 140 d of gestation (Littlejohn et al., 2016). From this group, 3 sexually mature control and 3 PNS Brahman bulls were mated with mature cows (20 cows per bull) to produce a second generation of calves. These crossbred calves were evaluated for temperament utilizing pen score (PS; 1 = calm and 5 = excitable), exit velocity (EV; m/sec), and temperament score (TEMP; PS+EV/2) at weaning (d 0; adjusted 205 d), d 28, and d 56. At these same time points body weights were recorded. All data were analyzed using Mixed Models Procedures of SAS. Treatment of sire and sex of calf were included as fixed effects. Male calves had greater birth weights compared to females ($P < 0.001$). Steers had greater adjusted 205 d, d 28, and 56 BW ($P < 0.005$) compared with heifers. Calves from PNS sires had greater ($P < 0.001$) adjusted 205 d BW compared to calves from CTRL sires but this did not carry through d 28 or 56. Male calves from PNS sires had greater ($P < 0.001$) adjusted 205 d BW, male calves from CTRL sires and female calves from PNS sires were intermediate and female calves from CTRL sires had the lowest adjusted 205 d BW. Male and female calves from CTRL sires had the greatest PS ($P < 0.002$), EV ($P < 0.05$) and TEMP ($P < 0.002$) scores at weaning compared to male and female calves from PNS sires. Individual sire influenced ($P < 0.05$) all measures of temperament and BW. Weaning TEMP score was highly ($P < 0.001$) correlated to TEMP scores at d 28 and 56 (0.66 and 0.68, respectively). Calves from CTRL sires had greater TEMP scores at weaning; however, by d 56 these differences had diminished. Calves from PNS sires had greater adjusted 205 d BW; however, these differences in BW at weaning, d 28 or 56 were not apparent where adjustments for age of dam and sex of calf were not included. Temperament measures in PNS were lower than for CTRL calves.

Key Words: beef calves, temperament, transgenerational

1124 DNA methylation is a possible basis of phenotypic alterations observed in suckling Brahman calves. B. P. Littlejohn[*1,2], D. M. Price[1,2], D. A. Neuendorff[2], C. R. Long[2], J. A. Carroll[3], R. C. Vann[4], T. H. Welsh, Jr.[1], and R. D. Randel[2], *[1]Texas A&M AgriLife Research and Department of Animal Science, College Station, [2]Texas A&M AgriLife Research, Texas A&M University System, Overton, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [4]MAFES-Brown Loam Experiment Station, Mississippi State University, Raymond.*

The objective of this experiment was to examine DNA methylation as a potential basis for phenotypic alterations observed in prenatally stressed (PNS) compared to control calves (Littlejohn et al., 2016). Previously, 41 of 85 mature Brahman cows were transported for 2-h periods at 60, 80, 100, 120, and 140 d of gestation, while the remaining cows were controls ($n = 44$). All calves born to control and transported dams (PNS group) were evaluated to determine phenotypic differences in temperament, circulating concentrations of cortisol, immune

Table 1124.

Table 1. Enumeration of strongly hypermethylated and strongly hypomethylated genes in PNS (n=7) compared to control (n=7) bull calves.

	Immune Function	Metabolic Function	Behavior/ Stress/Neural Function	Reproductive Function	Cell Signaling/Gene Function
Strongly Hypermethylated Genes	4	13	3	2	25
Strongly Hypomethylated Genes	14	15	9	2	23

function, and metabolism as suckling calves. At 28 d of age each calf was restrained for collection of jugular blood samples. Buffy coat cells were harvested from whole blood and stored at −80 C. DNA was isolated from buffy coat cells of 7 PNS and 7 control bulls using phenol-chloroform extraction procedures and the samples were analyzed using reduced representation bisulfite sequencing (Zymo Research; Irvine, CA) to determine differential methylation of DNA. Reported genes were differentially methylated ($P < 0.015$) in PNS compared to control calves (Table 1). Genes that were defined as strongly hypermethylated ($n = 41$) were $\geq$ 33% more methylated in PNS than control bulls, while genes that were defined as strongly hypomethylated ($n = 49$) were $\geq$ 33% less methylated than controls. Reported genes were related to immune function, metabolic function, behavior/stress/neural function, reproductive function, and cell signaling/gene function. Several genes were ascribed to multiple functions. Differentially methylated genes related to phenotypic alterations observed in PNS compared to control bull calves suggest epigenetic programming of biological systems in utero.

Key Words: calves, DNA methylation, prenatal stress

1125 Photoperiod manipulations during the dry period significantly impact mammary circadian clock in goats. S. J. Mabjeesh[*1], A. Shamay[2], K. Plaut[3], C. Sabastian[1], and T. M. Casey[3], *[1]Department of Animal Sciences, The Robert H. Smith Faculty of Agriculture, Food and Environment, The Hebrew University, Rehovot, Israel, [2]Institute of Animal Science, The Volcani Center, Bet Dagan, Israel, [3]Department of Animal Sciences, Purdue University, West Lafayette, IN.*

Exposing goats to short day photoperiod (SDPP; 8 h light:16 h dark) during the dry period increases milk production compared to long day photoperiod (LDPP; 16 h light:8 h dark) exposure, due in part to increased mammary cell proliferation rates. Photoperiod information is sent to the master clock in the suprachiasmatic nuclei (SCN) via the retinal nerve. In turn the SCN sends temporal information out to peripheral clocks located in every tissue of the body to synchronize physiological systems to time of day and season. Studies support mammary clock regulates cell proliferation, thus we hypothesized photoperiod effects on milk production are mediated in part by changes in the molecular clock located in mammary gland. The objective of this study was to determine the effect of photoperiod manipulation during the dry period in goats on core clock gene expression in mammary gland. Multiparous Israeli Saanen goats ($n = 6$) were blocked at dry off (?45 d prepartum) into 2 treatments: LDPP ($n = 3$) and SDPP ($n = 3$) based on body weight and previous milk production. All goats were housed in metabolism chambers equipped with two separate but identical environmentally controlled rooms in which photoperiod was adjusted according to the treatment. Goats were fed a total mixed ration in two equal meals at 0800 and 1500 to meet nutritional demands. Serial mammary biopsies were taken over a 24 h period from each goat during 3 wk prepartum at 4 h intervals (0900, 1300, 1700, 2100, 0100, 0500). Tissue was placed in Trizol and immersed in liquid nitrogen. Total RNA was isolated and q-PCR was used to measure expression of two reference genes (BACTIN and GAPDH) and the core clock genes CLOCK and ARNTL. Relative gene expression was calculated using delta-delta CT method with mean of SDPP treatment as normalizer. Exposure to SDPP significantly increased ARNTL ($P < 0.05$) while significantly decreasing CLOCK gene expression. CLOCK and ARNTL heterodimerize to function as a transcription factor, thus changes in their abundance due to photoperiod manipulation will affect expression of target genes, including those that regulate cell proliferation.

Key Words: ARNTL, CLOCK, photoperiod

1126 Management and genetic components of fertility indicators in dairy cattle. T. M. Goncalves[*1], D. Gonzalez-Pena[2], H. Jeong[1], P. J. Pinedo[3], J. E. P. Santos[4], G. M. Schuenemann[5], G. J. M. Rosa[6], R. O. Gilbert[7], R. C. Bicalho[8], R. Chebel[4], K. N. Galvão[9], C. M. Seabury[10], W. W. Thatcher[11], and S. L. Rodriguez Zas[12], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Zoetis, Kalamazoo, MI, [3]Colorado State University, Fort Collins, [4]University of Florida, Gainesville, [5]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, [6]University of Wisconsin-Madison, Madison, [7]Cornell University College of Veterinary Medicine, Department of Clinical Sciences, Ithaca, NY, [8]Cornell University, Ithaca, NY, [9]Department of Large Animal Clinical Sciences, University of Florida, Gainesville, [10]Texas A&M University, College Station, [11]Department of Animal Sciences, University of Florida, Gainesville, [12]University of Illinois, Urbana.*

Management and genetic strategies are employed to attain high fertility rates in dairy farms. These high rates in turn enable higher profits from higher milk production, higher replacement rates, higher genetic progress, and lower expenses compared to those in systems with lower fertility efficiency. The goal of this study was to characterize the joint effect of management and genetic variation on fertility indicators that are linked to the cost-effectiveness of diary production systems. Fertility, disease, production, environment, and pedigree records from over 6000 Holstein cows across the U.S Pacific, Southeast, Midwest, and Southwest regions were analyzed. Binary fertility variables included pregnancy at first and second artificial insemination (AI), pregnancy loss after first and second AI, ovarian cyclicity status, and open status +100 d after calving. Explanatory variables included AI method, farm, lactation number, season, body condition

score at 35 d post-calving, milk yield during the first three test-days, retained placenta, twin calving, dystocia, ovarian cyclicity status, open status +100 d after calving, pregnancy at first AI, and pregnancy loss after first AI. Sire of the cow was the random effect in the models. First lactation cows had significantly higher odds of pregnancy at first AI, higher odds of +100 d open status, lower odds of cyclicity than later lactation cows. The odds of pregnancy loss after first and second AI tended to be lower in first lactation cows relative to higher lactation cows. Cyclicity was significant and negatively associated with the odds of pregnancy loss at second AI and was positively correlated with pregnancy loss at first AI, albeit not significant. Calving of twins significantly reduced the odds of cyclicity. Retained placenta and timed AI were associated with significantly higher odds of +100 d open status than estrus-guided AI and not retained placenta, respectively. Higher body condition score was positively and significantly associated with odds of cyclicity. The odds of pregnancy after first and second AI were lower among cows calving during summer relative to winter; likewise, the odds of pregnancy loss after first and second AI were higher during the summer. Heritability estimates for the fertility variables studied ranged from 0.03 (pregnancy at first AI) to 0.12 (pregnancy loss at first AI). These results highlight availability of genetic variation and the major relevance of non-genetic component on fertility indicators. These findings contribute to a long-term multistate project database (USDA-NIFA-AFRI-003542) for direct measures of fertility.

Key Words: milk, pregnancy, reproduction

1127 Effects of OmniGen-AF® on superovulation response and embryo quality in donor beef cows.

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Superovulation is a required yet costly and biologically stressful procedure in cattle embryo transfer. High variation in the number of ova recovered, fertilization rates, and embryo quality result in inconsistent results and prevent full optimization of the procedure for genetic improvement. Inflammation and immune system dysregulation have been suggested to be one cause of this variability. Therefore, the objective of this study was to evaluate OmniGen-AF® (OG) supplementation on superovulatory response, embryo quality, and serum cortisol in beef cattle embryo donors using two doses of follicle stimulating hormone (FSH). Twenty-four cross-bred beef cows were split into four groups and superovulated with 200 or 400 mg FSH and fed OG at 0 or 56 g/hd/day. The feeding period was 49 d. The superovulation protocol was started on Day 28 of feeding and ova were nonsurgically recovered 7 d after estrus and artificial insemination. Good to excellent quality morulae and blastocysts were either fixed for staining or cultured to evaluate in vitro embryo development and plasminogen activator (PA) production. In cows superovulated with 400 mg FSH, feeding OG decreased the percent degenerate embryos recovered ($p = 0.08$). Embryos recovered from cows superovulated with 400 mg FSH and fed OG produced more total PA, with a trend for peak PA production to be higher at 72 h of culture ($p = 0.08$), compared to all other groups. In addition, serum cortisol concentration was significantly lower ($p = 0.049$) in donor cows fed OG at the last breeding of the superovulation protocol compared to controls. In summary, feeding OmniGen-AF may ameliorate negative effects of the higher FSH dose used in superovulation protocols resulting in more transferable and fewer degenerate embryos. Also based on PA production, there is a potential for healthier embryos, with a greater likelihood of developing beyond hatching in an embryo transfer procedure.

Key Words: embryo, OmniGen-AF®, superovulation

1128 OmniGen-AF® reduces basal plasma cortisol as well as cortisol release to adrencocorticotropic hormone or corticotrophin releasing hormone and vasopressin in lactating dairy cows under thermoneutral or acute heat stress conditions.

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Differences in the adrenal cortisol response of OmniGen-AF® (OG) supplemented and control dairy cows to a corticotrophin releasing hormone (CRH) and vasopressin (VP) or an adrenocorticotropic hormone (ACTH) challenge when housed at different temperature-humidity indices (THI) were studied. Holstein cows ($n = 12$; 162 ± 1 DIM) were balanced for milk yield, BW and DIM and randomly assigned to 1 of 2 trts: 1) OminGen-AF, supplemented with OG at 56 g/hd/day for 70 d; or 2) Control (CON), no supplement. Cows were moved to individual tie stalls in 1 of 2 temperature controlled chambers on d 45 and fitted with indwelling rectal temperature (RT) devices and jugular catheters on d 52. Initially THI was cycling at thermoneutrality (TN; THI < 72 for 24 h/d) for 10d, followed by heat stress (HS, THI > 72 for 12h/d) for 10 d. Cows were challenged with CRH (0.3 μg/kg BW) and VP (1 μg/kg BW) at 1000 h on d 6 of TN (d 53 of study) and d 1 of HS (d 57 of study), and with ACTH (0.1 IU/kg BW) at 1000 h on d 7 of TN and d 2 of HS. Blood samples were collected from −2 to 8 h at 30-min intervals relative to each challenge and serum was analyzed for cortisol and corticoid-binding globulin (CBG). Mean

serum cortisol concentration before challenge was lower in OG fed cows compared to CON (9.24 vs. 15.80 ng/ml, $P < 0.003$). Mean serum cortisol concentration was also lower in OG-fed cows compared to CON challenged with ACTH during both TN (27.2 vs. 43.4 ng/ml, $P < 0.01$) and acute HS (11.2 vs. 47.8 ng/ml, $P < 0.01$). Mean plasma cortisol concentrations tended to be lower in OG-fed animals compared to CON cows infused with CRH-VP during TN (38.2 vs. 44.9 ng/ml, $P < 0.06$) and were lower than CON cows infused with CRH-VP during acute HS (49.8 ng/ml vs. 78.3 ng/ml, $P < 0.01$). Mean serum CBG concentration was lower following ACTH infusion than following CRH-VP (753.2 vs. 913.3 ng/ml, $P < 0.01$). OG supplementation had no effect on serum CBG concentrations under TN or HS conditions in this study. However, serum CBG concentrations were elevated by HS in both CON and OG-fed animals following CRH-VP infusion, (1033 vs. 795 ng/ml, $P < 0.01$). Basal serum cortisol was reduced in cows supplemented with OG. In addition, the cortisol response to ACTH and CRH-VP was reduced in OG-fed cows compared to CON and this difference was enhanced during acute heat stress.

Key Words: ACTH, cortisol, heat stress, OmniGen-AF

1129 Reproductive performance with automated activity monitoring or a timed insemination program for first insemination in dairy cows.

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The objective of this study was to compare reproductive performance in lactating cows inseminated exclusively with timed artificial insemination (TAI) or with maximal use of an automated activity monitoring (AAM) system for the first insemination postpartum. From April 2014 to December 2015, a total of 998 cows in two herds in Ontario were randomly assigned to be inseminated at 85 ± 3 d in milk (DIM) following a Double Ovsynch protocol (DO), or be inseminated following detection of estrus by the AAM system between 50 and 75 DIM. In the AAM group, if estrus had not been signaled by 75 DIM, cows received the Ovsynch protocol and were inseminated at 85 ± 3 DIM. After first insemination, cows were managed according to routine herd management programs (combination of AAM and timed AI). The odds of pregnancy at first insemination and by 88 DIM were used as the outcome for logistic regression models. Models were adjusted for herd and parity as fixed effects, and interactions between treatment and covariates were tested. Analyses were done on cows that completed the protocol as assigned (completed protocol basis, $n = 719$) and on all cows that were not culled before first insemination (intention to treat basis, $n = 849$). The odds of being pregnant to first insemination were higher for cows in the DO group than in the AAM group in the intention-to-treat analysis (0.56 vs. 0.42, $P = 0.05$), but were not statistically significant (0.58 vs. 0.45, $P = 0.12$) for the completed protocol analysis. The odds of being pregnant by 88 DIM tended to be higher for cows in the AAM group than in the DO group, but was not statistically different for the completed protocol (0.74 vs. 0.59, $P = 0.13$) or the intention–to-treat analyses (0.70 vs. 0.56, $P = 0.11$).There was an interaction of treatment with herd in both models, such that more cows in the AAM group were pregnant by 88 DIM in one herd, but there was no difference in the other. In this study, the exclusive use of Double Ovsynch had a higher probability of pregnancy at first AI than AAM, but earlier insemination in the AAM group and the possibility of re-insemination resulted in no statistical difference in the proportion of cows pregnant by 88 DIM. There were differences in the relative performance of TAI and AAM between herds.

Key Words: automated activity monitoring, Double Ovsynch, reproductive performance

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1130 Establishing fertility benchmarks for in-line automated milk progesterone monitoring in postpartum dairy cows.

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Milk progesterone (MP4) concentrations in postpartum dairy cows are indicative of ovarian cyclicity. The adoption of automated in-line MP4 monitoring on farm has created the need for benchmarks to better understand MP4 data across cows, parities, farms, etc. The objective was to establish useful fertility benchmarks for in-line MP4 records. MP4 records ($n = 135,588$) from an automated milk progesterone sampling system (Herd Navigator; DeLaval International, Tumba, Sweden) were used. The records were from 1224 lactations of 1505 lactating cows in 4 European herds from January 2014 to December 2015. Farms started monitoring MP4 by 20 d postpartum. Excluded cows did not have MP4 samples before 30 d postpartum, lacked a defined ovulation (MP4 < 3ng/mL followed consecutively by MP4 > 3ng/mL), or lacked consistent MP4 records. The LIFETEST and GLM procedures of SAS 9.4 (Cary, NC) were used to test for differences among farm, parity, and milk yield for commencement of luteal activity (CLA) and length of postpartum estrous cycle. CLA was defined by MP4 > 3ng/mL on 20 to 22 d for initial samples or by a defined ovulation thereafter. Length of estrous cycle was the difference between the two ovulations. Cows were classified as primiparous, mature (2 to 4 lactations), or aged (> 4 lactations). The UNIVARIATE procedure was used to classify daily milk yield (Q1: < 25 kg/day, Q2: 25 to 33 kg/day, Q3: 34 to 41kg/day, Q4: > 41kg/day). The mean interval to CLA was 28.7 ± 14.6 d for all farms. Farm 4 had more cows (103/308 cows) not achieving CLA by 50 d postpartum than the other farms ($P < 0.001$). Aged cows (28/114, 25%) failed to achieve CLA by 50 d postpartum compared with primiparous cows (13/148; $P < 0.05$). Highest producing cows (Q4) failed to

achieve CLA by 40 d postpartum compared with cows producing less than 33kg/day ($P < 0.001$). Length of estrous cycle was shorter for farms 1 and 2 (21.8 ± 0.4d) compared with 22.7 ± 0.4 and 23.0 ± 0.4d for farms 3 and 4, respectively ($P < 0.05$). Length of estrous cycle differed ($P < 0.001$) for primiparous, mature, and aged cows, 21.3 ± 0.2d, 22.7 ± 0.2d, and 23.0 ± 0.5d, respectively. Strategic sampling of MP4 concentrations using an automated system identified differences between herds, parities, and milk production with respect to ovarian cyclicity. Establishing benchmarks based on these data will enable producers to assess ovarian function and the underlying causes of infertility in their herds.

Key Words: fertility, in-line milk progesterone, ovulation

1131 The effects of aspirin on pregnancy rates and pregnancy specific protein B in lactating dairy cows during the summer. J. A. Spencer*[1], K. G. Carnahan[1], B. Shafii[1], J. Dalton[2], and A. Ahmadzadeh[1], [1]*University of Idaho, Moscow,* [2]*University of Idaho, Caldwell.*

The occurrence of embryonic loss in cattle may be due to a hormonal imbalance and untimely secretion of $PGF_{2\alpha}$ around the time of maternal recognition on Days 14–16 after fertilization. The objective of this study was to examine the effect of aspirin, a non-steroidal anti-inflammatory drug, on pregnancy rates (PR) and blood pregnancy specific protein B (PSPB) in lactating dairy cows bred more than once and during the summer months. On Day 14 after two or more AI, 556 cows, from a commercial drylot herd in the Pacific Northwest, were assigned randomly to aspirin (total of 187.2 g; $n = 277$) or control ($n = 279$) treatment groups. Aspirin was administered orally with a balling gun 24 h apart on Day 14 and 15 (93.6 g/dose) after AI, whereas the control group was subjected to oral stimulation. On Day 25 following AI, blood samples were collected from a subset of cows ($n = 192$) and measured for PSPB concentrations. Pregancy status was determined by palpation per rectum between Day 32 to 40 post-AI. The maximum daily ambient temperature ranged from 27 to 39.4°C during the trial period. To estimate the effect of aspirin on PR/AI, a logistic regression model was used. Concentrations of PSPB were analyzed using the analysis of variance. There were no differences in PR/AI ($P > 0.05$) between aspirin (21.7%) and control (27.6%) groups. There was no effect of parity (primiparious 26.2% vs. multiparous 23.8%) or number of inseminations (TBRD) (second and third 26.2% vs. ≥ 4 21.5%) on PR/AI. There was also no effects of treatment or treatment by pregnancy status on PSPB concentrations ($P > 0.05$). Blood PSPB concentrations were 122.8 ± 8.1 and 127.8 ± 6.4 pg/mL for the aspirin and control groups, respectively. However, PSPB concentrations tended to be greater in multiparous cows compared with primiparous cows (132.7 ± 5.7 vs. 118.1 ± 7.3 pg/mL, $P = 0.07$). In addition, PSPB concentrations tended to be greater ($P = 0.07$) for second and 3rd TBRD (133.1 ± 5.3 pg/mL) than ≥ 4 TBRD (117.6 ± 7.8 pg/mL). These results indicate that aspirin may not have an effect on PR/AI or PSPB concentrations in lactating dairy cows subjected to two or more AI during hot summer months in the Pacific Northwest.

Key Words: aspirin, dairy cow, fertility

1132 Temporarily decreasing progesterone after timed artificial insemination decreased expression of ISG15 in blood leukocytes, serum PSPB concentrations, and embryo size in lactating Holstein cows. P. D. Carvalho, C. E. Consentini, S. R. Weaver, R. V. Barletta, L. L. Hernandez, and P. M. Fricke*, *Department of Dairy Science, University of Wisconsin, Madison.*

Our objective was to evaluate the effect of temporarily decreasing progesterone (P4) after timed artificial insemination (TAI) in dairy cows. Lactating Holstein cows ($n = 80$) were synchronized for first TAI using a Double-Ovsynch protocol, and were randomly assigned to receive 12.5 mg $PGF_{2\alpha}$ (dinoprost tromethamine) 5 d after the last GnRH treatment (LowP4) or serve as untreated controls (HighP4). Blood samples were collected thrice weekly from 5 to 32 d after TAI for all cows and from 32 to 67 d for pregnant cows, and were analyzed for P4 and PSPB concentrations. Expression of interferon-tau stimulated gene 15 (ISG15) was assessed in blood leukocytes 18 and 20 d after TAI. Pregnancy diagnosis was performed weekly using ultrasound from 32 to 67 d after TAI, and embryo size (crown-rump length) was measured 32, 39, and 46 d after TAI. Data were analyzed by ANOVA and logistic regression using the MIXED and GLIMMIX procedures of SAS. LowP4 cows had less ($P < 0.01$) P4 than HighP4 cows from 6 to 11 d after TAI, however, pregnancy outcomes 32 d after TAI [43% (17/40) for both treatments, $P = 0.97$] and pregnancy loss from 32 to 67 d after TAI [6% (1/17) vs. 6% (1/17) for LowP4 and HighP4, $P = 0.84$] did not differ between treatments. HighP4 cows diagnosed pregnant 32 d after TAI had greater ($P < 0.05$) expression of ISG15 20 d after TAI than LowP4 cows diagnosed pregnant 32 d after TAI (7.7 vs. 4.9-fold increase from d 4). Pregnant HighP4 cows had greater ($P < 0.01$) PSPB concentrations from 25 to 67 d after TAI than pregnant LowP4 cows. Embryo crown-rump length did not differ between treatments 32 and 39 d after TAI, but HighP4 cows had larger ($P < 0.05$) embryos 46 d after TAI (26.0 ± 1.0 vs. 23.5 ± 1.0 mm). We conclude that treatment with 12.5 mg of $PGF_{2\alpha}$ 5 d after induction of ovulation temporarily decreased P4 concentrations from 6 to 11 d after TAI without inducing luteal regression. Decreasing P4 after TAI decreased expression of ISG15 in blood leukocytes 20 d after TAI, serum PSPB concentrations 25 to 67 d after TAI, and embryo size 46 d after TAI but did not affect P/AI in lactating Holstein cows. Supported by USDA NIFA Hatch project 1006519.

Key Words: embryo, ISG15, progesterone, PSPB

1133 Effects for fertility of processing steps of a new technology platform for producing sexed sperm. M. A. Faust*, J. Betthauser, A. Storch, and S. Crego, *ABS Global, Inc., De Forest, WI.*

To understand the importance for fertility of key processing steps used in the production of sexed sperm, we conducted a series of field trials in U.S. dairy herds. Steps studied were: staining and processing in the absence of laser excitation (1), excitation laser power (2), and the presence of bisected sperm and debris resulting from laser-based cell destruction (3). For experiment 1, split or coincident collections from 8 dairy bulls were used to produce STAINED-L (2×10^6 motile sperm/straw) and untreated controls (CON-H, 10×10^6 sperm). The STAINED-L comprised sperm stained using Hoechst 33342 and subjected to all steps of the sexing process but with no exposure to laser excitation. Conception rates (CR) in Holstein heifers were 56.1% ± 2.8% (n = 312 pregnancy diagnoses) for STAINED-L and 66.7% ± 2.6% (n = 330) for CON-H. For experiment 2, one collection from each of 4 Holstein bulls was split to create untreated CON-L and stained treatments receiving low, medium, and high laser power during excitation. Post-thaw, these 4 treatments contained similar numbers of progressively motile sperm/straw (0.90 to 1.41 $\times 10^6$). When used in virgin heifers, CR for all laser excited treatments were lower than CON-L ($P < 0.01$), and were 58.7% ± 2.0% (n = 591) for CON-L and 45.2% ± 3.6% (n = 186), 44.9% ± 3.5% (n = 205), and 39.1% ± 3.5% (n = 192) for low, medium, and high laser excitation power, respectively. For experiment 3, TRT-L containing 3×10^6 bisected sperm + 2×10^6 unprocessed sperm was compared to matched untreated controls (CON-L, 2×10^6 sperm), and contemporaneously produced high dosage controls (CON-H, 10×10^6 sperm). The TRT-L was produced by processing an aliquot from each ejaculate through the laser detection + laser-destruction system set to bisect 90% of sperm and after each 1 h of collection, combining equal portions of bisected and unprocessed spermatozoa. Post-thaw, matched low dosage fractions contained similar numbers of progressively motile sperm/straw (1.1 to 1.7 $\times 10^6$ for TRT-L and CON-L), but differed markedly in percentage of bisected sperm (69 to 79% and 32 to 59% non-motile, respectively). For CR in virgin heifers, TRT-L did not differ from CON-L but was lower than CON-H ($P < 0.01$). Conception rates were 43.5% ± 1.9% (n = 666) for TRT-L, 43.7% ± 1.9% (n = 668) for CON-L, and 58.1% ± 1.4% (n = 1334) for CON-H. Staining of sperm, excitation laser power, and sperm dosage have implications for the fertility of sexed sperm produced using this novel technology. Contrary to theory, the presence of significant numbers of non-motile and bisected spermatozoa and their debris did not impact conception rates.

Key Words: conception rate, flow cytometer, sperm sexing

1134 Fertility and sex of calf results from a new commercial scale technology platform for producing sexed sperm. M. A. Faust*, J. Betthauser, S. Crego, and A. Storch, *ABS Global, Inc., De Forest, WI.*

By 2016, sexed sperm constitutes ~8% of AI breedings in dairy and beef cattle. Further growth in the application of sexed sperm is limited by the existing technology. We developed a novel technology for producing sexed sperm at commercial scale to better address current and future needs of genetics companies and their producer customers. For this new technology platform, purpose-built microfluidics and laser based cell destruction components were invented to enable accurate quantification of sperm DNA content and rapid and efficient destruction of unwanted cells while safeguarding sperm of the desired chromosomal content. To assess performance resulting from the sexed sperm, field trials were conducted in dairy herds across the U.S. Experiments compared sexed sperm (SEXED, 2×10^6 motile sperm per straw) and non-sexed controls (CON, 10×10^6 sperm) produced using split or contemporaneous collections from a total of 26 bulls (Holstein and Jersey). All treatments were packaged and cryopreserved in 0.25 mL straws. Quality checks for the new sexed sperm product were developed and included an estimate of numbers of progressively motile sperm per straw and a fluorescence in situ hybridization assay for determining sex chromosome content of live sperm. For experiment 1, post-thaw numbers of progressively motile sperm/straw ranged from 0.75 to 1.5 $\times 10^6$ for SEXED batches, 3.9 to 7.7 $\times 10^6$ for CON-Citrate, and 4.1 to 8.9 $\times 10^6$ for CON-Tris. Conception rates from virgin dairy heifers were 61.4% ± 1.5% (n = 1091 pregnancy diagnoses) for citrate control, 60.7% ± 1.5% (n = 1079) for CON-Tris, and 37.4% ± 1.5% (n = 1082) for SEXED. For experiments 2 and 3, no Tris control was used. Numbers of progressively motile sperm/straw ranged from 4.2 to 8.7 $\times 10^6$ for CON and from 0.74 to 1.6 $\times 10^6$ for SEXED batches. In experiment 2, conception rates in dairy heifers were 65.2% ± 1.5% (n = 1005 pregnancy diagnoses) for CON and 46.2% ± 1.6% (n = 1025) for SEXED. Conception rates for experiment 3 were equally favorable and were 64.1% ± 1.6% (n = 900) for CON and 48.3% ± 1.7% (n = 895) for SEXED. Sex chromosome content for live sperm was 87.2% X-bearing (weighted average) and ranged from 73% to 93% for individual batches of SEXED; as indicated by others, proportion of female calves as reported on-farm was somewhat lower at 84.6% ± 1.3% (n = 775, experiments pooled) for SEXED. Proportion of female calves for CON was 50.5% ± 1.4% (n = 1187, pooled). Our novel sexed sperm technology delivers a new platform enabling preselecting the sex ratio of offspring.

Key Words: conception rate, sexed sperm, sex ratio

1135 A meta-analysis of the impacts of maternal weight and fetal sex on uterine blood flow and maternal heart rate in beef cows from mid- to late-gestation. A. R. Tanner*[1], M. L. Bauer[1], V. C. Kennedy[1], B. Mordhorst[1], L. E. Camacho[2], K. C. Swanson[1], and K. A. Vonnahme[1], [1]*North Dakota State University, Fargo,* [2]*University of Arizona, Tucson.*

Uterine blood flow plays a critical role in the development of the conceptus, allowing for the maternal-fetal exchange of nutrients, hormones, and wastes. The objective was to examine the relationships between maternal BW, fetal sex, uterine blood flow, and maternal heart rate in beef cows during mid- to late-gestation. A total of 4 studies were used in the analyses which included 108 beef cows with blood flow measurements taken via Doppler ultrasonography on 4 d of gestation which resulted in 333 total observations. Fetal sex, BW class (45-kg increments), and body weight class by fetal sex interactions were analyzed with generalized least squares using the mixed procedure of SAS with repeated measures. Day of gestation was included as a covariate and treatment was nested within study. Linear, quadratic, and cubic orthogonal contrasts were tested. Cows carrying bull calves ($n = 82$) had greater ($P = 0.03$) uterine blood flow from d 100 to 250 of gestation compared to cows carrying heifer calves ($n = 26$; 18.46 ± 0.764 vs. 15.56 ± 1.04 L/min). As maternal BW increased, uterine blood flow tended ($P = 0.09$) to increase linearly (14.5 mL per kg). Maternal heart rate also increased linearly ($P = 0.02$) as maternal BW increased (0.03 beats per min per kg). Fetal sex did not impact maternal heart rate ($P = 0.13$). In conclusion, the increase in uterine blood flow for male progeny may be contributing to heavier birth weights when compared to their female counterparts. Also, increasing maternal weight may be associated with increased uterine blood flow and heart rate. Perhaps the reason bull calves are heavier than heifer calves at birth may be due to the male's ability to increase uterine blood flow.

Key Words: fetal sex, maternal body weight, uterine blood flow

1136 Validation of a chemical pregnancy test in dairy cows that uses whole blood, shortened incubation times, and visual readout. L. M. Mayo*[1], S. G. Moore[1], S. E. Poock[1], W. Silvia[2], and M. C. Lucy[1], [1]*University of Missouri, Columbia,* [2]*University of Kentucky, Deceased, Lexington.*

Chemical pregnancy testing is an alternative to traditional methods of pregnancy diagnosis in postpartum dairy cows. The objective was to validate a new chemical pregnancy test that confers the advantages of using whole blood (EDTA), plasma (EDTA), or serum, rapid incubation times, and visual readouts. Blood and milk samples were collected from Holstein cows ($n = 320$) 162 ± 62 d (Mean ± SD) postpartum on a confinement farm in Northeast Missouri at 28 d after timed artificial insemination (TAI). Cows were assayed for pregnancy-associated glycoproteins (PAG) by using a new rapid visual ELISA assay, and plasma and milk-based ELISA assays (IDEXX, Westbrook, ME). Transrectal ultrasonography (TU) diagnosis for pregnancy at 35 d or 38 d after TAI was the reference standard for all PAG tests. The optical density (OD) measured with a microtiter plate reader (plasma, milk, and rapid tests) or visual readout (rapid test) were used to diagnose pregnancy. When the OD was used, the percentage of pregnant cows ($n = 159$; TU diagnosed pregnant) classified correctly (sensitivity) for the plasma, milk, and rapid tests were 97 ± 1%, 96 ± 2%, and 95 ± 1% (± SE), respectively. The sensitivity of the rapid test when assessed visually was 98 ± 1%. The specificity (proportion of non-pregnant cows classified correctly) for the plasma, milk, and rapid was 94 ± 2%, 94 ± 2% and 93 ± 2%, respectively. The lesser specificity for visual readouts (85 ± 3%) was associated with faint visual signals that yielded false positive diagnoses. Primiparous cows had greater (0.35 ± 0.02) rapid OD than multiparous cows (0.30 ± 0.01; $P = 0.03$). First insemination cows had a greater signal than cows with multiple breedings at time of sampling for rapid, milk, and plasma PAG assay OD ($P < 0.001$). In a second experiment, lactating Holstein cows ($n = 291$) from 4 Kentucky commercial confinement dairy farms were tested for pregnancy 25 to 95 d after artificial insemination with the rapid visual test. The OD of the rapid visual test followed the known profile for PAG in circulation (high concentrations during early pregnancy followed by a period of lesser concentrations with increasing concentrations thereafter; $P < 0.05$). Overall, the new rapid visual test has equal sensitivity and accuracy to existing PAG tests.

Key Words: pregnancy-associated glycoprotein, pregnancy diagnosis, whole blood

1137 Effects of parity and mid-gestation nutrient restriction on umbilical blood flow, fetal and placental measurements, and birth weight in sheep. M. A. Vasquez*, K. C. Swanson, and K. A. Vonnahme, *North Dakota State University, Fargo.*

We recently reported that mid-gestation (d 50 to 90) nutrient-restriction decreases umbilical blood flow (UBF) and placentome area (PA), and increases pulsatility index (PI) and resistance index (RI) on Day 80 of gestation in multiparous Dorset ewes. The same nutritional restriction applied in nulliparous ewe lambs decreased UBF by d 70 (Lemley et al. (2012).AJP.302:R454). We hypothesized that multiparous ewes would be more resilient to restriction compared to nulliparous ewes. On d 50 of gestation, adult (15 mo) nulliparous (NUL; $n = 12$) and multiparous (MUL; $n = 16$) Dorset ewes carrying singletons were randomly assigned to receive 100% of NRC recommendations (CON) or 60% of CON (RES). On d 91, RES ewes were realimented to 100% of NRC

recommendations. On d 50, and every 10 d until d 110, fetal and placental measurements and umbilical hemodynamics were obtained via ultrasonography. Lamb birth weights were recorded. The study was conducted as a 2 by 2 factorial arrangement of treatments with repeated measures. Data were analyzed using the MIXED procedure of SAS. By d 60 RES ewes were lighter than CON ewes ($P < 0.01$), and remained lighter throughout the experiment. There were no three way interactions or main effects of treatments on UBF, PI, RI and PA ($P \geq 0.57$). There was a parity by day interaction ($P < 0.05$) for RI, but UBF was not affected by parity or diet. At birth no differences were observed in lamb weight ($P \geq 0.78$). Restriction from d 50 to 90 does not appear to impact umbilical hemodynamics or conceptus growth in adults, regardless of parity. Our laboratory's previous observation that reduced UBF in young ewes (6 mo old) resulting from nutrient restriction may be due to maternal age. Future studies investigating age, parity, and body fat reserves of the dam on umbilical hemodynamics are underway.

Key Words: pregnancy, realimentation, sheep

1138 Comparing two ultrasound devices to determine antral follicle counts in dairy cows.

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The determination of antral follicle count (AFC) in dairy cows and its association with fertility is an area of interest to many researchers. Different types of ultrasound scanning (US) devices are available in the market but their comparative efficacy in determining AFC is rarely reported. In this study, we compared the efficacy of EASI-SCAN (BCF Technology Ltd., Rochester, MN; 4.5–8.5 MHz linear array transrectal transducer) and ALOKA (Aloka Co Ltd., Tokyo, Japan; 7.5 MHz linear array transrectal transducer) in the determination of AFC in dairy cows. Eighteen lactating Holstein cows were randomly subjected to transrectal ultrasonography by EASI-SCAN and ALOKA scanners approximately 30 min apart. All scans were performed by the same individual and AFC of each ovary was recorded on separate sheets by a second individual who was blinded to the study. The MEANS procedure of SAS was applied to obtain the mean and standard error of mean for AFC on the left ovary, right ovary and in total. The AFC in left and right ovaries, and total AFC obtained by EASI-SCAN and ALOKA were compared using CORR procedure of SAS and differences determined by TTEST procedure of SAS. The mean (± SEM) AFC determined by EASI-SCAN and ALOKA for the left ovary, right ovary, and total AFC were 6.3 ± 0.7 vs. 9.5 ± 1.0, 7.2 ± 1.4 vs. 11.0 ± 1.8, and 13.6 ± 2.0 vs. 20.5 ± 2.7, respectively. Likewise, the range for the total AFC was lower with EASI-SCAN (4 to 35) than with ALOKA (7 to 46). Although AFC data obtained by EASI-SCAN and ALOKA were significantly correlated ($r = 0.90$; $P < 0.0001$), total AFC was approximately 34% lower ($P < 0.01$) with EASI-SCAN than with ALOKA. Findings indicated that the ALOKA (7.5 MHz transducer) is more precise in determination of AFC than EASI-SCAN (4.5–8.5 MHz transducer).

Key Words: antral follicle count, dairy cows, ultrasound scanner

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1139 The repeatability of antral follicle count and anti-Müllerian hormone concentration at two different postpartum stages in dairy cattle.

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Low antral follicle count (AFC) and low plasma anti-Müllerian hormone (AMH) concentrations are reportedly associated with poor reproductive outcomes in dairy cattle. The primary objective of this study was to evaluate the repeatability of AFC and plasma AMH concentrations at two different postpartum stages. The ovaries of 100 lactating Holstein cows were subjected to transrectal ultrasonography (Aloka Co Ltd., Tokyo, Japan) by a single individual using a 7.5 MHz linear array transducer to determine AFC at 14 ± 1 and 75 ± 1 d postpartum (second exam was approximately 48 h after the second GnRH of an Ovsynch protocol). Blood samples were also collected 14 ± 1 and 75 ± 1 d postpartum to determine plasma AMH concentrations. The MEANS procedure of SAS was used to obtain the mean and standard error of means for the continuous variables, and correlations between continuous variables were tested using the CORR procedure of SAS. The means (± SEM) for AFC determined at 14 and 75 d postpartum were 27 ± 1 and 23 ± 1, respectively. Likewise, the mean (± SEM) AMH concentrations determined at 14 and 75 d postpartum were 190.0 ± 12.8 and 224.8 ± 14.3 pg/mL, respectively. A moderate significant correlation ($r = 0.41$; $P < 0.01$) existed between AFC at 14 and 75 d postpartum. Concentrations of AMH at 14 and 75 d postpartum were strongly correlated ($r = 0.75$; $P < 0.01$). The correlation between AFC and plasma AMH was moderate at both 14 ($r = 0.57$; $P < 0.01$) and 75 d ($r = 0.59$; $P < 0.01$) postpartum. Results indicate that both AFC and AMH concentrations are repeatable at different stages postpartum, although the repeatability is significantly greater for AMH.

Key Words: anti-Müllerian hormone, antral follicle count, repeatability

1140 Dairy cows with shorter ano-genital distance may be more fertile than those with longer ano-genital distance. M. Gobikrushanth*[1], T. C. Bruinjé[1], M. G. Colazo[2], and D. J. Ambrose[1,2], [1]*Department of Agricultural Food and Nutritional Science, University of Alberta, Edmonton, Canada,* [2]*Livestock Research Branch, Alberta Agriculture and Forestry, Edmonton, Canada.*

The ano-genital distance (AGD) is the distance from anus to base of the penis in male, or clitoris in female mammals. The AGD is a reflection of testosterone exposure during in utero development. Thus, AGD in the adult is indicative of prenatal androgen exposure and reportedly associated with several reproductive health outcomes in humans and laboratory animals. The objectives of this preliminary study were: (1) to characterize variations in the measurements of AGD in a population of dairy cows and (2) to determine associations between categories of AGD and traditional reproductive indices. The AGD in 93 lactating Holstein cows (35 primiparous and 58 multiparous) were measured using a digital caliper. To increase precision, the average of three AGD measurements in each animal was used. All cows were subjected to fixed-timed AI at ~75 d postpartum following a Presynch/Ovsynch protocol. The traditional reproductive indices of first service conception rate, number of inseminations and days open were determined for the current lactation. Cows were ranked based on AGD, from shortest to longest, and those in the top and bottom 50th percentiles were classified into SHORT (n = 46) and LONG (n = 47) AGD categories. The continuous variables were analyzed using the MIXED procedure of SAS and first service conception rate was modeled against categories of AGD and parity as interactions between categories of AGD and parity were not significant, and analyzed using LOGISTIC procedure of SAS. The overall AGD ranged from 95.7 to 149.0 mm and mean (± SEM) AGD were 111.3 ± 0.9 and 129.2 ± 1.1 mm for cows categorized as SHORT and LONG AGD groups, respectively. Cows in the SHORT AGD group tended (P = 0.07) to have 2.4 times higher odds of becoming pregnant to the first insemination than cows in LONG AGD. Similarly, cows in the SHORT AGD group tended to have fewer days open (142.5 ± 10.4 vs. 169.5 ± 11.6 d; P = 0.10) and required less number of inseminations (2.3 ± 0.2 vs. 2.8 ± 0.2; P = 0.12) than those in LONG AGD. The AGD ranged from 95.7 to 142.7 mm (mean ± SEM; 119.6 ± 1.2 mm) for primiparous cows and from 100.0 to 149.0 mm (mean ± SEM; 120.8 ± 0.9 mm) for multiparous cows. The first service conception rate, number of inseminations and days open did not differ between primiparous and multiparous cows. In summary, findings of this preliminary study suggest that cows with shorter ano-genital distance tend to have better reproductive performance than cows with longer ano-genital distance.

Key Words: ano-genital distance, dairy cows, fertility

1141 Pregnancy Associated Glycoprotein (PAG) concentrations in early gestation from dairy heifers undergoing embryo transfer. S. Reese[1], M. H. Pereira[2], J. L. M. Vasconcelos[3], and K. G. Pohler*[1], [1]*University of Tennessee, Knoxville,* [2]*UNESP-FMVZ, Botucatu, Brazil,* [3]*Sao Paulo State University, Botucatu, Brazil.*

Diagnosing and identifying successful pregnancies early in gestation has important economic and management implications for dairy producers. The limitation of current ultrasound and chemical based pregnancy diagnosis methods are that they are most effective starting at Day 30 of gestation. Pregnancy associated glycoproteins (PAGs) are produced by the ruminant placenta and can be used to accurately detect pregnancy as early as Day 28 of gestation. More recent data indicate that circulating PAGs may also be a marker of embryonic viability and predictive of embryonic mortality after Day 28 of gestation. The objective of the current study was to determine if early gestation circulating PAG levels could be indicative of pregnancy for an individual heifer following a baseline sample. Our hypothesis was that Day 24 PAG levels could be predictive of pregnancy if there was a significant increase over a Day 17 baseline sample. In vitro produced embryos were transferred into synchronized virgin percentage Holstein dairy heifers (n = 206) using timed embryo transfer (TET). Blood was collected at Day 17 and 24 for PAG analysis as well as Day 31 for confirmation of pregnancy. Serum concentrations of PAG were quantified using an in house PAG ELISA with antibodies raised against PAGs expressed early in gestation (Green et al., 2005, Pohler et al., 2013). Following TET there were 101 heifers identified pregnant on Day 31 of gestation (49%) using ultrasound and PAG testing. Circulating concentrations of PAG were significantly different ($P < 0.05$) at d 24 of gestation between heifers that were pregnant (2.98 ng/mL) and non pregnant (0.69 ng/mL). In addition, when using receiver operating curve (ROC) analysis PAGs were 95% accurate in diagnosing pregnancy at Day 24 of gestation when circulating PAG levels reached 1.39 ng/mL (~50% of pregnant heifers). When determining pregnancy only based on subtracting the Day 17 sample (baseline) from Day 24, we were able to accurately diagnosis 79% of the heifers for pregnancy at d 31 of gestation. Interestingly, about 11% of heifers following TET that ended up being not pregnant at Day 31 of gestation had increased Day 24 circulating PAGs compared to the Day 17 baseline sample. Thus suggesting that pregnancy loss occurred between Day 24 and 31 of gestation in these heifers. In summary, early pregnancy detection may be possible by using PAGs; however more work is needed to refine this area.

Key Words: heifers, PAGs, pregnancy

1142 Protein kinase A directly phosphorylates GSK3β, and regulates β-catenin via phosphorylation in granulosa cells. B. H. Aloqaily*[1], C. A. Gifford[2], B. I. Gomez[1], and J. A. Hernandez Gifford[1], *[1]Oklahoma State University, Stillwater, [2]Department of Animal Science, Oklahoma State University, Stillwater.*

Estradiol serves an important role in female fertility and FSH drives estradiol production. Beta-catenin is a transcriptional co-factor that is required for FSH-induced estradiol production. Beta-catenin is activated via phosphorylation at Ser^{552} and Ser^{675} by protein kinase A (PKA) dependent event. Wingless-type mouse mammary tumor virus (WNT) also regulates the β-catenin pathway. Glycogen Synthase Kinase-3 β (GSK3β) is a component of the β-catenin degradation complex; canonical WNT signaling pathway phosphorylates protein kinase B (AKT) and inhibits GSK3β resulting in β-catenin accumulation in the cytoplasm. Work in our laboratory demonstrated that WNT downregulates steroidogenesis. Furthermore, AKT is required for β-catenin accumulation and FSH-induced estradiol production, suggesting convergence of the WNT and FSH pathways. We hypothesize that WNT inhibition of FSH signaling occurs through modulation of phosphorylation patterns on β-catenin. The objective of these experiments was to evaluate the phosphorylation pattern of β-catenin in response to PKA, AKT, and WNT signaling pathways. Granulosa cells (KGN cell line) were cultured and treated with vehicle control, phosphoinositide 3-kinase (PI3K) inhibitor LY294002 (LY) (30 μM; 30 min), Forskolin (FSK) (10 μM; 1.5 h), WNT (50 ng/mL, 30 min) and the combination of these treatments. Western blot was used to detect total and phosphorylated β-catenin and phosphorylated GSK3β. Protein abundances were analyzed using densitometry software and densitometry values for treatments were analyzed using the GLM procedure of SAS. When significant model interactions were detected, means were separated using PDIFF. Treatment of FSK combined with WNT and LY enhanced GSK3β phosphorylation compared to control ($P < 0.05$). Similarly, FSK alone or in combination with WNT and LY enhanced ($P < 0.05$) phosphorylation of β-catenin at Ser^{675} and Ser^{552}, but WNT did not alter β-catenin phosphorylation after FSK stimulation ($P > 0.10$). However, when the AKT pathway was blocked with LY, FSK, and WNT treatment increased phosphorylation of GSK3β and subsequently β-catenin at Ser^{552} suggesting that PKA can directly phosphorylate GSK3β. Results from these experiments demonstrate that WNT does not alter FSH-stimulated phosphorylation patterns of β-catenin indicating that WNT inhibits FSH signaling via other unknown mechanisms.

Key Words: beta-catenin, FSH, WNT

1143 Plasma anti-Müllerian hormone in dairy heifers and associations with reproductive performance in two reproductive programs for first artificial insemination. T. V. Silva[1], J. E. P. Santos[2], and E. S. Ribeiro*[3], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]University of Florida, Gainesville, [3]Department of Animal Biosciences, University of Guelph, Guelph, Canada.*

The objective was to investigate associations between plasma anti-Müllerian hormone (AMH) and reproductive performance in dairy heifers inseminated after detection of estrus or synchronized ovulation. Heifers ($n = 601$) in three farms were enrolled in the study 6 d before moving to the breeding pens. A randomized complete block design was used to assign one of two reproductive programs (RP) for first artificial insemination (AI): estrous detection (ED, $n = 297$) or timed AI (TAI, $n = 304$). Heifers in the ED group had their tailheads painted with chalk and were evaluated for signs of estrus once daily. Heifers receiving TAI were enrolled in the 5-d TAI protocol. On the day of enrollment, blood was sampled and analyzed for concentrations of AMH using an immune assay (AnshLite Bovine AMH CLIA). Within farm, concentrations of AMH in plasma were ranked and categorized as low (20% lowest values), high (20% highest values), or intermediate (60% intermediate values). Reproductive performance was evaluated for 84 d and the remaining AIs were performed after detection of estrus in both RP groups. Pregnancy was diagnosed on Days 32 and 60 after AI. Binary data were analyzed by logistic regression using the GLIMMIX procedure of SAS, and pregnancy rate was analyzed by the Cox's proportional hazard model using the PHREG procedure of SAS. Statistical models included the effects of AMH, RP, and their interaction, farm and semen. Concentration of AMH in plasma ranged from 2.6 to 566.3 pg/mL, and averaged 12.9, 30.9, and 85.4 pg/mL for low, intermediate and high AMH, respectively. Pregnancy per AI on Days 32 and 60 after first AI were not affected by AMH (d 32: 57.5, 65.9, and 64.2%, $P = 0.21$; d 60: 56.7, 62.6, and 58.3%, $P = 0.38$; for low, intermediate, and high AMH, respectively) or RP (d 32: 62.3, and 65.5%, $P = 0.16$; d 60: 58.2, and 62.8%, $P = 0.11$; for ED and TAI, respectively). Compared with low AMH, rate of pregnancy during the 84 d was similar for intermediate (AHR = 1.19, $P = 0.12$) and high AMH (AHR = 1.11, $P = 0.46$). Nonetheless, TAI had a faster rate of pregnancy (AHR = 1.58; $P < 0.01$) than ED. No interactions between AMH and RP were detected. In conclusion, plasma AMH was not associated with reproductive performance of dairy heifers in neither one of the two RP evaluated.

Key Words: AMH, heifers, timed AI

1144 Wingless-type mouse mammary tumor virus integration site (WNT) regulation of ovarian thec cells of cattle. L. J. Spicer*, *Oklahoma State University, Stillwater.*

During ovarian follicular development, granulosa and theca cell (TC) proliferation and differentiation are influenced by gonadotropins, insulin-like growth factors (IGF), and diverse intraovarian factors. Based on high-density microarray analysis comparing cystic and noncystic bovine follicles, we discovered that secreted frizzled related protein 4 (SFRP4) mRNA is downregulated in granulosa cells of cystic follicles suggesting that the WNT system may be involved in cyst formation. Numerous WNT ligands bind to several cognate Frizzled receptors (FZD), and SFRP4 is a truncated form of FZD capable of blocking the action of WNT ligands. Dickkopf-1 (DKK1) is another WNT antagonist and R-spondin-1 (RSPO1) one of a group of four secreted proteins that enhance Wnt/β-catenin signaling. Our overall hypothesis is that granulosa cells signal TC via SFRP4, DKK1, RSPO1, and WNT secretion to regulate TC differentiation and proliferation during follicular development. Therefore, in vitro experiments were conducted to study the effects of WNT family member 3A (WNT3A), RSPO1, DKK1, IGF1, and fibroblast growth factor-9 (FGF9) on bovine TC proliferation and steroidogenesis. TC of large (8 to 20 mm) follicles were collected from ovaries of beef cattle (n = 20 per replicate) and cultured for 48 h and then treated in serum-free medium for 48 h containing either no additions (control), 30 or 100 ng/mL of recombinant human WNT3A, RSPO1, DKK1, IGF1 and/or ovine LH. At least 7 follicles from 5 or more cattle were used to generate one biological replicate per experiment and this was repeated thrice. Each treatment within a biological replicate was replicated 2 or 3 times. For each set of replicated experiments, ANOVA was conducted using SAS. In experiment 1 using LH-treated TC, both IGF1 and WNT3A increased ($P < 0.05$) cell numbers and androstenedione production, whereas WNT3A inhibited ($P < 0.05$) progesterone production by 30%. In experiment 2 using IGF1 plus LH-treated TC, WNT3A (30 ng/mL) further increased ($P < 0.05$) IGF1-induced androstenedione production from 770 to 930 ± 60 pg/10^5 cells/24 h. Similarly, in experiment 3, 100 ng/mL of RSPO1 further increased ($P < 0.05$) IGF1-induced androstenedione production. In experiment 4, SFRP4 and DKK1 alone had no significant effect on TC proliferation or steroidogenesis. In experiment 5, FGF9 blocked ($P < 0.05$) the WNT3A-induced increase in androstenedione production. We conclude that the ovarian WNT system is functional in cattle, increasing proliferation and androstenedione production of TC.

Key Words: cattle, theca cells, WNT3A

1145 Plasma concentrations of glucagon-like peptide 1 and 2 in calves fed calf starters containing lactose. Y. Inabu*[1], A. Saegusa[2], K. Inouchi[2], M. Oba[3], and T. Sugino[1], *[1]Hiroshima University, Higashi-hiroshima, Japan, [2]ZEN-RAKU-REN, Nishi-shirakawa, Japan, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The objective of this study was to evaluate the effect of lactose inclusion in calf starters on plasma concentrations of glucagon-like peptide 1 (GLP-1) and 2 (GLP-2). Holstein bull calves (n = 60) were raised on an intensified nursing program using milk replacer containing 28.0% CP and 15.0% fat, and fed the texturized calf starter containing lactose at either 0 (Control), 5.0 (LAC5), or 10.0% (LAC10; n = 20 for each treatment) on a DM basis. All calf starters were formulated for 23.1% CP. Ethanol soluble carbohydrate concentration of Control, LAC5, and LAC10 starters were 7.3, 12.3, and 16.8%, respectively. Starch concentrations of Control, LAC5, and LAC10 were 29.7, 27.0, and 21.4%, respectively. All calves were fed treatment calf starters ad libitum. Blood samples were obtained weekly from 1 wk to 11 wk of age and used to measure plasma GLP-1, GLP-2, insulin, and β-hydroxyl butyric acid (BHB) concentrations. Plasma BHB concentrations were higher ($P < 0.01$) for LAC10 (169 ± 5.1 μmol/L; LSM ± SEM) compared with Control (153 ± 4.8 μmol/L) and LAC5 (148 ± 5.2 μmol/L). Plasma GLP-1 and GLP-2 concentrations were not affected by treatments. However, relative values of plasma GLP-1 concentrations compared with that of the baseline (1 wk of age) were higher ($P < 0.01$) for LAC10 (94.8 ± 5.01%) compared with LAC5 (66.5 ± 5.11%), and for LAC5 compared with Control (42.5 ± 4.73%), and similar tendency was observed for GLP-2 concentrations relative to that of the baseline (80.6 ± 5.42%, 74.7 ± 5.43%, and 73.3 ± 5.3%, respectively, for LAC10, LAC5, and Control, respectively; P = 0.09). Plasma insulin concentrations were lower ($P < 0.01$) for LAC5 (4.69 ± 0.58 ng/mL) and LAC10 (4.60 ± 0.58 ng/mL) compared with Control (5.52 ± 0.58 ng/mL). Lactose intake was positively correlated with plasma BHB concentrations (Spearman's correlation coefficient; $r_s = 0.87$, $P < 0.01$), and tended ($r_s = 0.41$, $P = 0.07$) to be positively correlated to plasma GLP-1 concentrations, but not correlated with plasma GLP-2 concentrations. In addition, plasma GLP-1 concentrations were positively correlated with plasma concentrations of BHB ($r_s = 0.85$, $P < 0.01$). In conclusion, these results indicate that inclusion of lactose in calf starters may contribute to maintaining high plasma concentrations of GLP-1, which was associated with greater plasma BHB concentrations.

Key Words: calf, glucagon-like peptide, lactose

1146 Metabolic profile and inflammatory response in calves with different intake of immunoglobulins.

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To achieve a successful passive transfer of immunoglobulins in newborn calves, it is recommended to feed the colostrum quickly after birth, paying attention to the quantity and quality of colostrum administered. The quality of colostrum is associated with content of Immunoglobulins G (IgG), which can vary dramatically among cows. The conventional strategy calls for feeding a calf of 45 kg first colostrum with at least 100 g of IgG. The adequate intake should be monitored measuring the concentration of IgG in the colostrum or in the blood of calves after 24–48 h from the first meal. Moreover, besides IgG for which determination is complex, other blood parameters might provide information on amount of IgG intake and eventual consequences on health. The aim was to assess the relationship among IgG intake with average daily gain (ADG), metabolic profile, inflammatory response and oxidative stress using 45 Holstein calves over the first month of life. After colostrum analyses, calves were retrospectively divided in two groups: G1 (n = 24), ingesting less than 100 g of IgG (average intake = 68 g) from first colostrum, and G2 (n = 21), ingesting more than 100 g of IgG (average intake = 133 g), from first colostrum (1.5 L of colostrum). Besides frequent blood samples, daily health status and body weight also were recorded. Our results showed a poor correlation between density and IgG content of colostrum (r = 0.34), while the correlation between blood IgG and gGT was high (r = 0.9 P < 0.001). During the first 4 wk of life, G1 compared with G2 calves had more clinical problems and lower ADG (0.27 vs. 0.40 kg/d, P < 0.01). At 7 d after birth, G1 calves had higher levels of haptoglobin (0.62 vs. 0.43 g/L, P < 0.02), ceruloplasmin (2.39 vs. 1.87 μmol/L, P < 0.01), and reactive oxygen metabolites (14.8 vs. 12.9 mg H_2O_2/100 mL, P < 0.03). These differences indicate that G1 calves (intake of IgG < 100 g with first meal) experienced important inflammatory events after birth, which increased the oxidative stress, impaired liver function, and strongly reduced the ADG. Therefore, to avoid these problems it is insufficient to only check first colostrum quality before feeding. Besides providing a better measure of the IgG intake, an evaluation of targeted blood parameters within 1 wk of life could give more detailed information on calf health and welfare.

Key Words: calves, colostrum, immunoglobulin, inflammation, metabolic profile

1147 Effect of the timing of addition of *trans*-10, *cis*-12 conjuaged linoleic acid and L-carnitine during culture on development and cryotolerance of bovine embryos produced in vitro.

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The objective was to determine whether embryo development and survival following cryopreservation were affected by the timing of addition of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) and L-carnitine during culture. Bovine embryos were produced in vitro using abattoir-derived cumulus-oocyte complexes. After fertilization, presumptive zygotes (n = 2804) were cultured at 38.5°C in a humidified atmosphere of 5% O_2, 5% CO_2, and 90% N_2 in synthetic oviductal fluid-bovine embryos 1 (SOF-BE1). Presumptive zygotes were randomly assigned to the following treatment groups: vehicle for the entire culture period, 100 μM CLA for the first 88 h, last 72 h, or the entire culture period and 0.75 mM L-carnitine for the first 88 h, last 72 h, or the entire culture period. At 88 h post-insemination, embryos were removed from culture, washed in HEPES-Tyrode's albumin lactate pyruvate, placed into their respective culture treatments and cultured for an additional 72 h. The proportion of oocytes that cleaved was assessed at 88 h (Day 4) after insemination and the proportion of oocytes that developed to the blastocyst and advanced blastocyst (expanded, hatching, and hatched) stages was determined on Day 7. Blastocysts and expanded blastocysts (n = 537) were harvested at Day 7 and subjected to controlled-rate freezing following equilibration in 1.5 M ethylene glycol. After thawing, embryos were cultured for 72 h in SOF-BE1 supplemented with 10% (v/v) fetal bovine serum and 50 mM dithiothreitol at 38.5°C in a humidified atmosphere of 5% O_2, 5% CO_2 and 90% N_2. Post-thaw re-expansion and hatching rates were determined at 24, 48, and 72 h. The experiment was replicated 14 times and data were analyzed by analysis of variance. There was no effect of treatment with CLA or L-carnitine on embryo development or post-thaw survival (Table 1.), regardless of whether treatment occurred during the first 88 h, the last 72 h or the entire culture period. While previous studies have reported beneficial effects of CLA and L-carnitine on embryo cryotolerance, the results of the present study indicate the effects of CLA and L-carnitine are likely not dependent on the timing of their addition during culture.

Key Words: conjugated linoleic acid, cryopreservation, L-carnitine,

1148 An insufficient supply of glucose substrates causes reduced lactose synthesis in lactating dairy cows fed cereal straws instead of alfalfa hay. B. Wang[*1], F. Zhao[1,2], B. X. Zhang[1], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]University of Vermont, Burlington.*

The objective of the present study was to investigate the nutrient supply for lactose synthesis in the mammary gland (MG) of lactating cows fed different sources of forage. Thirty Holstein cows were randomly assigned into three groups and fed 3 diets contained 30% corn stover (CS), 30% rice straw (RS), or 23% alfalfa hay plus 7% Chinese wild rye hay (AH) as forage sources, respectively, with identical total concentration and corn silage for 14 wk. Milk lactose, rumen VFA, blood glucose and hormones (n = 10), and mRNA abundance of genes related to glucose metabolism in liver and MG (n = 6) were analyzed in these cows. The data were analyzed using PROC MIXED program of SAS with a randomized complete block design with repeated measures. The percentage of milk lactose was always lower in the RS-fed cows than the cows fed AH or CS during the last 12 wk of feeding trial ($P < 0.01$). The ruminal propionate concentrations were also reduced in the RS group compared to the AH group ($P = 0.03$). The ratio of plasma insulin to glucagon in the mammary vein was greater in the AH group than in the CS or RS group ($P = 0.04$). The abundance of the pyruvate carboxylase mRNA in the liver was reduced in the RS group compared to the AH or CS groups ($P = 0.04$), whereas the mRNA abundance of mitochondrial phosphoenolpyruvate carboxykinase, insulin like growth factor-1 receptor, and phosphofructokinase-liver, -muscle, and -platelet in the liver was reduced in the RS group compared to the AH group ($P < 0.05$). The mammary glucose uptake was greater in the AH-fed cows than in the CS- or RS-fed cows ($P = 0.02$). The mRNA abundance of the glucose transporters in the MG was similar between the 3 treatments. The mRNA abundance of α-lactalbumin in the MG of the cows fed RS tended to increase compared to that of the cows fed AH or CS. The milk potassium concentration was increased in the cows fed RS compared to those fed AH or CS ($P < 0.01$). In summary, the insufficient ruminal propionate levels in the cows fed RS were associated with decreased gluconeogenesis in the liver, resulting in the shortage of the arterial glucose supply for mammary uptake and reduced lactose synthesis.

Key Words: cereal straw diets, glucose substrates, lactose synthesis

1149 Expression of genes involved in the initial steps of steroidogenesis in adipose tissue depots of dairy cows during the dry period and early lactation. A. Alizadeh[1,2,3], H. Sadri[1], J. Rehage[4], S. Dänicke[5], and H. Sauerwein[*1], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Bonn, Germany, [2]Department of Animal Science, Saveh Branch, Islamic Azad University, Saveh, Iran, [3]Department of Embryology, Reproductive Biomedicine Research Center, Royan Institute for Reproductive Biomedicine, ACECR, Tehran, Iran, [4]University for Veterinary Medicine, Foundation, Hannover, Germany, [5]Institute of Animal Nutrition, Friedrich-Loeffler-Institute (FLI), Braunschweig, Germany.*

In view of the significant changes in body fat content related to parturition and lactation in dairy cows, together with the role of adipose tissue (AT) not only as a store of steroid hormones but also as a potential site of steroidogenesis, mobilization of body reserves may also alter steroid hormone secretion and eventually reproduction. With this background, our research objectives were (1) to assess the expression of two rate-limiting factors of steroidogenesis, i.e., steroidogenic acute regulatory protein (StAR) and Cytochrome P450scc (CYP11A1) in bovine AT, (2) to characterize the time course of their mRNA abundance during late pregnancy and early lactation, and (3) to compare this time course in a subcutaneous versus a visceral fat depot. StAR triggers cholesterol delivery to the inner mitochondrial membrane (IMM) where CYP11A1 then initiates steroidogenesis by converting cholesterol to pregnenolone, the precursor of all other endogenous steroids. Biopsies were collected from 20 Holstein cows from the subcutaneous (sc) and the retroperitoneal fat depot (rp) on d −42 and d 1, 21, and 100 relative to calving. The mRNA abundance of StAR and CYP11A1 was assessed in the tissue samples by qPCR and normalized using the 4 most stable reference genes. Data were analyzed using the MIXED procedure of SAS. In scAT, the StAR mRNA abundance was lowest on d −42, increased on d 1 ($P < 0.05$) until d 21 to remain at this level at d 100 (~3-fold greater than on d −42; $P < 0.001$). Expression of StAR mRNA in rpAT increased with time of lactation, but differences between sampling days were limited to d −42 versus d 100 (3.3-fold increase; $P = 0.01$). Expression of CYP11A1 mRNA was not detectable in both AT with the protocol used herein (suitability of the protocol was confirmed with ovary as positive control). The increased expression of StAR mRNA abundance after calving in rpAT and scAT indicate an increased capacity for cholesterol uptake to the IMM. Given the apparently absent expression of CYP11A1, de novo synthesis of steroid hormones in bovine AT seems implausible and AT steroid metabolism likely depends on the uptake of preformed steroid precursors. Cholesterol reaching the IMM may thus rather be metabolized

to oxysterols which were suggested to have regulatory functions in adipocytes.

Key Words: adipose tissue, dairy cow, StAR

1150 Effects of a dietary supplementation of rumen-protected B vitamins on reproduction of dairy cows by measuring nutrigenomic parameters.

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It has been known that supplementary rumen-protected or injected B vitamins can improve dairy cow milk production and reproductive performance. Recently, it has been reported that B vitamins injections were having an impact on granulosa cells of the ovarian follicle when looking at gene expression profiling. Therefore, the aim of the present study was to assess whether rumen-protected B vitamins given as a dietary supplement can have an impact on gene expression in granulosa cells. The experimental design included 30 cows divided in three groups; 1) control, without any B vitamin supplementation, 2) injection, weekly intramuscular injections of 320 mg of folic acid and 10 mg of vitamin B12 starting from −21 to 60 d post calving, and 3) dietary supplementation of rumen-protected B vitamins as 50 g/cow/d of Transition VB™ (Jefo) from −21 to −1 calving, 100 g/cow/d of Transition VB™ from 1 to 21 d post-calving, 3 g/cow/d of Lactation VB™(Jefo) from calving to 60 d post calving. The follicles size was measured by laparoscopic transvaginal ultrasound from 40 d until OPU at 54 d post-calving. The cows were synchronized with two injections of PGF2α 12 d apart with first injection at 40 d. Granulosa cells were collected by OPU 53 h post second injection on the dominant follicle larger than 12 mm in diameter. Hybridization was done in dye swipe on EmbryoGENE microarray slides using three trios of animals. Differently expressed genes were analyzed through Ingenuity Pathway Analysis software. Selected genes were further assessed by RT-qPCR based on their functional significances. Based on estradiol and progesterone levels, the pattern of gene expression is supporting precocious granulosa cell differentiation toward an earlier response to LH (up-regulation of RGS2, NR3C1, OLR1, since significantly different ($p < 0.05$) from the control in both microarray analysis and RT-qPCR validation; downregulation of LHCGR, HSD3B1 and FST, since significantly different ($p < 0.05$) from the control) which may be the result of an increase in LH secretion. While comparing gene expression to superovulation conditions improving oocyte developmental competence, we observed genes commonly expressed with dietary supplementation of protected B vitamins (RGS2 and INHBA). The microarray data of granulosa cells from the dominant follicle are supporting the hypothesis that dietary supplementation of rumen-protected B vitamins is affecting granulosa cells differentiation toward an earlier LH response associated with genes expressed in conditions where oocyte developmental competence is improved.

Key Words: microarray, nutrigenomic, protected B vitamins, reproduction

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1151 Impact of dietary protein levels during late pregnancy on the number of binuclear cells in sheep.

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Angiogenic and vasoactive factors have been localized to binuclear cells (BNCs) located in the placenta of several species including sheep. During late gestation in the ewe, a low protein diet increased maternal blood pressure and uterine blood flow compared with a high dietary protein level. The objective of this study is to determine the effect of varying protein levels during late pregnancy in ewes on the number of BNCs. We hypothesized that low dietary protein during late gestation would increase the number of BNCs leading to the reported increase in uterine blood flow in ewes. At Day 100 of pregnancy, 18 ewes were randomly divided into three groups (6 each) and provided one of three diets containing different metabolizable protein (MP) levels: low protein level (L; 60% MP), control protein level (C; 100% MP), and high protein level (H; 140% MP). At Day 130 ± 1 of gestation dams were humanly euthanized and placentomes were removed for histology analysis. Histology sections were stained with biotinylated Dolichos biflurus (DBA) lectin, Texas red-avidin, and fluorescein (Fluorescien labeled Griffonia simplifolica lectin). There was no significant effect ($P = 0.90$) of maternal protein level on BNC number (180.0, 166.1, and 165.2 ± 28.41 for L, C, and H, respectively). Furthermore, there was no significant effect of maternal protein level on BNC size, proportion of the placentome occupied by cotyledon, nor number of BNCs per cotyledonary area. While we reject our hypothesis that BNC numbers are increased in protein deficient pregnant ewes, we will continue to evaluate if the ovine BNCs produce angiogenic or vasoactive factors that may influence placental function.

Key Words: binuclear cell, placentome, sheep

1152 Effect of serum concentration of β-carotene at AI on productive and reproductive parameters in lactating Holstein cows. A. M. L. Madureira*[1], T. Guzella Guida[1], R. L. A. Cerri[2], and J. L. M. Vasconcelos[1], [1]*Sao Paulo State University, Botucatu, Brazil,* [2]*Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada.*

The objective of this study was to determine the effect of β-carotene concentration in serum at the moment of artificial insemination (AI) on Holstein cows. A total of 497 lactating dairy cows were enrolled. All animals were assigned to a timed AI protocol (CIDR+ estradiol benzoate+GnRH-7d-PG-F-2d-CIDR-out+PGF+ECP-2d-timed AI). Blood samples and body condition score were collected at the moment of AI. The serum B-carotene was quantified in a single step denaturation and extraction into a solvent, followed by measurement using a portable spectrophotometer (iCheck; BioAnalyt, GmbH, Teltow, Germany). Milk production and herd health records were collected for the entire experimental period, and pregnancy diagnosis performed by ultrasound 31 d post-AI. Data were analyzed using the MIXED and GLIMMIX procedures of SAS. Animals with BCS $\leq$ 2.75 had lower ($P < 0.01$) concentration of B-Carotene compared with cows with BCS $\geq$ 3.0 (3.82 ± 0.09 μg/ml and 4.16 ± 0.06μg/ml, respectively). Multiparous cows had greater concentration of B-Carotene compared with primiparous ($P < 0.01$). The concentration of B-carotene at TAI was greater in cows with at least one disease episode between parturition and timed AI compared with healthy animals (3.95 ± 0.12 μg/ml vs. 5.12 ± 0.46 μg/ml). There was no correlation between milk production and concentration of B-carotene ($r < 0.01$), but a quadratic correlation between pregnancy per AI and concentration of B-carotene ($P = 0.03$) was found. When serum B-carotene was categorized as low (< 3.0 μg/ml), intermediate ($\geq$ 3.0– < 6.0 μg/ml) and high $\geq$ 6.0μg/ml, cows with intermediate concentrations were more fertile than the other two categories (29.0%; 38.9% and 22.6%, respectively; $P = 0.05$). In conclusion, the concentration of β-carotene was affected by BCS, parity, incidence of diseases. Animals with intermediate concentrations in serum had greater pregnancy per AI, suggesting a possible use as a marker for fertility in lactating dairy cows.

Key Words: β-carotene, fertility, pregnancy per AI

1153 Propionic acid decreased hepatic acetyl CoA content compared with glycerol within the timeframe of meals when infused abomasally. L. B. Gualdron-Duarte* and M. S. Allen, *Michigan State University, East Lansing.*

We previously reported that propionic acid (P) reduced dry matter (DMI) and metabolizable energy intake compared with glycerol (G) when administered as isoenergetic infusions to the abomasum of cows in the postpartum (PP) period. Our objective in this experiment was to evaluate short-term effects of P compared with G on hepatic acetyl CoA (AcCoA) content for PP cows. We hypothesized that P compared with G will decrease the AcCoA content in the liver within the time frame of a meal. Six ruminal cannulated cows in the PP period (15.2 ± 7.7 d PP) were used in a crossover design experiment to evaluate the effects of G and P pulse dosed to the abomasum on hepatic AcCoA content and plasma concentrations of metabolites and hormones. Cows were randomly allocated to treatment sequence (G-P and P-G) and each block was completed in 3 d with 2 collection days and a rest day between them. Two moles of P or G (2 mol/500mL, $\geq$ 99.5%) were dosed within 1 min to the abomasum 1 h before feeding. Liver tissue was biopsied and blood was collected immediately before dosing and at 30 and 60 min after dosing. Treatments interacted with time to affect AcCoA content ($P < 0.01$). At 30 min after dosing, P decreased AcCoA content by 34% while G increased AcCoA content by 32%, resulting in differences in AcCoA for P compared to G at 30 min (18.0 vs. 36.9 nM/g, $P < 0.0001$), which persisted at 60 min after dosing (21.9 vs. 32.8 nM/g, $P < 0.01$). Plasma BHBA concentration decreased and glucose concentration increased over time for both treatments ($P < 0.001$). While plasma NEFA concentration tended ($P = 0.059$) to be lower for P compared with G at 30 min, it was numerically higher by 60 min when hepatic AcCoA content was still lower. Therefore, the reduction of hepatic AcCoA content by P compared with G was likely because of oxidation in the tricarboxylic acid cycle. This is consistent with these treatment effects on DMI according to the Hepatic Oxidation Theory.

Key Words: acetyl CoA, hepatic oxidation, postpartum

1154 Feed restriction-induced negative energy balance alters the fatty acid profiles of adipose tissue and milk fat of dairy cows. S. E. Schmidt*, K. M. Thelen, C. L. Preseault, G. A. Contreras, and A. L. Lock, *Michigan State University, East Lansing.*

Negative energy balance (NEB) during early lactation results in extensive adipose tissue lipolysis in dairy cows. However, it is not clear if specific adipose depots or fatty acids (FA) are preferentially mobilized. Our objective was to characterize the FA profile of adipose depots and milk fat following feed restriction-induced NEB. Twelve multiparous late lactation (> 200 DIM) Holstein cows, in two experimental blocks, were subjected to treatments consisting of ad libitum feed intake (ADLIB; $n = 6$) or feed restriction (RESTR; $n = 6$) resulting in an energy balance of −13.3 ± 0.5 Mcal/d over 4 d. Milk samples were analyzed for FA composition and collected on d 4. Following the treatment period, all cows were slaughtered and tissue samples were collected from 6 adipose depots: omental, subcutaneous flank, tailhead, perirenal, inguinal, and sternal. Statistical analysis of adipose and milk FA composition was

performed using linear mixed models. RESTR increased the C14 desaturase index (*cis*-9 C14:1/(*cis*-9 C14:1 + C14:0)) of the sternal and tailhead depots ($P < 0.05$) and the C16 desaturase index (*cis*-9 C16:1/(*cis*-9 C16:1 + C16:0)) of the tailhead depot ($P < 0.01$). RESTR decreased C18:0 content of the tailhead depot (8.7 vs. 12.8 g/100 g FA; $P = 0.01$). Across all depots, RESTR increased the *cis*-9 C14:1 content of adipose tissue ($P = 0.04$). RESTR decreased daily yield of de novo-synthesized FA in milk ($P = 0.02$) but the yields of 16-carbon and preformed FA were not affected by treatment ($P \geq 0.20$). Compared to ADLIB, RESTR increased the C18 desaturase index (*cis*-9 C18:1/(*cis*-9 C18:1 + C18:0)) (0.73 vs. 0.66) and the C16 desaturase index (0.08 vs. 0.05) of milk fat ($P < 0.01$). RESTR increased the daily yields of *cis*-9 C16:1 and *cis*-9 C18:1 in milk fat compared to ADLIB (both $P < 0.05$), while the yields of C16:0 and C18:0 were not affected by treatment ($P \geq 0.24$). RESTR increased total monounsaturated FA yield in milk ($P = 0.03$), but treatment did not alter total saturated FA or polyunsaturated FA yields ($P \geq 0.11$). Alterations in adipose FA composition, suggesting mobilization of saturated FA, occurred only in the subcutaneous adipose depots, and most dramatically in the tailhead. However, increased desaturase activity in the mammary gland most likely prevented a subsequent increase in saturated FA yield of milk.

Key Words: adipose, energy balance, lipolysis

1155 Body condition score and body condition score change: Associations with fertility phenotypes in lactating dairy cows.

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The objective was to examine the associations between BCS and BCS change and utero-ovarian status in first and second parity dairy cows (n = 910; 22 commercial pasture-based dairy herds). Each cow was examined at wk 3 ± 1 and 7 ± 1 postpartum. Transrectal ultrasound exams were conducted to determine presence/absence of corpora lutea (CL). BCS was measured using a 1 to 5 scale, with increments of 0.25. Vaginal discharge score (VDS) of the contents of the vagina was assessed using the Metricheck device. For VDS, an objective scoring scheme on a 1 to 5 scale with 1 point increments was utilized (1 = no infection; 2 = mild infection; > 2 = severe infection). Binary data were analyzed using the GLIMMIX procedure of SAS. Dependent variables were CL and VDS at 3 and 7 wk postpartum. Independent variables were BCS and BCS change (loss, constant, or gain between 3 and 7 wk postpartum), with farm, parity, and DIM on the day of the exam included as adjustment variables. For CL, VDS score was included as an adjustment variable, whereas for VDS, CL was included as an adjustment variable. Fixed effects were tested and retained where $P \leq 0.1$. For variables with a binary distribution (CL) model-adjusted LSMEAN values are presented, whereas, for variables with a multinomial distribution (VDS), unadjusted raw mean values are presented. The proportion of cows that had a CL at wk 3 was 0.45 and 0.58 when cows had BCS $\leq$ 2.75 and $\geq$ 3.00, respectively ($P = 0.002$), and the corresponding figures at wk 7 were 0.74 and 0.89, respectively ($P < 0.0001$). There was no association between BCS change and CL at wk 3 ($P = 0.7$) or wk 7 ($P = 0.9$). At wk 3, the proportion of cows that were classified as having no infection, mild infection, or severe infection was 0.15, 0.23, and 0.62 for cows with BCS $\leq$ 2.75 and 0.15, 0.32, and 0.53 for cows with BCS $\geq$ 3.00, respectively ($P = 0.01$). At 6–8 wk, the proportion of cows that were classified as having no infection, mild infection, or severe infection was 0.46, 0.32, and 0.23 for cows with BCS $\leq$ 2.75 and 0.52, 0.30, and 0.18 for cows with BCS $\geq$ 3.00, respectively ($P = 0.05$). The findings highlight the importance of BCS during early lactation for restoration of cyclicity and uterine health status in pasture-based systems.

Key Words: BCS, utero-ovarian status

1156 Effects of Omnigen-AF supplementation on body temperature, milk production, and somatic cell count in lactating dairy cows.

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The objective this study was to evaluate the effects of Omnigen-AF (OMN; Phibro Animal Health, Teaneck, NJ) supplementation on body temperature, and production variables of lactating dairy cows. Thirty-two Holstein × Gir cows (100 ± 10 d in milk) were assigned to either control or OMN treated groups, balanced for previous milk production, parity, and body condition score. Dietary treatments were individually fed to cows once daily after the morning milking, at a rate of 56 g/day of kaolin (rumen-inert substance) or OMN added to 200 g of ground corn used as carrier for 56 d, and separated from the TMR diet that was fed ad libitum and formulated to meet or exceed cow nutritional requirements. Temperature and humidity loggers were used to record environmental data and temperature-humidity index. To assess body temperature, each animal was inserted with a thermometer coupled to an intravaginal device from d 15 to 28, and d 43 to 56 of the experiment. Thermometers were set to measure vaginal temperature every 10 min, and values were averaged hourly. Supplementation with OMN increased ($P < 0.01$) milk yield (21.3 vs. 20.1 kg/d for OMN and control, respectively; SEM = 0.13) and DMI (17.6 vs. 16.6 kg/d for OMN and control, respectively; SEM = 0.19), and decreased ($P = 0.06$) milk somatic

cells count (5.30 vs. 5.48 $\log_{10}$ cells/mL for OMN and control, respectively; SEM = 0.05). Treatment × time interactions were not significant ($P \geq 0.15$) for the production variables analyzed herein. Furthermore, when environmental temperature-humidity index was > 68, cows supplemented with OMN remained less ($P < 0.01$) time with body temperature above 39.1°C (38 vs. 45% for OMN and control, respectively; SEM = 0.05%). In conclusion, supplementing OMN to lactating dairy cows increased milk yield and DMI, decreased milk somatic cells count, and reduced incidence of rectal temperature above 39.1°C under heat stress conditions.

Key Words: dairy cows, dietary supplementation, heat stress

1157 The effects of stage of gestation and maternal nutrient status on binucleate cell numbers in the beef cow.

A. M. Peterson*[1], A. Reyaz[1], S. T. Dorsam[1], L. E. Camacho[2], K. C. Swanson[1], A. Grazul-Bilska[1], and K. A. Vonnahme[1], *[1]North Dakota State University, Fargo, [2]University of Arizona, Tucson.*

Our laboratory has demonstrated that maternal nutrition in beef cows can impact uterine blood flow and vascular function of excised placental arteries. However, there is little evidence to suggest that maternal nutrition is impacting capillary number. There is evidence in other species that multi-nucleated cells (i.e., binucleate cells; BNC) in the placenta may produce vasoactive factors. The objective was to test the hypothesis that maternal nutrient restriction followed by early realimentation would increase BNC numbers in the bovine placentome. On d 30 of pregnancy, multiparous, non-lactating cows (620.5 ± 11.3 kg) were assigned to 1 of 2 dietary treatments: control (C;100% NRC; $n = 18$) and restricted (R; 60% NRC; $n = 30$). On d 85, cows were slaughtered (C, $n = 6$; R, $n = 6$), remained on control (CC; $n = 12$) and restricted (RR; $n = 12$), or were realimented to control (RC; $n = 11$). On d 140, cows were slaughtered (CC, $n = 6$; RR, $n = 6$; RC, $n = 5$), remained on control (CCC, $n = 6$; RCC, $n = 5$), or were realimented to control (RRC, $n = 6$). On d 254, all remaining cows were slaughtered. Placentomes were collected and fixed in formalin. Tissue sections were stained using biotinylated lectin Dolichos Biflorus Agglutinin (DBA), Texas red avidin, and DAPI mounting media to visualize BNC. Using image analysis, BNC number, BNC size, and percentage BNC area per tissue area were determined. While there was no effect of diet ($P > 0.11$) on any measurement, there was a main effect of day ($P < 0.01$) where BNC numbers decreased as gestation advanced (572.5, 504.1, 489.1 ± 31.35 for d 85, 140, and 254, respectively). In addition, the BNC size decreased ($P < 0.01$) from d 85 to 140 of gestation, then increased until d 254 (63.1, 51.8, 65.2 ± 3.0 mm^2, respectively). Similarly, the percent BNC area per tissue area decreased ($P < 0.01$) from d 85 to 140 and then increased by d 254 (3.76, 2.78, 3.39 ± 0.20%, respectively). Thus, stage of pregnancy but not diet affected selected BNC measurements indicating a specific role of BNC as pregnancy progresses. Additional studies are currently underway to investigate expression of vasoactive factors (e.g., endothelial nitric oxide) by the bovine BNC, and if maternal diet can alter the expression of those factors.

Key Words: binucleate cell, cow, placentome

1158 Effects of post-AI supplementation with Ca salts of soybean oil on ovarian and pregnancy development in *Bos indicus* beef cows.

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The objective of this experiment was to compare corpus luteum (CL) and pregnancy development in beef cows supplemented or not with Ca salts of soybean oil for 21 d (CSSO) beginning after timed-AI. One hundred lactating multiparous Nelore (*Bos indicus*) cows (BW = 430 ± 5 kg, BCS = 2.87 ± 0.02; age = 8.5 ± 0.2 yr; days post-partum = 152 ± 1 d) were inseminated on d 0 of the experiment, and divided into 20 groups of 5 cows/group. Groups were randomly assigned to receive (as-fed basis) 100 g of protein-mineral mix + 100 g of ground corn per cow/d, in addition to: 1) 100 g/cow daily of CSSO ($n = 10$), or 2) 100 g/cow daily of kaolin (CON; rumen-inert indigestible substance; $n = 10$). Groups were maintained in 4 *Panicum maximum* pastures (5 groups from the same treatment within each pasture) with ad libitum access to forage. However, groups were segregated daily and offered treatments individually during the experimental period (d 0 to 21). Blood samples were collected and transrectal ultrasonography was performed to verify ovulation and corpus luteum (CL) volume immediately before AI (d 0), on d 7, and 15. Immediately after ultrasonography on d 15, 60 cows (30 cows/treatment, 3 cows/group) diagnosed without the presence of a CL on d 0, but with a CL greater than 0.38 cm^3 in volume on d 7 and 15, were assigned to embryo collection via uterine flushing with PBS. On d 30, final pregnancy status was determined via transrectal ultrasonography. No treatment differences ($P = 0.68$) were detected on dominant follicle diameter on d 0. However, mean CL volume on d 7 and 15 was greater ($P = 0.04$) for CSSO vs. CON cows (3.2 vs. 2.7 cm^3, respectively; SEM = 0.2). No treatment differences were detected ($P \geq 0.85$) for the proportion of cows that had an embryo on d 15 (40.0 vs. 39.2% for CSSO and CON cows, respectively; SEM = 8.9) or diagnosed as pregnant on d 30. However, embryos

collected from CSSO cows were longer ($P = 0.04$) compared with embryos collected from CSSO cohorts (2.57 vs. 1.15 cm, respectively; SEM = 0.59). In summary, supplementing beef cows with 100 g of CSSO beginning after AI increased CL and embryo development by d 15 of gestation.

Key Words: beef cows, Ca salts of soybean oil, embryo, ovary, pregnancy

PHYSIOLOGY AND ENDOCRINOLOGY SYMPOSIUM: PRE- AND POST-NATAL IMPACTS ON OFFSPRING PERFORMANCE

1159 Consequences of early nutritional insults on fetal hepatic glucose metabolism and insulin action. S. R. Wesolowski*, *University of Colorado School of Medicine, Aurora.*

Pregnancies complicated by placental insufficiency or reduced maternal nutrient supply produce fetuses with intrauterine growth restriction (IUGR). These in utero insults expose the fetus to a reduced supply of glucose, amino acids, and, in some cases, oxygen. The fetus adapts to these reductions in nutrient supply by reducing insulin secretion, increasing counter-regulatory hormone levels, and developing coordinated tissue-specific adaptations in glucose metabolism. Data from our fetal sheep model of IUGR demonstrate an early activation of hepatic glucose production and increased hepatic gluconeogenic gene expression (*PCK1*, *G6PC*) that are sustained during a hyperinsulinemic-euglycemic clamp, thus demonstrating the development of hepatic insulin resistance. This is liver specific insulin resistance because the IUGR fetus has a robust increase in non-hepatic insulin-stimulated glucose utilization in peripheral tissues. While this early activation of glucose production in utero may be an important adaptive response to produce glucose for other glucose-consuming fetal tissues, uncontrolled and dysregulated hepatic glucose production has adverse consequences postnatally and is a major component to diabetes in humans. The early mechanisms driving dysregulated hepatic glucose production and insulin resistance in the fetal liver are not fully understood. We have found that the AKT protein is robustly phosphorylated in the IUGR liver in response to insulin, yet downstream FOXO1 phosphorylation and nuclear localization is increased. We also find that despite decreased nutrient supply, stress signals like AMPK are not increased in the IUGR fetal liver. In addition to increased glucose production, our recent data also demonstrate decreased mitochondrial oxidation in the IUGR fetal liver and a compensatory increase in hepatic glycolysis, intrahepatic lactate production and utilization, and altered substrate preference for reduced hepatic oxidative metabolism. This combination of metabolic adaptations by the fetal liver may be necessary to activate and sustain GPR. However, decreased hepatic mitochondrial function that persists postnatally may underlie the development of hepatic steatosis in offspring who were IUGR. Overall, understanding the endocrine and molecular pathways responsible for these early metabolic adaptations in the fetus, will allow for development of targeted strategies to improve liver function in the fetus and improve postnatal growth and performance and decrease risk for diabetes and metabolic disease later in life.

Key Words: fetus, metabolic adaptations, nutrition

1160 Alterations in uteroplacental hemodynamics during melatonin supplementation in sheep and cattle. C. O. Lemley*[1] and K. A. Vonnahme[2], [1]*Mississippi State University, Mississippi State,* [2]*North Dakota State University, Fargo.*

Compromised placental function can result in fetal growth restriction which is associated with greater risk of neonatal morbidity and mortality. Large increases in transplacental nutrient and waste exchange, which support the exponential increase in fetal growth during the last half of gestation, are dependent primarily on the rapid growth and vascularization of the uteroplacenta. We are examining maternal nutritional plane along with therapeutic supplements, such as dietary melatonin, which impact placental vascularization, blood flow, and fetal development. Using a mid- to late-gestation ovine model of intrauterine growth restriction ($n = 31$), we examined uteroplacental blood flow and fetal growth during supplementation with 5 mg of dietary melatonin per day. Maternal nutrient restriction decreased uterine artery blood flow, while melatonin supplementation increased umbilical artery blood flow compared to non-supplemented controls. Although melatonin treatment did not rescue fetal weight in nutrient restricted ewes; we did observe disproportionate fetal size and fetal organ development. Moreover, fetal uptake of branched-chain amino acids was partially rescued by dietary melatonin supplementation. Elevated fetal concentrations of melatonin may result in altered blood flow distribution during important time points of development. These specific melatonin responses on umbilical artery hemodynamics and fetal development may be partially mediated through vascular melatonin receptors. Recently, we examined the effects of supplementing Holstein heifers ($n = 20$) with 20 mg of dietary melatonin per day during the last third of gestation. Uterine artery blood flow was increased by 25% and total serum antioxidant capacity was increased by 43% in melatonin supplemented heifers versus non-supplemented controls. In addition, peripheral concentrations of progesterone were decreased in melatonin supplemented heifers vs. non-supplemented controls. Using an in vitro model, melatonin treatment increased the activity of cytochrome P450 2C, a progesterone inactivating enzyme, which was blocked by treatment with the melatonin receptor antagonist, luzindole. Elucidating the consequences of specific therapeutic supplements on the continual plasticity of placental function will allow us to determine the proper timing

and duration for intervention and improvements in offspring growth and development.

Key Words: melatonin, umbilical blood flow, uterine blood flow

1161 Development of the fetus and fetal reproductive tract in gilts subjected to heat stress from week 4 to 8 of gestation. C. J. Bernhard*, T. J. Safranski, M. C. Lucy, W. R. Lamberson, S. G. Moore, L. M. Mayo, and R. Molina-Coto, *University of Missouri, Columbia.*

Gestational heat stress may lead to transgenerational changes in the reproductive capacity of boars and gilts. The objective was to assess fetal and placental development and the development of gonads in conceptuses whose mother was subjected to gestational heat stress (GHS; 28 to 38°C; 65 to 88% relative humidity; $n = 12$) or gestational thermoneutral (GTN; 17 to 22°C; 56 to 65% relative humidity; $n = 11$) conditions during pregnancy. Gilts were housed in the Brody Environmental Chambers from week (wk) 4 to 8 of pregnancy before sacrifice during the eighth wk of gestation for the collection of the reproductive tracts and fetal tissues. During pregnancy, GHS gilts had greater rectal temperature (38.5 ± .04 vs. 38.0 ± .04°C; $P < .001$), skin temperature (35.5 ± .2 vs. 28.7 ± .2°C; $P < .001$), and respiration rate (44.3 ± 2.6 vs. 19.5 ± 2.7 breaths per min; $P < .001$) compared with GTN. Sow was the experimental unit for analyses of fetal development. The weight of the pregnant tract (12.0 ± 1.2 vs. 12.5 ± 1.3 kg), number of viable conceptuses (13.8 ± .8 vs. 15.3 ± .9), the number of non-viable conceptuses (.3 ± .2 vs..1 ± .2), the number of mummies (.2 ± .1 vs..3 ± .1), and the % survival (number of viable conceptuses/number corpora lutea; 89 ± 4 vs. 90 ± 5%) did not differ ($P > .10$) for GHS vs. GTN (respectively). Upon dissection, the weight of the fetus (82.3 ± 3.6 vs. 84.9 ± 3.8 g), placenta (155.5 ± 14.7 vs. 170.1 ± 15.6 g), fetal fluid (80.4 ± 10.0 vs. 90.4 ± 10.6 g), and placental efficiency (fetal weight/placental weight; 0.60 ± .04 vs. 0.55 ± .05) did not differ ($P > .10$) for GHS vs. GTN (respectively). The ratio of male to female fetuses was similar ($P > .10$) for GHS (1.3 ± .3) and GTN (1.6 ± .3). The weight of male fetuses (86.2 ± 3.8 vs. 86.4 ± 4.0 g), combined testis weight (34.2 ± 1.4 vs. 32.8 ± 1.5 mg), and combined testis weight as a % of fetal weight (.040 ± .001 vs. .038 ± .001) did not differ ($P > .10$) for GHS vs. GTN (respectively). The weight of female fetuses (81.2 ± 3.6 vs. 83.5 ± 3.8 g), combined ovarian weight (25.2 ± 1.0 vs. 26.1 ± 1.1 mg), and combined ovarian weight as a % of fetal weight (.031 ± .001 vs..031 ± .001) did not differ ($P > .10$) for GHS vs. GTN (respectively). The conclusion was that heat stress from wk 4 to 8 of gestation in gilts did not change the growth of the fetus, placenta, ovary, or testis at mid-gestation. Research was supported by the National Pork Board.

Key Words: fetal development, gestation, heat stress

1162 The effects of under- and over-feeding ewes during gestation on offspring growth and stem cell function. K. E. Govoni*, S. A. Reed, M. L. Hoffman, S. M. Pillai, and S. A. Zinn, *Department of Animal Science, University of Connecticut, Storrs.*

Poor maternal nutrition during gestation has been linked to poor growth and development, metabolic dysfunction, impaired health, and reduced productivity of offspring in many species. Poor maternal nutrition can be defined as an excess or restriction of overall nutrients or specific macro- or micronutrients in the mother's diet during gestation. Interestingly, there are several reports that both over- and under-feeding during gestation negatively affect offspring postnatal growth with reduced muscle and bone, increased fat, and metabolic dysregulation through reduced leptin and insulin sensitivity. Our laboratory established a model to evaluate both under- and over-feeding during gestation in one population of ewes to evaluate effects on early postnatal growth of offspring. Specifically, ewes were under-fed (60% of NRC for TDN), over-fed (140% of NRC for TDN), or control-fed (100% of NRC for TDN) beginning at d 31 ± 1.3 of gestation. Blood and tissue samples were collected at birth and 3 mo of age. As previously reported, during the first 3 mo of postnatal growth, over-feeding during gestation increased body size, circulating growth factors and metabolic hormones in offspring. Both under- and over-feeding altered muscle growth, increased lipid content in the muscle and caused changes in expression of myogenic factors. Although the negative effects of poor maternal nutrition on offspring growth have been well characterized in recent years, the mechanisms are not well established. Our laboratory has focused on elucidating these mechanisms by evaluating changes in gene and protein expression and stem cell function. Through RNA-Seq analysis, we observed changes in expression of genes involved in protein synthesis, metabolism, cell function, and signal transduction in muscle tissue. We recently reported that satellite cells, muscle stem cells, have altered expression of myogenic factors in offspring from under-fed mothers. Mesenchymal stem cells, multipotent cells that contribute to development and maintenance of several tissues including bone, muscle and adipose, have a 50% reduction in cell proliferation ($P < 0.05$) and altered metabolism in offspring from both under- and over-fed mothers. These findings suggest that poor maternal nutrition may alter offspring postnatal growth by programming the stem cell populations. In conclusion, poor maternal nutrition during gestation negatively affects offspring postnatal growth, potentially through impaired stem cell function. Therefore, determining the mechanisms that contribute to fetal programming are critical to identifying novel methods to manage these offspring and improve efficiency of production.

Key Words: maternal nutrition, sheep, stem cells

1163 Postnatal reproductive development and the lactocrine hypothesis. F. F. Bartol[*1], C. A. Bagnell[2], and A. F. George[2], *[1]Auburn University, Auburn, AL, [2]Rutgers University, New Brunswick, NJ.*

Maternal contributions to development begin at conception. Prenatal conditions that evolve in utero through the course of gestation define the environment in which embryogenesis and fetoplacental development occur. Genotype notwithstanding, maternal effects on development from the time of conception can program cell fate and dictate offspring phenotype as defined by various aspects of performance and health, including fertility and fecundity. Maternal effects on development do not end at birth, but extend into postnatal life through signals communicated from mother to offspring in first milk (colostrum). Transmission of bioactive factors from mother to offspring as a specific consequence of nursing defines a lactocrine mechanism. The female reproductive tract (FRT) is not fully formed at birth. Data for both ungulate species and mice indicate that disruption of the developmental program during critical organizational periods of neonatal life can have lasting effects on the form and function of FRT tissues, including the uterus. Radial patterning of the uterine wall, reflected by differentiation and proliferation of nascent endometrial glands, is a postnatal event in most mammals. Both uterine growth and histogenesis proceed in an ovary-independent manner shortly after birth, suggesting that extra-ovarian inputs are important in this process. Data for the pig indicate that lactocrine signals constitute one source of such uterotrophic support. Disruption of lactocrine signaling by feeding gilts porcine milk replacer instead of colostrum for 2 d from birth (postnatal day = PND 0) retarded uterine gland genesis by PND 14. Differences in endometrial and whole uterine gene expression patterns between colostrum- and replacer-fed gilts were evident by PND 2, when RNA sequencing revealed over 800 differentially expressed, lactocrine-sensitive genes. Organizationally relevant, lactocrine-sensitive processes, pathways, and networks identified through transcriptomic studies included cell adhesion, cell-cell signaling, cytokine-receptor interactions, integrin cell surface interactions, ESR1 and Hedgehog signaling, and the plasminogen activating network. Lactocrine-sensitive expression of nine microRNAs with 115 potential mRNA targets was also identified. Results provide evidence of lactocrine-mediated, epigenetic effects on multiple elements of the uterine developmental program. A single oral dose of colostrum given at birth affects endometrial cell behaviors associated with uterine wall development by 12 h postnatal. Evidence that minimal colostrum consumption at birth is associated with reduced lifetime fecundity in adult sows indicates that lactocrine programming can affect reproductive efficiency. Data support a role for lactocrine signaling in regulation of postnatal reproductive tract development and function.

Key Words: development, lactocrine programming, reproductive tract, uterus

1164 Supplementation of corn-dried distiller's grains plus solubles to gestating beef cows fed low quality forage: neonatal calf performance. V. C. Kennedy[*1], J. J. Gaspers[1], B. Mordhorst[1], G. L. Stokka[2], M. L. Bauer[1], K. C. Swanson[1], and K. A. Vonnahme[1], *[1]North Dakota State University, Fargo, [2]Department of Animal Sciences, North Dakota State University, Fargo.*

We have previously reported that corn-dried distiller's grains plus solubles (DDGS) supplementation to low quality forage during late gestation results in a tendency for heavier calves at birth and larger weaning weights compared to no DDGS (CON). To investigate if birth and weaning weight differences were due to metabolite or hormonal status, calf blood samples were collected during early life. Multiparous beef cows (n = 27; 674 ± 17 kg) were divided randomly into 2 pens equipped with Insentec feeders to monitor individual intake of corn stover and silage. For 10 wk, both treatment groups were fed the basal diet for ad libitum intake while one group was supplemented (SUP; n = 12) with DDGS at 0.3% of BW during the last third of gestation. Following parturition, all cows received the same diet for an additional 8 wk. At calving (0 and 24 h) and weekly for 56 d, blood samples were obtained from calves for analysis of NEFA, urea, glucose, cortisol, thyroxine (T_4) and triiodothyronine (T_3). From 0 to 24 h, NEFA concentrations did not differ between treatment groups, but were greater at 0 h (571 vs. 366 ± 40 μM, $P < 0.01$). Neither urea nor cortisol differed by treatment or hour at 0 and 24 h, however, treatment interacted with time for glucose, where SUP calves had the greatest concentration at 24 h (6.83 ± 0.32 mM). Glucose decreased from birth onward ($P < 0.01$), with treatments beginning to separate near d 56. Both T_3 and T_4 decreased ($P < 0.01$) from birth to d 56. Neither NEFA nor cortisol differed ($P \geq 0.95$, $P \geq 0.35$, respectively) by day or treatment. Urea was influenced by day ($P = 0.06$), but with little overall deviation from concentrations at birth. While there was no impact of diet on dystocia ($P = 0.39$), calves from SUP cows were heavier ($P = 0.01$) at birth than CON calves, which may have impacted their greater glucose concentration at 24 h. It appears that heavier weaning weights observed in calves from SUP cows were not influential on the measured metabolites and hormone profiles at birth and through early life.

Key Words: beef cows, metabolites, neonatal life

1165 The effects of nutritional restriction on endogenous retroviruses and placentation during the first 50 d of gestation in beef heifers.
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The objectives of this study were to evaluate the effects of maternal nutrient restriction and day of gestation on mRNA expression of *syncytin-Rum1*, bovine endogenous retrovirus K1 (*BERV-K1*), interferon-tau (*INF-τ*), and pregnancy specific protein B (*PSP-B*). At breeding (0 d), crossbred heifers ($n = 49$; ~15 mo of age; initial BW = 324.9 kg) were assigned to dietary treatments, control (fed to gain 0.45 kg/d BW gain) or restricted (60% of control). Heifers were ovariohysterectomized at d 16, 34, or 50 resulting in a 2 × 3 factorial. Non-bred, non-pregnant heifers ($n = 6$; NP), on the control diet, were ovariohysterectomized as baseline controls on d 16 of the estrous cycle. The tissues collected consisted of pregnant horn caruncle (P-CAR), pregnant horn inter-caruncle (P-ICAR), non-pregnant horn caruncle (NP-CAR), non-pregnant horn inter-caruncle (NP-ICAR), and fetal membrane (chorioallantoic; FM). Relative gene expression was calculated using the delta delta Ct method with β-actin as the reference gene and NP as the control tissue. Data were analyzed using PROC GLM of SAS with the model including d of gestation, nutritional treatment, and their interaction. There was significant d of gestation × nutrition interaction for expression of *BERV-K1* in NP-CAR and *INF-τ* in FM while all other interactions were not significant ($P > 0.08$). Expression of *INF-τ* was influenced by d of gestation and nutritional treatment in FM, with d 16 restricted being greatest (5781 fold; $P < 0.01$) followed by d 16 control FM (3324 fold); the remaining d and treatments were not different. In FM, *BERV-K1* was greatest ($P < 0.01$) on d 34 (2961 fold) compared with d 16 and 50 (5 and 1861 fold, respectively). *Syncytin-Rum1* increased ($P = 0.04$) in FM throughout the first 50 d (375 fold) of gestation. *Syncytin-Rum1* expression in P-ICAR was greatest ($P = 0.01$) at d 16; however, *syncytin-Rum1* expression in P-CAR tended ($P = 0.09$) to be greater at d 50. Expression of *PSP-B* increased ($P < 0.01$) throughout early gestation until d 50 in both NP-CAR (316 fold) and P-CAR (18,215 fold). Although nutritional restriction did not influence endogenous retrovirus expression in maternal or fetal tissues, it did influence *INF-τ* expression. These data suggest that both BERV-K1 and syncytin-Rum1 may interact with PSP-B during the establishment of the feto-maternal interface and syncytial plaques.

Key Words: beef heifers, early gestation, endogenous retroviruses, nutrient restriction

PHYSIOLOGY, ENDOCRINOLOGY, AND EXTENSION SYMPOSIUM: ENHANCING ADOPTION OF REPRODUCTIVE MANAGEMENT TOOLS FOR BEEF AND DAIRY PRODUCERS

1166 History of the development of the Beef Reproduction Task Force (BRTF) and impacts of the BRTF on beef cattle reproductive management.
S. Johnson[*1], R. F. Cooke[2], G. R. Dahlke[3], R. N. Funston[4], J. B. Hall[5], D. J. Kesler[6], G. C. Lamb[7], J. Lauderdale[8], D. J. Patterson[9], G. A. Perry[10], D. R. Strohbehn[3], and A. L. Van Eenennaam[11], *[1]Kansas State University, Colby, [2]Oregon State University-EOARC Burns, Burns, [3]Iowa State University, Ames, [4]University of Nebraska, North Platte, [5]University of Idaho Nancy M. Cummings Research, Extension Education Center, Carmen, [6]University of Illinois at Urbana-Champaign, Urbana, [7]University of Florida, North Florida Research and Education Center, Marianna, [8]Lauderdale Enterprises, Inc., Augusta, MI, [9]University of Missouri, Columbia, [10]Department of Animal Science, South Dakota State University, Brookings, [11]University of California, Davis.*

The Beef Reproduction Task Force (BRTF) was formed during a period of evolving science that resulted in systems to allow producer-acceptable results with a single fixed-timed insemination. The group organized and developed goals to enhance productivity and profitability of U.S. beef herds by integrating research and extension efforts with the intent of more effectively transferring the use of reproductive technologies to the field. A key early step was to coordinate efforts in identifying effective breeding management protocols for beef cattle and to clarify their associated acronyms. A short-list of recommended protocols and their acronyms for synchronization of estrus and ovulation in beef cattle was developed based on results from peer-reviewed, published research and a comprehensive review of data collected from the field. The list of recommended protocols was developed by the BRTF in cooperation with veterinarians and representatives from associated industries. The synergies of this larger industry-centered working group have resulted in ideas for research and broader educational reach. Together the group has planned and hosted 17 in-depth meetings at locations in key cow-calf areas across the country since 2002. These "Applied Reproductive Strategies in Beef Cattle" workshops targeted beef producers, AI industry personnel, veterinarians, allied industry representatives, and academicians. A national media sponsor has provided online coverage of the meetings (www.appliedreprostrategies.com) since 2008. The effectiveness of the team was recognized with the NIFA Partnership Award for

Multistate Efforts in 2013. A 2013 national survey of AI users indicated 97% of respondents (n = 425) were familiar with the BRTF recommended protocol lists. Recommendations from these guidelines were generally used by 65% and sometimes or occasionally used by 20% of respondents. Resources developed by the group include the Estrus Synchronization Planner in a mobile and spreadsheet version, tools to evaluate cost differences of AI and natural service breeding and numerous publications and support materials on a beefrepro.info website. The group has set in place a plan to bring in new members to help address changing industry needs. The multi-state research and extension effort combined with the industry group's insight and support have provided valuable information in a growing beef AI industry.

Key Words: artificial insemination, beef, synchronization of estrus

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1167 History of the development of the Dairy Cattle Reproduction Council (DCRC) and impacts of the DCRC on dairy cattle reproductive management.

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The DCRC was founded in 2006 in response to a decline in lactating dairy cow fertility that was occurring worldwide. The initial founders included academicians, allied industry professionals, veterinarians, and producers. The established goals of the organization are to educate and provide support for the development and implementation of new technologies that will sustain and improve reproduction in dairy cows and heifers. The organization is guided by a series of principles that were established by its founding members, the most important of which was to be science-based and non-commercial. The group is inclusive and seeks to involve all individuals with an interest in dairy reproduction. A professional and discounted student membership is offered. Members have full access to past proceedings and newsletters. Officers, directors, and committee members of the DCRC serve on a voluntary basis. There are four primary mechanisms through which the DCRC achieves its stated goals. First, a meeting is held annually that includes invited presentations on relevant topics. An invited poster session is also held during the meeting. The meeting is moved to different locations within the United States to facilitate participation by individuals from different dairy regions. Second, an awards competition is sponsored that identifies and recognizes dairy herds with the best reproduction by using objective criteria. Awardees are invited to participate in the annual meeting and are also recognized in trade magazines. Third, resource materials are prepared that include protocol sheets with diagrams of reproductive protocols for both dairy cows and heifers. The protocols depicted on the sheets are vetted annually by a committee so that the information is current and based on the most-recent scientific findings. The protocol sheets are printed in both English and Spanish languages. Finally an electronic newsletter is published six times each year that includes a president's message, research summaries, technical information, a member profile, and a meeting calendar. The 2015 meeting held in Buffalo, NY was the largest meeting to date. The continued growth of the DCRC and recognized improvements in dairy reproduction in the past 10 yr speak to the success of the organization.

Key Words: cow, dairy, fertility

1168 Physiological and management advances enhancing adoption of applied reproductive management procedures in beef cattle.

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Advances in research over the past two decades expanded our understanding of the bovine estrous cycle and led to improvements in methods to more effectively control estrus and ovulation in beef heifers and cows. Precise monitoring of ovarian follicles and corpora lutea over time by transrectal ultrasonography expanded our understanding of the changes that occur during a follicular wave. Consequently, we now know that precise control of estrous cycles requires the manipulation of both follicular waves and luteal lifespan. As a result, breeding management technologies are currently available or emerging that offer the potential to more effectively manage reproduction, expedite genetic progress, enhance efficiencies of production, and add value to beef cattle produced and marketed in the U.S. Until recently, the inability to predict time of estrus for individual cows or heifers in a herd was the primary reason beef producers viewed AI as being impractical to use because of the labor required to detect estrus. However, improvements in methods to control estrus and ovulation in beef heifers and cows provide the opportunity to expand the use of AI by reducing the period of time required to detect estrus or eliminate estrus detection entirely. Protocols for inducing and synchronizing a fertile estrus in which progestins are used strategically with gonadotropin releasing hormone and prostaglandin F2α provide opportunities for beef producers to synchronize estrus and ovulation and facilitate fixed-time AI. Procedures used to control estrous cycles in cattle include synchronization of estrus and ovulation in estrous cycling females, and induction of estrus accompanied by fertile ovulation in heifers that have not yet reached puberty or among cows that have not

returned to estrus after calving. These strategies provide opportunities for producers to utilize sires of elite genetic merit, reduce length of the breeding and calving seasons, produce more uniform calf crops, and improve reproductive rates of replacement beef heifers and the mature cow herd. Collectively, advancements in applied reproductive technologies afford beef producers the flexibility to match specific breeding management protocols to a defined management system, thereby creating the opportunity to significantly expand use of AI in beef herds across the United States and enhance profitability of the beef enterprise.

Key Words: beef, estrus synchronization, fixed-time AI

1169 Physiological and management advances enhancing adoption of applied reproductive management procedures in dairy cattle.

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Since the first meeting of the Dairy Cattle Reproduction Council in 2006, several advances occurred to upgrade reproductive management programs in dairy herds. Many advancements are refinements of the currently applied standard 7-d Ovsynch program (GnRH [d 0; G1]; $PGF_{2\alpha}$ [1 dose on d 7]; GnRH [G2; d 9.5]; and AI 16 h after G2). Key advances: (1) including GnRH in presynchronization programs to facilitate ovulation before first or repeat AI to change the proportion of cows with a corpus luteum (CL) and more moderate progesterone concentrations to start Ovsynch, thus increasing G1-induced LH release and subsequent ovulation to G1 and greater pregnancy per AI (P/AI). (2) Clarifying the specific role of progesterone in targeted sub-fertile populations before first or repeat AI of cows without a CL to facilitate greater P/AI compared with non-progesterone treated controls without a CL, but similar P/AI to cows starting Ovsynch in diestrus. (3) Applying increased dosages or additional injections of $PGF_{2\alpha}$ to enhance luteolysis before timed AI to increase P/AI in cows treated with either the 5- or 7-d Ovsynch program. (4) Increasing dosages of GnRH at G1 or G2 to increase ovulation incidence did not always increase P/AI. (5) Diagnosing pregnancy via blood or milk pregnancy-associated glycoprotein (PAG) tests beginning 28 d post-AI to spare veterinarians' time to address other health issues. (6) Field testing the role of a 5- or 7-d Ovsynch program with progesterone inserts to facilitate timed AI in dairy heifers to increase early pregnancy in replacement heifer programs and reduce days on feed before first calving. (7) Incorporating gender-selected semen in AI programs to increase herd size from within, allow for more selective culling, and less outsourced heifer purchases. (8) Applying software tools to project revenues and costs associated with various timed AI and estrus-detection AI programs. (9) Detecting ovarian structures to more accurately diagnose large anovulatory follicles or ovarian cysts, early pregnancy, and subsequent embryo survival via diagnostic transrectal ultrasonography. (10) Applying technologies such as activity monitors to assess increased physical activity associated with estrus, monitor rumination and ear temperature, and RFID for accurate cow identification. (11) Clarifying the role of postpartum health (clinical and subclinical disease) on subsequent P/AI. (12) Applying genomics and fertility-selection traits to enhance fertility. These physiological advances have impacted reproductive management, increased P/AI, and promoted sustainability of dairy herds to provide dairy products to feed a hungry world.

Key Words: dairy, fertility, management

1170 Impacts of temperament on reproductive performance of *Bos indicus* and *B. taurus* beef females.

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Temperament is defined as the fear-related behavioral responses of cattle when exposed to human handling. Our group evaluates cattle temperament using: 1) chute score; 1 to 5 scale that increases according to excitable behavior during restraint in a squeeze chute, 2) exit velocity; speed of an animal exiting the squeeze chute, 3) exit score; dividing cattle according to exit velocity into quintiles using a 1 to 5 scale (1 = cattle in the slowest quintile; 5 = cattle in the fastest quintile), and 4) temperament score; average of chute and exit scores. Subsequently, cattle are assigned a temperament type; adequate temperament (ADQ; temperament score ≤ 3) or excitable temperament (EXC; temperament score > 3). To assess the impacts of temperament on reproductive efficiency in beef production systems, our group associated these evaluation criteria with puberty attainment and pregnancy rates in *Bos taurus* and *B. indicus*-influenced females. Cattle classified as EXC had greater plasma cortisol vs. ADQ cattle during handling, independent of breed type (*B. indicus* × *B. taurus*, $P < 0.01$; *B. taurus*, $P < 0.01$; *B. indicus,* $P = 0.04$) or age (cows, $P < 0.01$; heifers, $P < 0.01$). In regards to reproductive variables, *B. taurus* and *B. indicus* × *B. taurus* EXC heifers reached puberty at older ages ($P < 0.05$) compared with ADQ cohorts. Cows classified as EXC had reduced annual pregnancy rates vs. ADQ cows across breed types (*B. taurus*, $P = 0.03$; *B. indicus* × *B. taurus,* $P = 0.04$; *B. indicus*, $P = 0.05$). Moreover, *B. taurus* EXC cows also had decreased calving rate ($P = 0.04$), weaning rate ($P = 0.09$), and kg of calf weaned/cow exposed to breeding ($P = 0.08$) vs. ADQ cohorts. Our group also reported that acclimating *B. indicus* × *B. taurus*or *B. taurus* heifers to human handling improved temperament ($P \leq 0.02$), reduced plasma cortisol ($P < 0.01$), and hastened puberty attainment ($P \leq 0.02$). Hence, strategies to improve herd temperament, including selection for this trait and acclimation of young animals to human handling, are imperative for optimal reproductive efficiency of beef operations based on *B. taurus* and *B. indicus* influenced cattle.

Key Words: beef cattle, reproduction, temperament

1171 Estrus: Association with productive parameters and implications to fertility. R. L. A. Cerri*[1], B. F. Silper[1], T. A. Burnett[1], A. M. L. Madureira[2], J. L. M. Vasconcelos[2], and L. Polsky[1], [1]*Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada,* [2]*Sao Paulo State University, Botucatu, Brazil.*

Comparison between the fertility of timed-AI protocols vs. AI based on spontaneous or induced estrus is often inadequate. Day post-partum at AI and the consequent grouping of animals with different cyclic status, BCS, and overall health status is a confounding factor caused by many experimental designs. Previous studies observing the effect of concentration of progesterone during diestrus, concentration of estradiol and length of proestrus and follicular dominance minimize or neglect the effect of the expression of estrus on parameters such as fertilization rate, embryo quality, and endometrium receptivity. In one study, the likelihood of ovulation was greater for high vs. low relative increase estrus, but a more detailed experiment also showed slight differences in the timing of ovulation. Expression of estrus near AI also modified the expression of genes related with the immune system, adhesion molecules and prostaglandin synthesis in the endometrium (*MX1*, *MX2*, *MYL12A*, *MMP19*, *CXCL10*, *IGLL1*, *SLPI, OTR*, and *COX-2*) and those related with apoptosis, P4 synthesis, and prostaglandin receptor (*CYP11A*, *BAX*, and *FPr*) in the CL. The expression of estrus was associated with increased P/AI for timed-AI (38.9 vs. 25.5%) and embryo transfer (46.2 vs. 32.7%) protocols. Moreover, there was a decrease in pregnancy loss in both programs. Data from other recent studies involving spontaneous and estradiol cypionate induced estrus have shown that greater relative increase and longer duration of estrus, captured by different activity monitors, have a significant impact on P/AI (over 12% points across different studies). Intensity and duration of estrus were correlated with BCS, parity, and secondary behavior signs as expected, but only weakly associated with milk production. Follicle diameter and concentration of estradiol at estrus were also weakly correlated with estrus expression. Collectively, ovulation could partly explain the observed reduction in fertility, but it is clear that the endometrium and the CL play an important role that is independent of parameters such as parity, BCS, and milk production. Quantitative information from estrus events could be used to improve estrus detection quality and develop decision-making strategies at the farm level. Further studies in this field should aim to 1) better understand ovarian, embryo and endometrium mechanisms associated with either the expression or intensity of estrus and, 2) refine the collection of phenotypes related to estrus (i.e., relative increase, absolute increase, baseline levels, duration, and repeatability within cow) to improve estrus detection and possibly genetic selection.

Key Words: dairy cow, estrus expression, fertility

PRODUCTION, MANAGEMENT, AND ENVIRONMENT

1172 Use of evaporative cooling systems and their effects on core body temperature and lying times in lactating dairy cattle. J. R. Johnson*[1], L. G. D. Mendonça[2], J. P. Harner[3], and M. J. Brouk[1], [1]*Department of Animal Sciences and Industry, Kansas State University, Manhattan,* [2]*Kansas State University, Manhattan,* [3]*Department of Biological and Agricultural Engineering, Kansas State University, Manhattan.*

A study was completed to assess the effect of an evaporative cooling system on respiration rates, rear udder skin temperature (T_u), core body temperature (CBT), and resting time in lactating dairy cows. There were two environmental treatments in this study: FAN (Cyclone fans only, no fog); and FANFOG (Cyclone fans and fog on). Cows exposed to these 2 environments were either housed in a bedded pack barn equipped with an evaporative cooling system (Cyclone fans, Chippewa Falls, WI) or a tie-stall barn equipped with cooling cells. Cows were divided into 2 treatment groups with 8 cows/treatment: TIE which spent 50% of the time in the tie-stall barn and 50% of the time in the bedded pack barn, and PACK which also spent 50% of the time in the tie-stall barn and 50% of the time in the bedded pack barn but opposite of TIE. Each cow was fitted with a vaginal temperature logger (HOBO U12, Onset Computer Corporation, Pocasset, MA), a neck collar that contained a sensor (HOBO Pro V2, Onset Computer Corporation, Pocasset, MA) to track temperature and relative humidity of the environment, and an electronic data logger (HOBO Pendant G Acceleration Data Logger, Onset Computer Corporation, Pocasset, MA) to track lying times. Ambient temperature and relative humidity (RH) were also collected and all devices recorded at 1 min intervals. During FANFOG, PACK cows had reduced ($P < 0.05$) respiration rates (breaths per minute) compared with TIE (69 vs. 76 ± 2.4 BPM). Breaths per minute also increased significantly throughout the day for TIE but this was not the case for PACK. No differences were found in T_u between treatments. CBT data were divided into the following categories: < 38.6°C, ≥ 38.6°C, and ≥ 39.0°C. When exposed to the FANFOG environment, cows spent decreased ($P = 0.05$) time above 39°C CBT when compared with FAN (9.2 vs. 14.6 h/d, respectively), while PACK cows during FAN and FANFOG spent fewer hours/day above 39°C CBT vs. TIE ($P < 0.05$). TIE showed numerically greater total daily lying times during FAN and FANFOG compared with PACK ($P > 0.10$). These results confirm that evaporative cooling systems (Cyclone fans and fog) are effective at decreasing respiration rates and CBT thus improving cow comfort, while having no

effect on T_u and lying times in lactating dairy cows.

Key Words: core body temperature, evaporative cooling, heat stress

1173 Relationship between blood parameters, physiological changes, and behavior pattern in Korean native steers under cold stress. W. S. Kim*, U. S. Jung, M. J. Kim, S. W. Jeon, D. Q. Peng, Y. S. Kim, M. H. Bae, J. S. Lee, S. R. Lee, and H. G. Lee, *Department of Animal Science and Technology, College of Animal Bioscience and Technology, Konkuk University, Seoul, Korea.*

The performance, health, and behavior of cattle are strongly affected by climate. The objective of this study was to investigate the relationship between blood parameters, rectal temperature, heart rate, and rumination time in Korean native steers under cold stress. Data were collected from four Korean native steers (331.6 ± 6.46 kg BW and 343.5 ± 3.48 d age), which were kept in three designated temperature levels based on ambient temperature: HCS; high cold stress (−15 to −10°C) period, MCS; medium cold stress (−10 to −5°C) period, and LCS; low cold stress (−5 to 2°C) period. According to the ambient temperature, blood was collected after 3h feeding (at 1100). The blood metabolites and hormone as stress-related indicators were analyzed using biochemical analyzer-T-BA-40FR. Complete Blood Count (CBC) test was conducted to determine the change in blood cells, and rectal temperature (RT) and heart rate (HR) were measured at the same time points. Feed and water intake were recorded daily (at 0900 h), and rumination time (RMT) was monitored through a video monitoring system. Data were analyzed using the JMP 5.0 procedures of SAS. The results showed that the level of serum cortisol ($P = 0.027$) as an indicator of stress steroid hormone was significantly increased in the HCS period compared with the LCS period. Also, RT ($P = 0.003$) and HR ($P = 0.01$) were significantly increased in the HCS period compared with the LCS period. However, RMT ($P = 0.011$) was decreased in the HCS period compared with the LCS period. Feed, water intake, and blood parameters were not associated with RT ($P > 0.10$). In contrast, RMT and HR influenced RT ($P < 0.01$). Serum cortisol, platelet, and RMT were affected in HR ($P < 0.05$). This means that the lower temperature is related to high stress in Korean native steers, and there were close correlations between RT, HR, and cortisol. In conclusion, HR and RT were very important stress indexes in cold season, which has a very close relationship with the concentration of cortisol and RMT. In addition, an increase in cortisol level probably activates the sympathetic nerve system to cause an increase in the heart rate of Korean native steers. This relationship with this physiological action explains that it would be an important factor to reduce stress.

Key Words: blood parameters, cold stress, Korean native steer

1174 Effects of exit-lane water drenching using showers on lactating dairy cow vaginal temperature. A. R. Lee*, S. M. Smith, D. L. Ray, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

Dairy producers can help mitigate the negative effects of high temperature and humidity by implementing cow cooling methods. The objective of this study was to quantify the changes in vaginal temperature after drenching cows with water using showers on parlor exit. Forty-five lactating Holstein cows (Parity = 1.89 ± 1.21, days in milk = 244.58 ± 127.58) at the University of Kentucky Coldstream Dairy were enrolled in a 4 wk crossover study from August 31 to September 24, 2013. Vaginal temperature measurements were recorded every 6 min for 7 d using Thermochrom iButtons (Embedded Data Systems, Lawrenceberg, KY) placed in a vaginally inserted blank CIDR (Zoetis, Florham Park, NJ). Vaginal temperature was used as a measure of core body temperature. Cooling Sense showers (Edstrom Industries, Waterford, WI) were installed in 2 parlor exit lanes and automatically activated at morning or afternoon milking when ambient air temperature was ≥ 18.3°C. Showers sensed approaching cows and drenched water for 5 s, as cows walked through each respective exit lane. Showers ran for 5 s, although cows may have received no, some, or all of the drench. Cows were randomly balanced by days in milk and parity into two pens. Cows in pen 1 received 4 d of showers and 3 d of washout during weeks 1 and 3. Cows in pen 2 received 4 d of showers and 3 d of washout during weeks 2 and 4. All other times, cows in pen 1 or pen 2 did not have showers. Shower time was characterized as the time before or after the cow entered the shower. The MIXED procedure of SAS (SAS 9.3, SAS Inst., Inc., Cary NC) was used to analyze the effects of shower time, shower use, and milking sessions on vaginal temperature. Stepwise backward elimination was used to remove nonsignificant interactions ($P \geq 0.05$). Vaginal temperature was lower ($P < 0.01$) 1 h and 2 h after drench than 1h and 2h before drench (LSMean ± SE; 39.1 ± 0.04°C vs. 39.2 ± 0.04°C) and (39.1 ± 0.03°C vs. 39.2 ± 0.04°C), respectively. Morning or afternoon milking had a significant effect on vaginal temperature at 5 min, 10 min, 30 min, 1 h, and 2 h after milking ($P < 0.01$). The use of showers on parlor exit reduced vaginal temperature by 0.1°C for up to 2 h following drenching with showers.

Key Words: cow cooling, shower, vaginal temperature

1175 The effects of zinc amino acid complex on biomarkers of gut integrity and metabolism in heat-stressed steers. M. Abuajamieh*[1], S. K. Kvidera[1], E. A. Horst[1], E. J. Mayorga[1], J. T. Seibert[1], J. S. Johnson[1], J. W. Ross[1], M. A. Al-Qaisi[1], P. J. Gorden[2], J. DeFrain[3], R. P. Rhoads[4], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Veterinary Diagnostic and Production Animal Medicine, Iowa State University, Ames, [3]Zinpro Corporation, Eden Prairie, MN, [4]Virginia Tech, Blacksburg.*

Supplemental Zn improves monogastric intestinal integrity during heat stress (HS), but its ability to improve ruminant gut health is unknown. Forty Holstein steers (173.6 ± 4.9 kg) were used in a replicated, incomplete 2 x 3 factorial design to determine the effect of Zn source ($ZnSO_4$ vs. Zn amino acid complex [CZ; Availa®Zn, Zinpro Corporation]) and environment (thermal neutral [TN] conditions or cyclical HS) on biomarkers of intestinal integrity and villi morphology. Steers were fed ad libitum (AL) one of two diets for 21 d: 1) 75 mg/kg of Zn from $ZnSO_4$ or 2) 35 mg/kg Zn from $ZnSO_4$ and 40 mg/kg Zn from of CZ. Steers remained on assigned diets and were then housed in environmental chambers. The experiment consisted of two periods (P): P1) 5 d of baseline in TN-AL conditions (20.2 ± 1.4°C, 30.4 ± 4.3% RH) and P2) 6 d of environment implementation followed by euthanasia. During P2, steers received one of five diets by environment combinations: 1) TN fed AL 75 mg/kg of Zn from $ZnSO_4$ (Ctrl; n = 8), 2) TN pair-fed (PF) 75 mg/kg of Zn from $ZnSO_4$ (0CZPF, n = 8), 3) HS (27.1 ± 1.5 to 35.0 ± 2.9°C, 19.3 ± 3.5% RH) and fed AL 75 mg/kg of Zn from $ZnSO_4$ (0CZHS; n = 8), 4) TN and PF 35 mg/kg of Zn from $ZnSO_4$ and 40 mg/kg of Zn from CZ (40CZPF, n = 8), and 5) HS and fed AL 35 mg/kg of Zn from $ZnSO_4$ and 40 mg/kg of Zn from CZ (40CZHS; n = 8). The Ctrl, 0CZPF, and 40CZPF steers remained in TN continuously. The 0CZPF and 40CZPF steers were fed to their 0CZHS and 40CZHS counterparts, respectively. Data were analyzed with repeated measures using PROC MIXED in SAS and P1 data used as a covariate. Preplanned contrasts evaluated Zn source and environment. Regardless of environment, 40CZ tended to increase DMI (10%; P = 0.09) relative to 0CZ (P < 0.01). Compared to TN, HS decreased NEFA, serum amyloid A and increased BUN, insulin:DMI, and L-lactate (P < 0.01). 40CZHS calves had reduced rectal temperature compared to 0CZHS (0.24°C; P < 0.01). Compared to PF, HS calves had increased (P < 0.01) goblet cell numbers in the duodenum, jejunum, ileum, and colon. 40CZHS decreased duodenum villi width and increased both jejunum villi height and villi height:crypt depth relative to 0CZHS (P < 0.01). Feeding CZ improved DMI, reduced rectal temperature, and altered intestinal morphology; changes indicative of improved intestinal barrier function during HS.

Key Words: gut health, heat stress, intestine, zinc

1176 Effect of OmniGen-AF® supplementation to heat stressed cows during late gestation on blood parameters and immune cells of their calves. A. L. Skibiel*[1], J. L. Powell[1], T. F. Fabris[1], Y. M. Torres[1], F. N. Corra[1], J. D. Chapman[2], D. J. McLean[2], D. Kirk[2], G. E. Dahl[1], and J. Laporta[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]Phibro Animal Health Corporation, Quincy, IL.*

Exposure to heat (HT) stress during the dry period negatively impacts cow immune status. Feeding OmniGen-AF® (OG) has been shown to improve the immune status of the HT cow, but the effect on the calf is unknown. We evaluated the effect of OG supplementation pre-calving (56 g/d, for approximately 105 d) to cows under HT (shade) or cooled (CL; shade, fans, soakers) environmental conditions during the dry period (~56 d) on the immune and stress response of their calves. The experimental design was a 2 x 2 factorial with four treatments: CL (n = 4), CLOG (n = 6), HT (n = 6), HTOG (n = 7). Data were analyzed with a one- or two-way ANOVA, d as a repeated measure. At birth, heifers were fed maternal colostrum (5.7 L, two meals the first 24h). Blood samples were collected at 0 h, 24 h, d 10, and d 28 to measure cortisol, haptoglobin, (HPT), and serum amyloid-A (SAA). Hematology parameters and immune cell counts were assessed in the circulation of calves at birth and at 24 h (before and after colostrum feeding). Total cortisol concentrations were elevated at birth, but markedly decreased after feeding colostrum and on d 10 (P < 0.01) for all groups. Calves born to OG fed cows tended to have increased circulating cortisol (P = 0.09). Haptoglobin and SAA levels were higher on d 10 for all groups except for the CL calves (P < 0.01). Calves born to OG fed cows, and those born to HT cows, had higher SAA on d 10 (P < 0.03). White blood cell counts were similar at birth, and increased at 24 h after colostrum feeding except in the calves born to CLOG cows. Red blood cell counts (RBC) were elevated at birth and decreased significantly at 24 h for all groups (P < 0.05), except for the CL calves. Calves born to OG fed cows had more RBC (P < 0.02). Neutrophil counts were similar for all groups at birth and increased, after colostrum feeding, only for the HT and CL calves. Calves born to OG fed cows had more lymphocytes at birth compared to those born to cows not fed OG (P < 0.05). Heifers born to HT cows had fewer lymphocytes compared to CL if they weren't fed OG, but if they were born to HTOG cows their lymphocyte count was similar to the CLOG. In summary, in-utero exposure to heat stress during late-gestation negatively affects the immune and stress responses of the calf ex-utero. OmniGen-AF® supplementation to the dam could potentially benefit the offspring.

Key Words: calves, immunity, OmniGen-AF, stress

1177 Effects of cooling and dietary zinc source on the inflammatory responses to an intra-mammary lipopolysaccharide challenge in lactating Holstein cows during summer. A. P. A. Monteiro*[1], X. Weng[1], J. Guo[1], J. K. Bernard[1], J. DeFrain[2], and S. Tao[1], *[1]University of Georgia, Tifton, [2]Zinpro Corporation, Eden Prairie, MN.*

Milk somatic cell count increases during summer and dietary zinc supplementation has been shown to improve mammary health. The objective was to determine the effect of active cooling and dietary zinc source on an intra-mammary lipopolysaccharide challenge during summer. Twenty lactating multiparous Holstein cows were randomly assigned to one of 4 treatments with a 2 × 2 factorial arrangement (n = 5/treatment), including two environments: cooled (CL) or not cooled (NC), and two sources of Zn: 75 ppm ZnCl, or 35 ppm ZnCl+40 ppm Zn-methionine complex. From d 0 to 84 of the trial, all cows were cooled (fans and misters over the freestall and feeding areas, temperature-humidity index = 73). Starting at d 85, NC cows were deprived of cooling (temperature-humidity index = 78). At d 118, cows received infusions of 10 μg of lipopolysaccharide and saline in the left (LQ) and right (control, CQ) rear quarters, respectively. Rectal temperature was assessed. Individual quarter milk samples were collected at −12, −4, 0, 6, 12, 24, 48, 72, 96, 120, 144, and 168 h relative to infusion and analyzed for composition. Plasma was collected at the same time points (with an additional sample at 3 h) for analyses of lactose and Zn, and complete blood count was performed for samples collected within the first 24 h. Treatments did not affect DMI, whereas milk yield tended to be greater for NC at d 6 than CL cows (environment × d, P < 0.10). CL cows tended to have higher somatic cell score at 96, 120, and 144 h in LQ, and at 24 h in CQ than NC cows (environment × h, P < 0.10). Compared with CL, NC cows had higher rectal temperature at 12 h and tended to have higher at 120 and 144 h (environment × h, P = 0.01). CL cows had higher milk protein percentage in CQ, but lower in LQ ($P \leq$ 0.05) than NC. Relative to CL, NC cows had higher milk urea nitrogen in CQ (P = 0.04). Solids-not-fat percent tended to be higher for CL than NC cows in CQ (P = 0.07). Relative to CL, NC cows had higher plasma lactose at 3 h (environment × h, P = 0.02) and lower plasma Zn at 6 and 12 h (environment × h, P < 0.01). NC cows had a greater reduction in blood neutrophils at 3 h (environment × h, P < 0.01) and lymphocytes at 3 and 6 h (P = 0.05) than CL. Active cooling mitigated the inflammatory responses to an intra-mammary lipopolysaccharide challenge; however, dietary Zn source had no impact.

Key Words: cooling, intra-mammary lipopolysaccharide challenge, zinc

1178 Survey of facility design and heat abatement strategies in progressive Central California dairies. A. H. Souza*[1], E. O. S. Batista[2], B. Gonzales[3], and F. Doricci[4], *[1]Ceva Animal Health, Libourne, France, [2]University of Sao Paulo, Pirassununga, Brazil, [3]Large Animal Veterinary Practitioner-Campestre Dairy, Sao Pedro, Brazil, [4]University of Sao Paulo, Sao Paulo, Brazil.*

An on-farm survey was performed to assess type of facilities and common practices used to mitigate heat stress in progressive Central California dairies. A total of 18 dairies (10 drylot, 8 free-stall herds) classified as in the top quartile in terms of milk production and reproduction performance according to DHIA benchmarking for herds in Central California agreed to participate in the on-farm data collection procedure, which consisted of ~1 h walk through on all facilities in the dairy plus a 20 min interview with herd managers. Data collection and recording were performed by the same trained technician and all herd visits were performed in the morning hours from June to October of 2014. Complete sanitization of clothes and rubber boots used during the visit occurred after all visits and an interval of at least 72 h between visits was respected for biosecurity reasons. All participating dairies purposely chosen to avoid breed-related facility variations milked predominantly (≥ 90% of the cows in the herd) Holstein cows with an average herd size of 1959 lactating cows (range 703 to 5987). In terms of heat abatement strategies, all herds had shade, soakers, and fans in their pre-milking holding areas. Most herds (15) had fans in the holding area positioned to the opposite side of the milking parlor, but 3 of them had fans positioned toward the milking parlor. In addition, 11 herds had functioning under-wash systems in their holding areas. However, only 6 herds had showers, 13 had water troughs, and 7 had rubber-mattress in the return alleys after milking time. Interestingly, only 1 herd had shade provided in the return alleys from milking parlor to all milking pens. Thirteen herds used dry-manure beddings, 3 had compost-manure beddings, and 2 used sand-based bedding systems. Out of the herds that used stalls in the bedding area (9), stall front width averaged 121.3 cm. All herds used head-locks instead of neck-rails in the feeding lane, all had shaded areas for resting in the yard, all had soakers, and only 12 herds had shaded feed-bunks. Interestingly, only 3 herds had fairly clean water troughs in their barns, and most herds should implement more frequent routines to improve water trough cleanness. In conclusion, top performing dairy herds in CA use several strategies to mitigate detrimental effects of heat stress and keep cows comfortable while housed in confined systems.

Key Words: dairy cow, facility design, heat stress

1179 The effect of vaginal temperature on expressed physical activity of lactating Holstein cows following induced estrus. L. Polsky*[1], A. M. L. Madureira[2], E. L. Drago Filho[2], J. L. M. Vasconcelos[2], and R. L. A. Cerri[1], *[1]Applied Animal Biology, Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada, [2]Departamento de Produção Animal-FMVZ-UNESP, Botucatu, Brazil.*

The objective of this study was to determine the effect of vaginal temperature on levels of physical activity expressed by lactating Holstein cows following induced estrus. Lactating Holstein cows (n = 641; 41.5 ± 9.4 kg milk/d) were fitted with a leg-mounted pedometer (AfiActII, Afimilk, Israel) resulting in 843 evaluated activity episodes of estrus. Vaginal temperature was monitored using thermometers (Thermochron iButton −40°C thru +85°C), attached to an intravaginal device (CIDR) as part of a timed-AI protocol (CIDR+estradiol benzoate+GnRH-7d-PGF-2d-CIDR out+PGF+ECP-2d-timed AI), which recorded vaginal temperature every 10 min for 3 d. Ambient temperature and relative humidity were monitored using an external thermometer placed in the center of each pen. Milk production and BCS were collected at time of thermometer insertion. All statistical analysis was performed in R and R Studio using GLM and ARM packages. Heat stress was calculated based on the percentage of time the cow spent with a vaginal temperature greater than 39.1°C (HS). The mean HS was 36.8 ± 24.5%, whereas the mean maximum (MaxVT) and minimum (MinVT) vaginal temperatures were 39.7 ± 0.5°C and 38.0 ± 0.8°C, respectively, with an average amplitude (AMP) 1.71 ± 0.9°C. Mean peak activity (PA) at estrus was 237.0 ± 160.0% relative increase. Increasing MaxVT negatively affected mean PA (ODDS = 0.67, $P < 0.01$). PA was significantly affected by parity as multiparous cows expressed lower PA compared to primiparous cows (ODDS = 0.76, $P < 0.01$). MinVT, AMP, and HS had no significant effects on mean PA, but cows displaying greater PA at estrus had greater P/AI compared with lower PA (28% vs. 18%$P < 0.003$). The P/AI at 32 d was significantly reduced by increasing MaxVT (ODDS = 0.67 $P < 0.05$); however HS, MinVT, and AMP did not significantly affect P/AI. Future research should aim to refine variables related to hyperthermia as well as further effects of body temperature on physical activity behaviors such as lying time, bout, rumination, and subsequent effects on estrous expression and pregnancy rates.

Key Words: estrus, heat stress, physical activity

1180 Partial carbon footprint of milk and interaction between enteric methane and nitrous oxide emissions in grazing dairy farms: The case of Costa Rica. M. A. Wattiaux*[1], J. P. Iñamagua-Uyaguari[2], F. Casasola-Coto[3], L. Guerra-Alarcón[4], and A. Jenet[3], *[1]University of Wisconsin-Madison, Madison, [2]Universidad de Cuenca, Cuenca, Ecuador, [3]Centro Agronómico Tropical de Investigación y Enseñanza (CATIE), Turrialba, Costa Rica, [4]Université Laval, Québec, Canada.*

Pasture-based dairy production systems in Costa Rica vary considerably from the tropical coastal areas to the temperate highlands (1600 to 2400 m above sea level). The objective of this study was to identify indicators of on-farm partial carbon footprint (PCFP) of milk among 31 variables describing farm conditions (e.g., altitude, rainfall, temperature), farm structure (e.g., stocking rate, breed), feeding and housing management practices (e.g., concentrate fed, intake from pasture), and pasture management (e.g., fertilization rate, hours in pasture). A second objective was to explore the correlation between methane (CH_4) and nitrous oxide (N_2O) emissions. Farm records and face-to-face survey data from 104 farms of the Dos Pinos cooperative were collected to estimate PCFP based on enteric CH_4 of lactating cows and N_2O from commercial fertilizers applied to grazed pastures (Fertilizer-A), cut-and-carry pastures (Fertilizer-B), and estimated manure N deposited during grazing. The PCFP ranged from 0.378 to 1.054 with CH_4 ranging from 0.310 to 0.692, and N_2O ranging from 0.056 to 0.609 kg CO_2eq./kg of fat-and-protein corrected milk (FPCM). Contribution of enteric CH_4, Fertilizer-A, Fertilizer-B and manure N to PCFP averaged 69.5, 9.2, 0.7 and 20.7%, respectively. Forward regression analysis indicated that the three most important variables explaining the PCFP were (all $P < 0.001$) feed efficiency (FPCM (kg/d)/dry matter intake (kg/d)), which ranged from 0.49 to 1.36 (partial r^2 = 0.52), Fertilizer-A, which ranged from 0 to 1058 kg/ha per year (partial r^2 = 0.16), and estimated dry matter intake from pasture, which ranged from 0 to 15.6 kg/d (partial r^2 = 0.08). Pearson correlation between CH_4 and N_2O emissions was 0.41 ($P < 0.001$). The contribution of CH_4 to PCFP was determined primarily by feed efficiency and estimated dietary dry matter digestibility, whereas the contribution of N_2O to PCFP was determined primarily by Fertilizer-A, feed efficiency, stocking rate (lactating cows per ha), hours of the day that cows were in pasture, and cow N use efficiency (milk N (g/d)/intake N (g/d)). Thus feeding practices had a substantial impact on both CH_4 and N_2O emissions. The relationship between CH_4 and N_2O emission was mediated in part through hours of the day that cows are in pasture, estimates of pasture consumption and pasture digestibility. In some farms PCFP of milk could be reduced readily simply by reducing excess fertilizer application. However, the adoption of management practices aimed at reducing enteric CH_4 may substantially alter pasture

N_2O emission and possibly vice-versa.

Key Words: climate change, greenhouse gases, LCA

1181 WS Effects of dry and wet conditions during the pre-weaning phase on subsequent feedlot performance and carcass composition of beef cattle. G. A. Gatson[*1], B. L. Vander Ley[2], W. D. Busby[3], P. J. Gunn[4], and A. M. Meyer[1], *[1]Division of Animal Sciences, University of Missouri, Columbia, [2]College of Veterinary Medicine, University of Missouri, Columbia, [3]Tri-County Steer Carcass Futurity, Lewis, IA, [4]Department of Animal Science, Iowa State University, Ames.*

The objective of this study was to determine the effects of dry and wet conditions during the pre-weaning phase of beef cattle production on subsequent feedlot performance and carcass characteristics. Steers (n = 7439) and heifers (n = 2380) finished in 16 feedlots in southwestern Iowa through the Tri-County Steer Carcass Futurity Cooperative (Lewis, IA) were used for a retrospective analysis. Cattle originated in the Midwest, were born in February, March, or April, and were slaughtered between 2003 and 2014. Feedlot performance and carcass composition data were obtained for each animal. Palmer Drought Severity Index (PDSI) values were obtained for each animal for the pre-weaning forage growing season on a monthly basis. These values were used to classify conditions as dry (mean PDSI value ≤ -2.00), normal (mean PDSI value > -2.00 and < 2.00), or wet (mean PDSI value ≥ 2.00) for the cool season, warm season, and combined seasons. Mixed models were used to evaluate the effects of dry and wet conditions on subsequent performance. Birth year, feedlot, and sex were included as fixed effects. Average daily gain was greater ($P < 0.03$) for cattle from the dry class than those from the wet class during the cool season and the combined seasons. Cattle from the dry and normal classes for both the cool season and combined seasons had greater ($P < 0.02$) final BW than those from the wet class. During the cool season, HCW was greater ($P < 0.0001$) for the normal class than wet class, although HCW was greater ($P < 0.04$) for the dry class compared with normal and wet during the combined seasons. Calculated yield grade was improved ($P < 0.01$) for the normal class during the cool season compared with the dry and wet classes. For both the warm and combined seasons, the dry class had improved ($P < 0.02$) calculated yield grade compared with normal and wet classes. For the cool season, the dry and normal classes had greater ($P < 0.03$) marbling scores than the wet class. For marbling score in the warm season, the normal and wet classes were greater ($P < 0.02$) than the dry class. In conclusion, this study indicates that both dry and wet conditions during the pre-weaning phase may impact ultimate feedlot performance and carcass composition.

Key Words: carcass, drought, feedlot

1182 Predicting manure volatile solid output of lactating dairy cows. R. Appuhamy[*1], L. Moraes[1], C. Wagner-Riddle[2], D. P. Casper[3], and E. Kebreab[1], *[1]University of California, Davis, Davis, [2]University of Guelph, Guelph, Canada, [3]Dairy Science Department, South Dakota State University, Brookings.*

Organic matter (OM) in livestock manure consisting of biodegradable and non-biodegradable fractions are known as volatile solids (VS). According to Intergovernmental Panel on Climate Change Tier 2 (IPCC-Tier 2) guidelines, methane emissions from manure is determined based on VS. However, only biodegradable OM generates methane. So methane emissions should be based on biodegradable VS (dVS, dVS = VS – lignin). The objective of the study was to develop mathematical models for estimating VS and dVS outputs by lactating dairy cows. Dry matter intake, dietary nutrient contents, milk yield and composition, body weight, and days in milk were used as potential predictor variables. Multicollinearity, model simplicity, and random study effects were taken into account during model development that used 588 VS and dVS measurements (kg/cow/d) from 43 studies. New models and the IPCC-Tier 2 model [VS = {fecal energy (MJ/d) + urinary energy (MJ/d)} × fecal OM/18.45] were evaluated with an independent set of VS and dVS measurements (n = 244) made on Holstein cows in the United States. Dry matter intake (kg/d) and dietary CP and NDF contents (% of DM) were significantly associated ($P < 0.001$) with VS. A model including these variables [VS = 0.364 ± 0.007 × DMI + 0.026 ± 0.004 × NDF– 0.078 ± 0.008 × CP] fitted best to data. When evaluated with independent data, the new model had a root mean square prediction error, as a percentage of average observed value (RMSPE%), of 14.0%. More than 93% of the error was due to random variability of data. Under the assumptions that feed digestibility = 66%, energy intake partitioning to urine = 0.04, and fecal OM = 0.92, the IPCC-Tier 2 model also performed well on independent data and had a RMSPE of 14.5%. A model including DMI, and dietary CP and hemicellulose (HC, HC = NDF– ADF in % of DM) contents as predictor variables fitted best to dVS data [dVS = 0.334 ± 0.007 × DMI + 0.029 ± 0.006 × HC– 0.058 ± 0.008 × CP] and performed well, when evaluated with independent data (RMSPE = 13.9%). The majority of the error (95.7%) was due to random variability of data. The study offers empirical models that can predict VS. and dVS of lactating dairy cows accurately and thereby, could assist in determining methane emissions from manure successfully.

Key Words: dairy cow, manure, prediction model, volatile solid

1183 The effects of vermifiltration on gaseous emissions from dairy lagoon water. *E. Lai*, Y. Zhao, Y. Pan, and F. M. Mitloehner, University of California, Davis, Davis.*

Dairy lagoon water contains high concentrations of nitrogen (N), which has the potential to pollute groundwater and the atmosphere. To reduce N loading of an anaerobic lagoon at a commercial dairy, a pilot project vermifilter was installed, which used earthworms embedded in woodchips to enhance removal of solids and contaminants. The objective was to mitigate nitrogenous gases, greenhouse gases (GHGs), volatile organic compounds (VOCs), and criteria pollutants from lagoon water using this new technology. Specifically, emissions of ammonia (NH_3), nitrous oxide (N_2O), carbon dioxide (CO_2), methane (CH_4), hydrogen sulfide (H_2S), and ethanol (EtOH) were measured using Thermo analyzers (Franklin, MA) that were housed inside a Mobile Agricultural Air Quality Lab. To assess whole filter system performance, emissions were measured from the untreated dairy lagoon water (LAG), as well as from the vermifilter's influent (INF), effluent (EFF), the top (TOP), and bottom (BOT) of the filter. Gases were measured using a flux chamber approach for LAG, INF, and EFF, a triangle wind tunnel for the TOP, and an inlet threaded to the bottom of the filter for BOT. Results for EFF vs. INF showed a 90.2% reduction of NH_3 emissions without increasing emission of N_2O, CO_2, CH_4, H_2S, and EtOH from the rest of the vermifilter's system. The vermifilter's ability to reduce nutrient loading and subsequent NH_3 emissions without producing other detrimental gaseous emissions needs to be replicated across more dairy operations. However, this new technology has the potential to be a viable candidate for nitrogen removal particularly in regions like the San Joaquin Valley of California, where dairy air and water quality issues are most sensitive.

Key Words: dairy wastewater, emissions, nitrogen

1184 Trends in milk urea nitrogen, milk composition, and milk yield in dairy farms in the Northeast U.S. A. N. Hristov[*1], M. T. Harper[1], J. Oh[1], F. Giallongo[1], J. C. Lopes[1], G. Cudoc[2], J. Clay[3], and L. E. Chase[4], *[1]The Pennsylvania State University, University Park, [2]Dairy One Coop., Inc., Ithaca, NY, [3]Dairy Records Management Systems, Raleigh, NC, [4]Cornell University, Ithaca, NY.*

The main objective of this survey was to examine trends in milk urea nitrogen (MUN) in DHI herds (all dairy cattle breeds were included) in the Northeast U.S. Data for milk fat and true protein concentrations, milk yield, days in milk (DIM) on test day, and lactation number of the cows were also collected. Close to 11 million historical (2004 to 2015) records from the Dairy Records Management Systems (Raleigh, NC) for 14 states (CT, DE, MA, MD, ME, NC, NH, NJ, NY, PA, RI, VA, VT, and WV) were included in the analysis. Average (across states and years) MUN, milk fat, milk true protein, milk yield, DIM, and lactation number were (mean and SD): 13.3 (0.65) mg/dL, 3.85 (0.07)%, 3.13 (0.04)%, 31.6 (0.86) kg/d, 178 (19.2) d, and 2.3 (0.04) lactations. MUN was 13.3 mg/dL in 2004, decreased to 12.4–12.6 mg/dL in 2009–10, steadily increased to 14.6 mg/dL by 2013, and then decreased to 13.0 and 12.4 mg/dL in 2014 and 2015, respectively. Milk fat concentration steadily increased from 3.69 in 2004 to 3.92–3.93% in 2013–14 and decreased to 3.87% in 2015. Milk true protein was 3.01% in 2004, increased to 3.15–3.16% in 2008–09 and declined to 3.13–3.11% thereafter. Except for 2004 (33.5 kg/d), milk yield steadily increased from 30.7 in 2005 to 32.3–32.8 kg/d in 2014–15. The likely explanation for the higher average milk yield in 2004 was the lower average test day DIM (119 d) in that year vs. all other years (184 d, SD = 4.3). In an effort to explain the observed trends in MUN, we investigated variability in dairy feed cost in PA and the U.S. (Northeast data were not available). Average dairy feed cost in PA (for a cow producing 29.5 kg milk/d) increased from $3.08 in 2005 to $5.22 in 2008, declined to $4.01 by 2010, increased again to $6.03 in 2012, and then declined to $5.07/d in 2015. Dairy feed cost for the U.S. followed similar trends. It was apparent that high MUN coincided with high feed cost and vice versa. Therefore, our conclusion from this survey was that MUN in Northeast dairy herds fluctuated following trends in feed cost; however, ration data are not available to better define the reasons for the variations in MUN levels.

Key Words: dairy cow, milk composition, milk urea nitrogen, northeast U.S.

1185 Effect of time and storage conditions on cow urine pH. M. C. Lewis*, S. A. Armstrong, J. P. Jarrett, and D. J. McLean, *Phibro Animal Health Corporation, Quincy, IL.*

Analysis of bovine urine pH is a common practice for dairy professionals wishing to evaluate the efficacy of a negative dietary cation anion difference (DCAD) diet in pre-fresh transitional dairy cows. However, immediate measurement of urine pH on collection is not always possible in an on-farm setting, and information regarding how storage conditions and time impact changes in urine pH is not available. The objective of this study was to analyze the effect of various storage conditions over time on the urine pH of dairy cows fed a fully-acidified and non-acidified diet. This information will be used to advise professionals on the best method of urine storage to consistently obtain accurate urine pH values. Urine from three randomly selected Jersey cows was collected and an initial time zero pH reading was taken with a pre-calibrated Milwaukee portable pH meter, model MW101. Samples were aliquoted and assigned for either 2, 4, 6, and 24 h of storage in triplicate, then placed at 4°C, 20°C, 37°C, and field conditions at temperatures ranging from 0.5°C to 7°C and 81% to 100%

humidity. Urine pH was measured at the indicated storage time intervals. Study one (S1) measured sampled urine from cows on a fully acidified diet, while study two (S2) measured sampled urine from cows without diet acidification. Data were analyzed as change in pH units from the pH value at initial collection (time = 0), using two way ANOVA procedure in graph pad Prism 6.03 with storage method and time as fixed effects. Significance was declared at $P < 0.05$. The urine pH values from the fully-acidified cows had a significant storage effect ($P < 0.0001$) as well as a significant time effect ($P < 0.0001$) while the interaction of storage and time was not significant. Urine pH values were not different across time when collected from non-acidified cows, however storage temperature conditions did significantly change sample pH values ($P < 0.0001$), and the interaction between time and storage was significant ($P < 0.0001$). Diet acidification influenced urine pH values for all storage methods ($P < 0.05$). In cows fed both fully-acidified and non-acidified diets, urine stored at a temperature closest to the animal's normal internal temperature of 38.5°C had the least amount of change in pH units from initial collection, indicating that keeping samples at 37°C or 20°C produces significantly less pH variation than at cooler temperatures.

Key Words: dairy cows, dietary cation anion difference, urine pH

1186 Farm gate environmental impacts of beef production in the Northern Plains and Midwest regions of the U.S. S. Asem-Hiablie, C. A. Rotz*, and R. C. Stout, *USDA-ARS Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Cradle-to-farm gate environmental impacts of beef production in two cattle producing regions were assessed as part of an ongoing national sustainability study of the U.S. beef value chain launched by the Beef Checkoff. Region-specific data on common ranch and feedlot management practices were characterized from producer surveys and site visits in each of the 10 states within the Midwest and Northern Plains regions. This management information was used along with appropriate climate and soil data to simulate representative operations and predict environmental impacts with the Integrated Farm System Model (IFSM). The representative ranch and feedlot operations were then linked to form full production systems in each region. Weighted averages of the environmental footprints for the regions were determined using animal distribution data from both the producer survey and the National Agricultural Statistics Service. Preliminary results gave footprints of total carbon emission, reactive nitrogen loss, and energy and non-precipitation water use for the two regions as 19.7 ± 1.5 kg CO_{2e}, 158 ± 12.9 g N, 48 ± 4.3 MJ, and 1106 ± 154 L per kilogram of carcass weight produced, respectively. The carbon and reactive nitrogen footprints were greater in the Midwest than the Northern Plains, but water use was greater in the Northern Plains. These farm-gate results will be linked with post-farm gate impacts for each of seven study regions to provide the basis for a full national life cycle assessment of beef production and consumption.

Key Words: beef production, environmental footprint, sustainability

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118 Effect of temperature on ammonia emissions from feedlot cattle manure. K. M. Koenig* and S. M. McGinn*, Agriculture and Agri-Food Canada, Lethbridge Research and Development Centre, Lethbridge, Canada.*

Livestock feeding operations are the largest contributor to anthropogenic ammonia emissions affecting air quality and terrestrial and aquatic ecosystems. Ammonia emissions are highly temperature dependent and can be expected to vary through the production cycle from the major cattle producing regions of Western Canada that experience environmental extremes of cold winters and hot, dry summers. A study was conducted to simulate and quantify the effects of temperature on ammonia emissions from manure of feedlot cattle. Fresh feces and urine were collected separately for 24 h from eight beef heifers fed high concentrate, barley grain-based diets (14.8% CP). Urine was collected using bladder catheters into collection vessels submerged in an ice-slurry. Feces and urine were each pooled, sampled for chemical composition, divided into subsamples, and frozen. Feces and urine were thawed, equilibrated to treatment temperatures, combined to constitute manure (1:1 wt/wt wet basis), and ~2.25 kg of the manure were incubated in each of four open flow-through chambers. Chambers were housed within a walk-in controlled environment room with a fresh air exchange rate to prevent build-up of gases. Air flow through the chambers was 1.5 m/s and was subsampled by pumping 200 mL/min through sorbent tubes fitted on the inlet and exhaust ports at 24, 48, 72, and 96 h at temperatures of 5, 10, 15, 20, and 25°C. Flux and cumulative NH_3–N emissions were analyzed with a mixed model with experimental temperature as a fixed effect and chamber as a random effect and the experimental unit. Orthogonal contrasts were applied to determine linear and quadratic effects of temperature on emissions. Manure contained 17.6% DM and 1.12% N (as-is basis) of which 54.2% was urea-N. Increasing the temperature from 5 to 25°C increased the NH_3–N flux (g N/m^2) and cumulative emissions (g N/96 h, % of total N, and % of urea-N; linear and quadratic, $P < 0.001$). Cumulative NH_3–N emissions expressed as a percentage of total manure N for the 96-h incubations were 6.3, 21.2, and 30.8% at temperatures of 5, 15, and 25°C, respectively. Cumulative NH_3–N emissions expressed as a percentage of manure urea-N were 20.3, 38.3, and 58.7% for 5, 15, and 25°C, respectively. Temperature had a marked effect on volatilization of NH_3–N from feedlot manure and was reduced by 75% as temperature decreased from 15 to 5°C and increased

by 50% as temperature increased from 15 to 25°C.

Key Words: ammonia emissions, feedlot cattle, temperature

1188 A novel method for collecting gas produced from the in vitro ANKOM gas production system.

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Enteric methane produced by ruminants is a source of greenhouse gas emissions. One method for investigating methane production from ruminants is the in vitro method which when compared with in vivo methods is faster and less expensive. The ANKOM™ system is an in vitro system that periodically releases excess gas during the incubation to prevent it from diffusing into the medium. For this reason, a gas sample taken from the module's headspace at the conclusion of the incubation period may not be representative of the gas produced during the entire fermentation period. This study tested two methods that enable the collection of released gases. Yeast and sugar were incubated for 24 h in 310 mL ANKOM™ bottles equipped with an ANKOM module to regulate headspace pressure through ventilation. Incubations were made with three different methods: vented gas not collected (NC); vented gas collected in gas bags through a 304 cm gas sample line with an internal diameter (ID) of 1.0 mm (C304); and vented gas collected in gas bags through a 22 cm extension tube with an ID of 4.0 mm (C22). Each method was conducted using four different venting pressures (0.4, 0.6, 0.8, and 1.0 psi). When total gas production was calculated from absolute pressure measurements made by the pressure transducer in the ANKOM module, the mean of total gas production (ml) for the C304 method was significantly ($P < 0.05$) greater (125.3 ± 1.9) than either the C22 method (114 ± 1.9) or the NC method (115 ± 1.7), while the C22 method was not different from the NC method. There was no effect of venting pressure across treatments on estimated total gas production. It is concluded that the C22 method for collecting gas can be used in gas production studies with the ANKOM system as it does not interfere with measurement of gas production.

Key Words: enteric methane, gas collection technique, in vitro gas production

1189 Effect of forage source of dairy cow diets on methane emission from enteric fermentation and manure storage.

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The aim of this study was to determine the effect of corn silage (CS), barley silage (BS), alfalfa silage (AS), and timothy silage (TS) on CH_4 emissions from enteric fermentation and manure storage of dairy cows. For this purpose, 3 experiments (9 cows; replicated 3 × 3 Latin square design; 32-d periods) were conducted. Forages included at 60% of diet DM were, in study 1: 100% CS (0% AS), 100% AS (0% CS), and 50:50 mix CS:AS; in study 2: 100% CS (0% BS), 100% BS (0% CS), and 50:50 mix CS:BS; and study 3: 100% AS (0% TS), 100% TS (0% AS), and 50:50 mix AS:TS. Cows were fed for ad libitum intake and enteric CH_4 emission was determined (3 d) using respiration chambers. Manure excretion was measured over 5 d. Manure CH_4 emissions were estimated using the Eq. [10].23 of the IPCC (2006). Total CH_4 emissions are the sum of enteric and manure CH_4 emissions. Data were analyzed using the MIXED procedure (SAS) and differences between treatments were declared significant at $P \leq 0.05$ using the Tukey multiple comparison test. Overall, 72% of total CH_4 emission was from enteric source and 28% was from manure storage. In study 1, enteric CH_4 emissions (17.7 vs. 20.5 g/kg DMI) and manure CH_4 emissions (6.78 vs. 7.50 g/kg DMI) were lower in cows fed 100% CS compared to cows fed 100% AS or 50:50 mix CS:AS. Consequently, total CH_4 emissions were also lower in cows fed 100% CS compared to cows fed 100% AS or 50:50 mix CS:AS (24.4 vs. 28.0 g/kg DMI). Similarly, in study 2, enteric (19.1 vs. 22.1 g/kg DMI), manure (7.59 vs. 9.04 g/kg DMI) and total (26.7 vs. 31.1 g/kg DMI) CH_4 emissions decreased in cows fed 100% CS compared to cows fed 100% BS or 50:50 mix CS:BS. In study 3, no treatment effect was observed on enteric CH_4 (19.8 g/kg DMI), manure CH_4 (7.16 g/kg DMI), and total (27.0 g/kg DMI) emissions. Results of this study show that replacing AS or BS with CS in dairy cow diets is expected to lower total CH_4 emissions (g/kg DMI) because of reduced enteric and manure CH_4 emissions. However, no effect on CH_4 emissions (enteric, manure, and total) can be expected by replacing TS with AS in dairy cow diets.

Key Words: enteric/manure, forage, methane

1190 Intake, milk production, and methane emission of dairy cows fed diets that differ in ruminal in vitro NDF digestibility. *M. J. Aguerre*[*1], M. J. Powell[2], A. R. Pelletier[1], and M. A. Wattiaux[1], [1]University of Wisconsin-Madison, Madison, [2]USDA-ARS, US Dairy Forage Research Center, Madison, WI.*

The objective of this study was to determine how feeding diets that differed in dietary ruminal in vitro NDF digestibility (IVNDFD) affected DMI, milk production, and CH_4 emission from lactating dairy cows. Twenty four multiparous Holstein cows (mean ± SD; 717 ± 67 kg of BW; 160 ± 49 d in milk) were randomly assigned to four dietary treatments in a randomized complete block design study. Four levels of dietary IVNDFD (digestibility determine after 30 h of incubation) were achieved by substituting corn stover (15% of dietary DM) with alkaline-treated corn stover (at 7.0% $Ca(OH)_2$ of stover DM; stover DM was 50%) in stepwise increments (0, 5, 10, and 15% of dietary DM). Following a 2-wk covariate adjustment period, cows were assigned to dietary treatments for 6 wk. Cows were fed a total mixed ration with (DM basis) 55% forage, 45% concentrate, 16.6% crude protein, 28.7% NDF, and 23.7% starch once daily. Replacing untreated corn stover with 5, 10, and 15% treated corn stover increased dietary IVNDFD by 2.2, 4.3, and 6.2% units, respectively. Performance and CH_4 emission measurements were conducted in four tie-stall emission chambers during three consecutive days the last week of the covariate and experimental periods. Treatment effects are presented as covariate-adjusted least squares means (± SEM). Increasing IVNDFD in the diet had no effect on DMI (21.3 ± 1.3 kg/d), milk yield (32.1 ± 2.2 kg/d), fat-and-protein corrected milk yield (FPCM; 29.9 ± 2.3 kg/d), FPCM/DMI (1.42 ± 0.1), CH_4 emission (524 ± 35 kg/d), and CH_4/FPCM (18.4 g/kg ± 1.7). However, with increasing levels of IVNDFD in the diet there was a linear decrease ($P = 0.02$) in CH_4/DMI from 26.4 to 23.3 (g/kg) and a tendency ($P = 0.06$) to reduce CH_4/milk from 18.8 to 14.4 (g/kg). Also, a tendency ($P = 0.08$) for a quadratic response was observed for CH_4/milk; increasing dietary IVNDFD by 2.2 and 6.2% units decreased CH_4/milk to 17.7 and 14.4 g/kg respectively, compared with 15% untreated corn stover diet (18.8 g/kg), but a 4.4% increase on IVNDFD resulted in the highest yield of CH_4/milk (20.0 g/kg). Under the conditions of this study increasing IVNDFD in the diet by as much as 6.2% units had little impact on performance or emission of CH_4 (g/d), but decrease CH_4 emission per unit of DMI by 12% and decreased CH_4 emission per unit milk by 23%.

Key Words: dairy, forage, greenhouse

1191 Life cycle energy and greenhouse gas comparison of co-located organic and conventional dairy systems. B. J. Heins*, M. Reese, J. Tallaksen, and E. Buchanan, *University of Minnesota West Central Research and Outreach Center, Morris.*

The objective of this study was to directly compare life cycle fossil energy use and greenhouse gas (GHG) emissions in an organic and conventional dairy system at a site that utilizes both systems. The study was conducted at the University of Minnesota's West Central Research and Outreach Center, Morris, MN with SimaPro software. Conveniently, the on-site conventional and organic cropping systems provide comparable feed sourcing data. The life cycle assessment (LCA) is a cradle to gate study, with a functional unit of 1 kg of energy and fat corrected milk (EFCM). In terms of GHG, as measured by equivalents of CO_2, the organic system is greater (1.36 kg CO_2 equivalent per kg EFCM) compared to the conventional system (0.975 kg CO_2 equivalent). The organic dairy had higher emissions (1.3 and 0.0596 kg CO_2 equivalent) for animal maintenance/feeding and milk harvesting compared to the conventional herd (0.94 and 0.0351 kg CO_2 equivalent), respectively. In terms of fossil energy use, the organic system required more of fossil energy (3.47 MJ/kg EFCM) than the conventional system (2.72 MJ/kg EFCM). Fossil energy use for animal/maintenance and milk harvesting was similar for greenhouse gases for the organic system (1.87 and 1.6 MJ) compared to the conventional system (1.78 and 0.941 MJ), respectively. The largest factor influencing these results is the relative productivity of the organic and conventional herd. The organic herd is a pasture based low maintenance system, whereas the conventional herd is a more confinement based system. The conventional herd (20.9 kg/d) had greater milk production compared to the organic herd (12.3 kg/d). Another key difference between these systems is the feed use, which is higher per kg of milk produced in the organic system because of the greater use of pasture and high forage diets. The conventional system is able to use co-products such as DDGS and beet pulp to fulfill dietary requirements. With co-products, GHG and fossil energy impacts are spread between the main product (i.e., ethanol or sugar), resulting in a lower impact feed. It is important to note that this is an ongoing study and that additional data analysis may likely change the findings as the study progresses.

Key Words: greenhouse gas emissions, LCA, organic

1192 Effects of canola meal and soybean meal as protein sources on methane and ammonia emissions of high producing dairy cows.

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Manipulating dietary ingredients may effect greenhouse gas emissions by dairy cows. The objective was to determine CH_4 and NH_3 emissions of lactating cows fed canola meal (CM) or soybean meal (SBM) as the main protein source at either a high (HI; 17.6%) or low (LO; 15.4%) CP concentration. Twenty-four multiparous Holstein cows (mean ± SD; 120.5 ± 3.24 DIM; 2.71 ± 0.81 parity) were assigned 1 of 4 treatment diets at calving in a randomized complete block design with a 2 x 2 factorial arrangement of treatments. After wk 16 of lactation, cows were randomly assigned to 1 of 4 air-flow controlled chambers. Cows remained in the chamber for 6 d. Performance and emission data were measured on the last 3 d of each block. Diets were formulated to contain 55.0% forage (39.6% corn silage, 15.4% alfalfa silage) and 45% concentrate on DM basis. CM was included at 19.4% and 11.9% DM and SBM was included at 14.5% and 8.9% DM for the HI and LO diets, respectively. Soyhulls were included to balance nutrients and alter CP concentration. All other ingredients were the same across diets. Data were analyzed using the MIXED procedure of SAS. Cows fed either source or CP concentration of protein did not differ in DMI (mean ± SEM; 26.67 ± 0.75) or 4% fat-corrected milk (FCM; 53.89 ± 2.04 kg/d). Milk yield (59.1 vs. 53.3 ± 2.48 kg/d; $P = 0.095$) and feed efficiency (FCM/DMI; 2.11 vs. 1.95 ± 0.09; $P = 0.082$) tended to be greater for cows consuming HI protein compared to LO protein diets. Milk urea N (MUN) was lower for cows fed LO protein compared to HI protein (9.14 vs. 12.93 mg/dL; $P < 0.001$). There was a source x CP concentration interaction for CH_4 emission. Cows fed HICM produced less CH_4 than those consuming HISBM and LOCM (465.7 vs. 528.5 and 537.9 ± 28.7 g/d; $P = 0.036$). CH_4 expressed per unit of DMI (19.3 ± 1.24) or FCM (9.23 ± 0.71) did not differ among treatments. NH_3 tended to be higher for cows fed HI protein compared to LO protein (29.5 vs. 24.6 ± 2.31 g/d; $P = 0.062$). Milk N (g/d) and NH_3 emission expressed per unit of milk N was not affected by diet. NH_3 tends to increase with added protein inclusion in the diet and CM may reduce methane under specific feeding strategies.

Key Words: canola meal, greenhouse gas, methane

1193 Optimizing nitrogen efficiency on commercial dairy farms: Impact on production performance and herd profitability.

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Nitrogen efficiency (milk N/dietary N; NE) can be used as a tool for the environmental management of dairy herds. The aim of this study was to identify factors affecting NE and assess its impact on herd profitability. One hundred dairy herds comprising 17 to 117 lactating cows and located in the province of Québec, Canada were visited from October 2015 to June 2016. Feed intake was measured over 24 h. Samples of each feedstuff were taken and sent to a commercial laboratory for analysis of chemical composition. Particle size distribution of silages and total mixed ration was determined using the Penn State Particle Separator. Feeding management and feed prices were recorded. Milk yield was recorded and milk samples were collected over two consecutive milkings. Fat, protein, lactose, and milk urea nitrogen (MUN) were analyzed. Farms were divided according to their NE as low NE (L-NE) and high NE (H-NE) by the 25th and 75th percentiles, respectively. Differences between these groups were analyzed with the GLIMMIX procedure of SAS. Metabolizable protein (MP supply–MP requirements) and rumen degradable N (RDP supply–RDP requirement) balances were calculated according to NRC (2001). Income over feed cost was also calculated. Milk production was higher for H-NE than for L-NE (32.5 vs. 29.4 kg/d; $P < 0.001$) whereas MUN was lower for H-NE (11.1 vs. 12.8 mg/dL; $P < 0.01$). Herds with H-NE received diets with higher non-fiber carbohydrate (NFC; 41.1 vs. 37.3; $P < 0.01$), physically effective NDF (6.9 vs. 3.7; $P < 0.05$) and TDN (74.0 vs. 71.0; $P < 0.01$), and lower CP (11.1 vs. 12.8; $P < 0.01$), NDF (36.5 vs. 40.0; $P < 0.001$), lignin (3.0 vs. 4.0; $P < 0.001$) and soluble protein (4.6 vs. 5.3; $P < 0.05$) than herds with L-NE. Metabolizable protein and RDP balances were lower for H-NE than L-NE (−320 vs. 206 g/d; $P < 0.001$ and 314 vs. 525 g/d; $P < 0.001$, respectively). Furthermore, the negative MP balance for H-NE herds indicates that NRC (2001) may have overestimated the MP requirements for this group. Finally, income over feed cost was higher for H-NE (0.56 vs. 0.50 $/kg; $P < 0.001$). In conclusion, herds with H-NE had lower MUN and less CP, but higher NFC contents in the diet, which suggest a greater energy availability allowing a better efficiency of N utilization. This strategy was shown to be economically profitable.

Key Words: lactating dairy cows, milk urea nitrogen, nitrogen efficiency

1194 Including corn in crop rotations is profitable for dairy farms and does not result in greater greenhouse gas emissions at the whole-farm level. V. Ouellet*[1], D. Pellerin[1], M. Chantigny[2], and E. Charbonneau[1], [1]*Département des sciences animales, Université Laval, Quebec, Canada,* [2]*Soils and Crops Research and Development Centre, Agriculture and Agri-Food Canada, Quebec, Canada,*

Corn silage is recognized as a palatable and digestible source of energy for dairy cows. On the other hand, corn silage production is widely criticized as it may carry more environmental risks than perennial forages. Our objective was to use the whole-farm model N-CyCLES to assess the effect of different crop rotations with varied levels of environmental risks on dairy farm profits, N and P balance, and greenhouse gas emissions, while optimizing the management practices required to achieve maximum profits. Adaptations made to the model included modification to rotations, adjustment in the optimization constraints, evaluation of crop production cost, evaluation of forage nutritive value, and update in fertilization requirements. Data representative of an average dairy farm from Centre-du-Quebec region in Quebec, Canada were used. Four crop rotation scenarios considered to have different environmental impact were built in the model, and compared: corn grain-soybean-corn silage-alfalfa-alfalfa (very high negative impact, +++); corn grain-soybean-corn silage-alfalfa/timothy-alfalfa/timothy-alfalfa/timothy (moderate negative impact, ++); cereal-alfalfa/timothy-alfalfa/timothy-alfalfa/timothy-naked oats (low negative, +); cereal-alfalfa/timothy-alfalfa/timothy-alfalfa/timothy-alfalfa/timothy-mixed grains (positive impact,-). Results showed that the highest dairy farm profits (0.12 $/kg of FPCM) were associated with the (++) rotation, whereas the lowest profits (0.05 $/kg of FPCM) were associated with the (-) rotation. The lowest farm-gate to farm-gate greenhouse gas emission allocated to milk production (0.98 CO_2 eq./kg of FPCM) was predicted for the (+++) rotation, whereas the highest value (1.03 CO_2 eq./kg of FPCM) was predicted for the (-) rotation. This result is mainly explained by the lack of cash crop sold and the lower NFC and higher N content in cow's diet for the farm with (-) rotation. The highest N and P balances (20.1 g/kg of FPCM and 1.185 g/kg of FPCM, respectively) were predicted for the (-) rotation since more corn grain was bought (156.5 t/yr) to compensate for the absence of corn grain and corn silage produced on the farm. Moreover, the lowest N and P balances (12.8 g/kg of FPCM, 0.465 g/kg of FPCM) were predicted for the (++) rotation. These results suggested that including corn silage in the crop rotation do not carry a greater environmental risk on the considered output than crop rotations without corn and that growing corn silage is profitable when the whole farm is considered as a single unit of decision. Sound practices still need to be developed to improve other environmental considerations such as soil structure and erosion.

Key Words: corn silage, crop rotation, whole-farm model

1195 Effect of baling or grazing of corn residue on the subsequent crop yields. K. M. Ulmer*[1], J. L. Cox[1], M. K. Rakkar[1], R. G. Bondurant[1], M. E. Drewnoski[1], J. C. MacDonald[1], H. Blanco-Canqui[2], and R. J. Rasby[1], [1]*University of Nebraska, Lincoln,* [2]*Department of Agronomy and Horticulture, University of Nebraska, Lincoln.*

The amount of corn residue in the Midwest has increased with the increased corn production. Producers have utilized this resource as a feedstuff for cattle for grazing in the fall and winter and as a baled feed resource for future feeding. The objective of this 2 yr study was to determine how grazing or baling of corn residue affects subsequent grain yield and harvest index in multiple regions across Nebraska. In year 1, there were three locations and in year 2, an additional two locations were added. At each location, there were 3 treatments: grazed (GZD), baled (BLD), and no graze-no bale (NGNB) with 2–3 reps per treatment per location. Hand harvest yield estimates were collected once the corn reached black layer stage of maturity. Corn plants were cut from 5.33 m rows (3 rows per rep), corn grain was removed, then the grain and remaining plant material were weighed separately and subsequently subsampled for dry matter analysis (60°C). Dry matter measurements from the grain and stover were used to calculate corn yield and stover (total biomass minus the grain) per ha. Harvest index was calculated based on the percentage of dry grain out of total biomass (grain plus stover). Data were analyzed using the MIXED procedure of SAS with yield, location (nested within year), and treatment as fixed effects. There were no interactions ($P \geq 0.15$) between location and treatment for all analyses, but location was significant ($P \leq 0.01$). No differences were observed among treatments for grain yield ($P = 0.137$) with BLD having yields of 14,918 kg grain DM/ha, GZD with 14,689 kg grain DM/ha and NGNB with 13,682 kg grain DM/ha (SEM = 306). Across location, grain yields ranged from 11,981 to 17,085 kg DM/ha across locations. There was no difference ($P = 0.87$) in stover yield among treatments (8974, 9137, and 8743 ± 237 kg/ha stover DM for BLD, GZD, and NGNB, respectively). Stover yield ranged from 7649 to 11,562 kg DM/ha across locations. There was no difference ($P > 0.40$) in harvest index among treatments (62.2, 61.5 and 61.0 ± 0.57% for BLD, GZD, and NGNB, respectively). Harvest index ranged from 55.1 to 63.0% across locations. Results indicate that in the short term, removing corn residue provides a potential feed resource with no negative impact on grain yield or harvest index.

Key Words: baling, corn residue, crop yields, grazing

1196 Use of a novel continuous culture fermentor system for in vitro determination of enteric methane output from ruminants. A. I. Roca-Fernandez*, S. L. Dillard, M. D. Rubano, R. J. Tillmann, and K. J. Soder, *USDA-Agricultural Research Service, University Park, PA.*

Continuous culture fermentor systems (CCFS) serve to evaluate the effect of diet on in vitro nutrient digestibility, fermentation, and microbial protein synthesis. Limitations of CCFS are: maintaining protozoa populations, and avoiding accumulation of undigested material in the vessels. Therefore, a 4-unit, 3-L bioreactor CCFS (Applikon Biotechnology Inc., Foster City, CA) was adapted to determine pH, DM, protozoa numbers, and enteric CH_4 output of a forage diet. Each unit was fed 82 g DM/d of 50% orchardgrass (*Dactylis glomerata*) + 50% alfalfa (*Medicago sativa*) in equal portions, 4 times daily (07:30, 10:30, 14:00, and 19:00 h) throughout 10-d periods ($n = 4$, 7 d adaptation and 3 d collection). The CCFS was programmed to maintain temperature = 39°C, stirrer = 255 rpm, and CO_2 flux = 1 mL/min. Temperature and pH were recorded every 2 min. On d 1 of each period, 1500 mL of rumen fluid + 32 g of digesta were collected from a fistulated cow and added to each fermentor. Vat volume was maintained at 1500 ± 200 mL during the 10 d. Solid mean retention time, solid dilution rate, and liquid dilution rate were adjusted daily to 24 h, 4%/h, and 11%/h, respectively, by regulation of buffer input and effluent removal. Effluent and fermentation vats were sampled daily to determine protozoa numbers and DM. Gas samples for CH_4 analysis were collected 6 times daily (07:25, 09:00, 10:00, 13:55, 15:30, 16:30 h) during the 3-d collection periods and analyzed by GC (Varian CP 3800, Agilent Technologies, Santa Clara, CA). Data were analyzed using PROC GLIMMIX (SAS Inst. Inc., Cary, NC). There were no differences ($P \geq 0.067$) in total buffer and effluent volume, effluent DM, and CH_4 output between periods or among days within a collection period. There were no differences in pH or vat DM ($P \geq 0.445$) between periods. However, pH was greater ($P < 0.001$) on d 10 than d 8 or d 9 (6.51, 6.43, and 6.45, respectively). Preliminary results show fewer ($P < 0.001$) protozoa during the adaptation vs. collection period ($11.5 \pm 2.82 \times 10^4$ and $34.0 \pm 3.95 \times 10^4$ cells/ml, respectively). There was no difference ($P = 0.786$) in protozoa during the 3 d of the collection period ($34.0 \pm 2.25 \times 10^4$cells/ml). This CCFS not only provides a stable fermentation environment, but also preserves protozoal populations, which better simulates in vivo ruminal fermentation conditions compared with previous CCFS methods.

Key Words: continuous culture fermentor, methane, ruminants

1197 Effect of introducing legumes containing condensed tannins in an orchardgrass diet on forage nutritive value and enteric methane output in continuous culture. A. I. Roca-Fernandez*, S. L. Dillard, M. D. Rubano, C. J. Dell, and K. J. Soder, *USDA-Agricultural Research Service, University Park, PA.*

Legumes containing condensed tannins (CT) have been shown to reduce enteric CH_4 in ruminants; however, research is lacking on how increased CT levels affect forage nutritive value and CH_4 output. A 4-unit, dual-flow continuous culture fermentor system was used to assess CH_4 output of CT legumes in an orchardgrass diet (*Dactylis glomerata*). Treatments included: alfalfa (ALF, *Medicago sativa*) used as control, birdsfoot trefoil (BFT, *Lotus corniculatus*) as a low CT legume (7% CT, DM basis), crown vetch (CV, *Coronilla varia*) as an intermediate CT legume (12% CT, DM basis), and sericea lespedeza (SL, *Lespedeza cuneata*) as a high CT legume (31% CT, DM basis). Treatments were randomly assigned to fermentors in a 4 × 4 Latin square design using 7 d for adaptation and 3 d for collection. Feedings (82 g DM/d) occurred 4 times daily (07:30, 10:30, 14:00, and 19:00 h) throughout 4, 10-d periods. Treatments consisted of 50% orchardgrass and 50% legume. Forage samples were analyzed for DM, OM, CP, soluble and degradable protein, fiber, lignin, and NE_L. Gas samples for CH_4 analysis were collected 6 times daily (07:25, 09:00, 10:00, 13:55, 15:30, 16:30 h) during the last 3 d of each period and analyzed by GC (Varian CP 3800, Agilent Technologies, Santa Clara, CA). Methane data were analyzed using the GLIMMIX procedure of SAS (SAS Inst. Inc., Cary, NC) with treatment and period as fixed effects and fermentor as random effect. Pearson correlation coefficients between CH_4 output and forage characteristics were determined using PROC CORR, and stepwise linear regression analysis was conducted according to PROC REG to detect predictive statistical associations between CH_4 output and forage characteristics. Methane output of SL was 60, 68, and 73% less ($P < 0.012$) compared to CV, BFT, and ALF, respectively. Crown vetch reduced ($P < 0.025$) CH_4 output by 33% compared to ALF. There were no differences ($P > 0.200$) in CH_4 output between BFT and ALF or BFT and CV. Correlation analysis revealed a positive relationship between CH_4 output and degradable protein ($r = 0.630$, $P = 0.009$). An inverse relationship was found between CH_4 output and OM ($r = -0.520$, $P = 0.039$). Stepwise regression analysis revealed that degradable protein explained 40% of the variation in CH_4 output across all CT legumes. In summary, inclusion of legumes containing CT reduces CH_4 output and was affected by nutrient content of the forage.

Key Words: condensed tannins, enteric methane, legumes

1198 Effect of summer annuals on ruminal fermentation and methane output in continuous culture. *S. L. Dillard*[*1], *A. I. Roca-Fernandez*[1], *A. N. Hafla*[1], *M. D. Rubano*[1], *A. F. Brito*[2], *and K. J. Soder*[1], [1]*USDA-Agricultural Research Service, University Park, PA,* [2]*University of New Hampshire, Durham.*

Summer annuals (SA) provide forage during the summer "forage slump", yet research on ruminal fermentation and CH_4 output of SA is lacking. A 4-unit, dual-flow continuous culture fermentor system was used to assess nutrient digestibility, VFA production, bacterial protein synthesis, and CH_4 output of SA. Treatments were randomly assigned to fermentors in a 4 × 4 Latin square design using 7 d for adaptation and 3 d for collection. Treatments were: 1) 100% orchardgrass (*Dactylis glomerata*) herbage (HERB), 2) 50% herbage + 50% Japanese millet (*Echinochloa esculenta*; MIL), 3) 50% herbage + 50% sorghum × sudangrass (*Sorghum bicolor* × *S. bicolor var. sudanense*; SSG), and 4) 50% herbage + 25% MIL + 25% SSG (MIX). Feedings (60 g DM/d) occurred 4 times throughout four, 10-d periods; fermentors were fed orchardgrass herbage at 730 and 1030 h. At 1400 and 1900 h, SA treatments received SA supplements while HERB received orchardgrass. Samples for CH_4 were collected 6 times daily (725, 0900, 1000, 1355, 1530, 1630 h) during d 8, 9, and 10; samples for NH_3–N, VFA, and pH were taken on d 8, 9, and 10. Samples were also analyzed for DM, OM, CP, and fiber fractions for determination of nutrient digestibility, and estimation of bacterial protein synthesis. Data were analyzed using MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Apparent DM, NDF, and ADF, and true DM digestibilities were not different ($P > 0.062$) among treatments. True OM and CP digestibilities, and apparent OM digestibility, were not different ($P > 0.084$; 76 ± 2.3, 93 ± 2.4, and 66 ± 2.6%, respectively) among treatments. Total N intake was not different ($P = 0.389$) among treatments (2.3 ± 0.01 g N/d), but bacterial N was greater ($P = 0.013$) in MIL and MIX than HERB (0.33, 0.34, and 0.25 ± 0.020 g N/d). There was no difference ($P = 0.296$) in total VFA concentration among treatments (57.5 ± 1.16 mmol/L). There was no difference ($P > 0.178$) in daily CH_4 output (6.7 ± 2.14 mmol/d) or CH_4 per gram OM fed (1.9 ± 0.62 mg CH_4/g of OM fed). Addition of SA to an herbage-based diet provided similar nutrient digestibility, VFA production, and CH_4 output as HERB, suggesting SA would produce similar animal performance to that of HERB.

Key Words: methane, pasture, summer annuals

1199 Analysis and review of publicly available GreenFeed results. S. Zimmerman* and P. R. Zimmerman, *C-lock, Inc., Rapid City, SD.*

The GreenFeed is a novel tool for measurement of enteric methane (CH_4) from ruminant animals. The GreenFeed method uses repeated short-term measurement of CH_4 emitted from the animal in a feed trough while animals are receiving a feed reward. To date, over 50 papers, conference proceeding, and reports are available that have used GreenFeed. The research covers a wide range of applications including method comparisons, animal genetics and dietary studies, and on-farm use. In many studies, variability and repeatability of the GreenFeed data are reported. The objective of this study was to aggregate the public data, analyze the results for overall accuracy compared to reference methods, summarize variability and repeatability of CH_4 emissions across applications, and to determine the strength of individual animal ranking relationships. Overall, 22 method comparison trails ranging in herd averaged emission from 150–485 g/d have been completed comparing GreenFeed to either the Sulfur Hexafluoride tracer method (SF_6, 11 trials), respiration chambers (9 trials), or model predictions (2 trials). The herd averaged results for the reference method compared to GreenFeed showed no significant slope bias (Reference = 0.99 × *g*reenFeed, $R^2 = 0.99$) and the average absolute mean error for all trails was 6.4%. For individual animal CH_4 emissions, GreenFeed measured CH_4 emissions were positively and moderately-to highly correlated with respiration chamber, SF_6, or modeled CH_4 in all but 4 trials. In the 4 trials with less agreement for individual animals, the number of GreenFeed samples per animal was very low for some animals (4–10 samples) or there was no chamber replication. GreenFeed measured CH_4 for individual animals also showed moderate correlations with DMI in three studies ($r^2 = 0.73$, $r^2 = 0.61$, $r = 0.77$), and in other studies was found to be higher ($r^2 = 0.42$ and $r^2 = 0.47$) than for SF_6 ($r^2 = 0.17$, $r^2 = 0.08$). Between animal variation in GreenFeed CH_4 emissions were found to be the same, or lower than between animal variation in DMI, BW, or Respiration Chambers, or SF_6 in all but one trail. Long term repeatability (R) of GreenFeed CH_4 emissions on forage based diets was $R = 0.70$- 0.88 in 7 different trials. Overall, the GreenFeed method produced similar absolute CH_4emissions estimates to reference methods, demonstrated the ability to rank animals, produced low but accurate between animal variability, and was highly repeatable on forage diets.

Key Words: emissions, GreenFeed, methane

1200 Evaluation of an enteric methane emissions measurement system for cattle. E. M. Andreini*[1,2], M. S. Calvo-Lorenzo[1,3], C. J. Richards[1], J. E. White[1], and S. E. Place[1], [1]*Oklahoma State University, Stillwater,* [2]*University of California, Davis,* [3]*Elanco Animal Health, Fayetteville, AR.*

Growing concern about climate change and sustainability has increased societal pressures toward livestock production to quantify and reduce its environmental impact. Through enteric fermentation, ruminants produce the greenhouse gas methane (CH_4), and to improve emission inventories and evaluate mitigation techniques, several methods (i.e., whole animal and head chambers, SF_6 tracer technique) of measuring emissions have been developed. The objectives of this study were to evaluate a ventilated head box system capable of measuring CH_4 and carbon dioxide (CO_2) emissions, and oxygen (O_2) consumption from cattle and to compare emissions across ad libitum and restricted intake periods. An additional objective was to provide insight to animal comfort while housed in the head box system. Six Holstein heifers (n = 6), initial live weight between 364 and 430 kg, were used to measure CH_4 and CO_2 emissions and O_2 consumption from two ad libitum intake periods (ADAPT and ADLIB) and one period (RESTRICT) with intake restricted to 2% of body weight on a dry matter basis. In the head box system, ambient air was circulated around the animal's head, and expired air was collected. Emissions were determined by calculating the difference in gas concentrations between ambient and expired air. As a measure of comfort in the head box system, all cattle were assessed for lying time, and respiration rates and THI were evaluated for thermal comfort. During ADAPT and ADLIB, DMI in individual pens (10.40 ± 0.41 kg and 11.00 ± 0.41 kg, respectively) was higher ($P < 0.0001$) than DMI during gas measurement (9.20 ± 0.45 kg and 9.80 ± 0.45 kg, respectively). During RESTRICT, DMI in individual pens (8.40 ± 0.44 kg) did not differ ($P > 0.05$) from DMI during gas measurement (8.40 ± 0.45 kg). Methane and CO_2 emissions were lower ($P < 0.05$) during RESTRICT as compared to ADAPT and ADLIB (Table 1, next page). Oxygen consumption rates differed for each period (Table 1). Lying time while in the head box system was similar to lying behaviors of dairy

Table 1200.

Table 1. Least-squares means (n = 6) of heifer emissions and lying time[v] by period for periods ADAPT, ADLIB, and RESTRICT[+].

	Period					
	ADAPT		ADLIB		RESTRICT	
Item	LS mean	SE	LS Mean	SE	LS Mean	SE
CH_4 Production (L/day)	235.00[a]	6.19	228.26[a]	6.18	193.19[b]	8.88
CO_2 Production (L/day)	3627.47[a]	90.72	3632.35[a]	90.47	3183.95[b]	104.79
O_2 Consumption (L/day)	3390.59[a]	99.77	3453.90[b]	99.57	3001.81[c]	111.36
Lying Time (Min/day)	779.17[a]	31.19	768.79[a]	31.19	842.78[a]	31.19

[a, b, c] Least-squares means within row without common superscript letters differ ($P < 0.05$).

[+] For periods ADAPT and ADLIB heifers were fed *ad libitum* feed intake. For period RESTRICT, feed was restricted to 2% of body weight on a dry matter basis 4 days prior to and for the duration of the 3-day gas measurement.

[v] Lying time measurement refers to average time spent lying during the 3-day gas measurement at the end of each period.

heifers reported in previous literature. There was no difference ($P > 0.05$) in THI and respiration rate across all periods, and THI and respiration rate were positively correlated ($R^2 = 0.381$; $P < 0.0001$). The head box system evaluated will be useful in examining the effects of emissions mitigation strategies, and variation in emissions caused by different feeds and throughout the 24-hour cycle of a day.

Key Words: cattle, enteric methane, measurement

1201 Impact of corn or soybean in crops and lactating cow diets on estimated greenhouse gas emission from Wisconsin certified organic dairy farms.

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This study used a partial life cycle assessment approach to estimate the impact of feeding strategies and associated cropping systems on greenhouse gases emission intensity (GHG-EI, kg CO_2–eq/t energy corrected milk, ECM) from Wisconsin certified organic dairy farms. Gases and sources of emissions included in the study were: nitrous oxide (N_2O) from fields (row crop and pasture), enteric methane (CH_4), and manure management (N_2O and CH_4). An earlier study had identified four clusters from a survey dataset of 69 organic dairy farms. In cluster 1, 2, 3, and 4 daily DMI of lactating dairy cows was 22.1, 15.2, 20.9, and 18.1 kg/d, amount of concentrate fed was 8.0, 2.0, 6.0, and 6.0 kg/d, time grazing on pasture was 39.2, 53.5, 38.6, and 47.7% of the year, and ECM was 6657, 3857, 7666, and 5495 kg/yr per cow, respectively. Three combinations of corn grain (CG) and soybean (SB) as concentrate (100%CG, 75%CG+25%SB, and 50%CG+50%SB) were assigned to each cluster to study the substitution effect of protein vs. energy supplementation. Overall, GHG-EI was 1273 ± 235 kg CO2-eq/t ECM with contributions of 57.4, 34.1, and 8.5%, for enteric fermentation, manure management, and field emissions, respectively. There was a strong inverse relationship between level of production and GHG-EI, which averaged 1209, 1622, 996, and 1264 kg CO2-eq/t ECM for cluster 1, 2, 3, and 4, respectively. Grazing time was positively related with GHG-EI in part because longer grazing time was associated with lower ECM production and increased N_2O emission from manure deposited on pasture during grazing. The GHG-EI was the greatest in Cluster 2 with 50%CG+50%SB and the lowest in Cluster 3 with 100%CG (1635 vs. 983 kg CO_2–eq/t ECM). The GHG-EI was predicted to increase with increasing SB in all four clusters and on average GHG-EI was 1260, 1273, and 1285 kg CO_2–eq/t ECM for 100%CG, 75%CG+25%SB, and 50%CG+50%SB, respectively. Planting soybean decreased N_2O emission from cropland due to lower intensity of N fertilization and greater reliance on biological N-fixation compared with planting corn. Lowering CG for more SB in the diet reduced enteric CH_4 emission (because of greater fat content in the latter) but increased N_2O emission from manure (because of greater CP content of the latter). This study suggested that growing and feeding CG or SB might explain only a small fraction of the large differences in emission observed among clusters.

Key Words: carbon footprint, LCA, organic dairy farms

1202 Winter feeding systems and farm greenhouse gas emissions.

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Overwintering beef cows is a major cost in Canadian cow-calf production systems and swath grazing is a potential alternative to reduce winter feeding cost relative to the traditional drylot feeding systems. The objective was to estimate and compare greenhouse gas (GHG) emissions from winter feeding systems: i) swath grazing on triticale, ii) swath grazing on corn, and iii) conventional drylot feeding systems (control). Data were obtained from a study conducted over three production cycles (2008/2009, 2009/2010, 2010/2011) at the Lacombe Research Center in western Canada. Greenhouse gas emissions were estimated by calculating methane (CH_4), nitrous oxide (N_2O) and carbon dioxide (CO_2) emissions from different sources using Intergovernmental Panel on Climate Change (IPCC) Tier 2 approach. Methane emissions were estimated from enteric fermentation and manure, N_2O emissions from fertilization and manure, and CO_2 emissions from energy use for farm activities related to feed production and processing, feed and bedding delivery and manure removal. Total emission expressed per kg of feed produced and fed were significantly ($P < 0.001$) lower for both the swath grazing treatments relative to the control treatment. Emissions per cow varied among treatments ($P < 0.001$), higher for control (12.3 kg CO_2e cow-d^{-1}) than corn (9.4 kg CO_2e cow-d^{-1}), with triticale (11.0 kg CO_2e cow-d^{-1}) intermediate. In all the treatments, the largest fraction of emissions was enteric CH_4 (69–76%), followed by N_2O (14–24%). The contribution of energy-derived CO_2 emissions for total GHG emissions was lower in swath grazing treatments (5–7%) compared to a traditional feeding system (11%) due to their minimal energy use. Farm activity related energy use was 9.4, 11.5, and 21.4 MJ cow-d^{-1} for triticale, corn, and conventional drylot feeding, respectively. This study indicated that swath grazing on triticale or corn can be an effective alternative winter feeding systems to reduce GHG emissions and increase energy use efficiency of Canadian beef cattle industry.

Key Words: greenhouse gas, swath grazing, winter feeding

1203 Grazing management and farm greenhouse gas emission intensity of beef production systems.
A. W. Alemu*[1], H. Janzen[1], S. Little[1], X. Hao[1], D. Thompson[1], V. Baron[2], A. D. Iwaasa[3], K. A. Beauchemin[1], and R. Kröbel[1], *[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, Canada, [2]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Lacombe, Canada, [3]Agriculture and Agri-Food Canada, Swift Current, Canada.*

The objective of the study was to evaluate the impact of grazing management on greenhouse gas (GHG) emission intensity at the farm-gate for beef production systems in western Canada using life cycle analysis. A life cycle analysis over an 8-yr period was conducted on a beef farm that managed 120 cows, 4 bulls, and their progeny. Calves were stocked on pasture and market cattle were finished on grain for 136 d. Four grazing management systems were evaluated: i) light continuous grazing (LC), ii) heavy continuous grazing (HC), iii) light continuous grazing for the cow-calf pairs and moderate deferred-rotational grazing for the stocker cattle (LCDR), and iv) heavy continuous grazing for the cow-calf pairs and moderate deferred-rotational grazing for the stocker cattle (HCDR). Primary data for pasture quality, animal performance and soil were from short- and long-term grazing studies. GHG emissions from different sources within the farm were estimated using the whole-farm model, Holos. Soil carbon change related to the different grazing managements was estimated using the Introductory Carbon Balance Model. Emissions intensity of beef varied among grazing management strategies and ranged between 14.4–15.9 kg CO_2e kg^{-1} live weight. Emissions intensity decreased with increasing stocking rate where the LC management had 9% greater GHG emission intensity than the HC treatment (14.4 kg CO_2e kg^{-1} live weight). There was no difference in emission intensity estimates between LC and LCDR or between HC and HCDR, indicating that the use of moderate deferred-rotational grazing for the stocker operation in LCDR and HCDR has no effect on emission intensity. However, the LCDR management had 7% greater emission intensity than HCDR (14.5 kg CO_2e kg^{-1} live weight). Regardless of the grazing management, methane emission from enteric fermentation was the major contributor (67–68%) followed by nitrous oxide from manure management (14–16%). Similarly, in all the grazing managements, emissions from the cow-calf herd were the major contributor (68–70%) for the total farm GHG emissions. When soil carbon sequestration was included into the total farm emissions, intensity estimate was reduced by 25–30% and were similar among the grazing management scenarios. Overall, the outcome from our study emphasizes the impact of grazing management on farm emissions as well as the importance of accounting for all the emission sources and sinks within the beef production system while estimating its environmental footprint.

Key Words: grazing management, life cycle analysis, soil carbon

1204 A life cycle assessment of a beef feedlot finishing ration supply chain in California.
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A life cycle assessment (LCA) was conducted for the feed supply chain (FSC) of a total mixed ration (TMR) typical of finishing feedlot cattle produced in California, USA. The goal was to determine the global warming potential (kg CO_2e kg^{-1} TMR) associated with the FSC along with the associated impacts of the FSC on the total life cycle of feedlot cattle produced in California. The methodology used followed the Livestock Environmental Assessment and Performance (LEAP) Partnership guidelines for FSC. System boundaries included feed production (crops and feed additives), transportation (from field or factory to feedmill), and TMR compound feed production (i.e., at the feedmill). Life cycle inventory data for a typical finishing TMR was collected. Given the scope of the study, primary data were limited. In accordance with LEAP guidelines, secondary data were sourced from national databases and Ecoinvent™ unit process data. Three scenarios were assessed as a result of allocation at the transportation step. Scenario A, B, and C assumed that once a feed ingredient was transported to the feedmill, 100%, 50%, and 0% of the empty return load would be allocated to TMR production, respectively. Additionally, the impacts of feed production in relation to the entire feedlot cattle production life cycle, for Scenario A, was determined. Total GHG emissions were determined to be 0.630 kg CO_2e/kg TMR for Scenario A, 0.576 kg CO_2e/kg TMR for Scenario B, and 0.521 kg CO_2e/kg TMR for Scenario C. Corn production, feed transportation, and liquid premix production were the main contributors to the life cycle impacts of the TMR. When assessing the entire feedlot life cycle for Scenario A, total GHG emissions were determined to be 0.824 CO_2e/kg TMR. Additionally, for scenario A, feed production in the Angus and Holstein feedlot scenarios was found to contribute approximately 76% and 58% of total feedlot emissions, respectively. The FSC is a major contributor of emissions to the total life cycle of feedlot cattle production and knowledge thereof is a first step in improving efficiencies and reducing emissions.

Key Words: feedmill, greenhouse gas, sustainability

1205 Estimating farm-gate ammonia emissions from Canadian beef production in 1981 as compared with 2011.

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The quantity of beef produced per animal in Canada over the past three decades has increased significantly as a result of improvements in production efficiency and increases in carcass weights. This resulted in a decline in greenhouse gas emissions per kilogram beef. As NH_3 volatilization from beef cattle manure is also a major environmental concern, the present study compared the NH_3 emissions of Canadian beef production in 1981 and 2011. A nation-wide mass balance approach based on total ammoniacal nitrogen (TAN) content in animal manure was used to estimate NH_3losses from housing, grazing, manure storage, and land spreading. Temporal and regional differences in cattle categories, feed types, and management systems, average daily gains and carcass weights were considered. On average, 21% to 22% of the total nitrogen (N) consumed by Canadian beef cattle was lost as NH_3–N in both years. Highest losses were observed in finished cattle where approximately 43% of the N consumed was lost as NH_3–N. Contribution of NH_3 from the various cattle classes differed between years and was mainly due to differences in the type of feeds used, and proportions of breeding stock and cattle finished in feedlots. Emission sources were generally consistent in both years, with average values of 12%, 40%, 28%, and 21% associated with animal housing, animal grazing, manure storage and land spreading, respectively. Total NH_3 emissions from the production of Canadian beef cattle (standardized on the basis of the size of the breeding herd within the reference year) was 27% higher in 2011 than they were 1981. The average emissions per animal in 1981 and 2011 were 14.2 and 15.7 kg NH_3/animal/yr, respectively. On an intensity basis, however, kilogram of NH_3 emitted per kilogram of beef decreased by 20%, from 0.17 in 1981 to 0.14 in 2011. The reduction in NH_3 intensity is mainly attributed to increase in reproductive efficiency, average daily gain and slaughter weights, and the resulting improvement in productivity per breeding herd over the study period. Differences in intensity may also be attributed to increased use of extended grazing (*e.g.*, swath, stockpiled and bale grazing) in 2011 compared to 1981. As management practices are altered in response to changes in profitability and policy, further studies are necessary to assess the impact of the beef industry on NH_3 emissions and air quality at the local, regional and national scale.

Key Words: ammonia emission intensity, beef, Canada.

1206 The effect of reduced crude protein, synthetic amino acid supplemented diets on nutrient excretion in wean to finish swine.

C. E. Vonderohe[*1], K. M. Mills[1], M. D. Asmus[1], E. R. Otto-Tice[1], J. Ni[1], C. V. Maxwell[2], B. T. Richert[1], and J. S. Radcliffe[1], *[1]Purdue University, West Lafayette, IN, [2]Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville.*

Seven hundred twenty mixed-sex pigs were placed in 12 rooms at the Purdue University Swine Environmental Research Building to study the effect of reduced crude protein diets supplemented with synthetic amino acids on nutrient excretion from wean-finish. Pigs were blocked by BW and gender, and randomly assigned to a room and pen (10 pigs/pen). There were two deep pits per room and three pens over each pit. Each room was fed one of three diets: 1) control diet (Control) balanced to the first limiting amino acid with no synthetic amino acids, 2) a low crude protein (2X), high synthetic amino acid diet that balanced to the seventh limiting amino acid, and 3) an intermediate CP diet (1X) formulated to have a CP concentration intermediate to the Control and 2X diets, with a moderate level of synthetic amino acid inclusion. This resulted in approximately a 3 and 5%-unit reduction in CP, respectively for 1X and 2X diets. Pig BW, feed intake, and manure pit depths were determined at each diet phase change. Pit vacuum samples were collected at the end of each growth phase and frozen at −20°C for subsequent analyses. Data were analyzed using the GLM procedure in SAS. Reductions in dietary crude protein resulted in a linear reduction in ammoniated N excretion per kg of BW gain in both Nursery (Control = 8.6 g/kg gain, 1X = 7.2 g/kg gain, 2X = 5.5 g/kg gain; $P < 0.0001$) and Grow-Finish (Control = 18.0 g/kg gain, 1X = 14.3 kg/kg gain, 2X = 10.1 g/kg gain; $P < 0.0001$) phases. Reductions in dietary CP, with synthetic amino acid supplementation also resulted in a linear reduction in total N excreted per kg gain in the Grow-Finish phase (Control = 18.5 g/kg gain, 1X = 14.9 g/kg gain, 2X = 13.1 g/kg gain; $P < 0.0001$) and overall (Control = 17.4 g/kg gain, 1X = 15.4 g/kg gain, 2X = 13.1 g/kg gain; $P = 0.0009$). Total mineral excretion (Ash) per kg gain was reduced in the 1X and 2X diets compared to the control (Control = 39.6 g/kg gain, 1X = 36.0 g/kg gain, 2X = 33.4 g/kg gain; $P = 0.0046$). There was no effect of diet on total manure volume or P excreted per kg gain. These results indicate that reductions in dietary crude protein of ~3 and 5%-units from wean-finish result in reductions of total N excretion of 11.7 and 24.4%, respectively.

Key Words: crude protein, excretion, swine

1207 Oxalic acid production by *Aspergillus niger* when using whey permeate lactose as a carbon source.
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When manure is applied to crops on a nitrogen basis, it often creates a buildup of phosphorus (P) in the soil. Phosphorus recovery by struvite precipitation is one strategy to capture excess P before land application. However, daily operating costs are expensive due to chemical inputs. Dairy cow manure contains larger concentrations of calcium compared to other livestock manure, which requires an acid addition to break the calcium phosphate bonds. Oxalic acid is desirable because, in addition to breaking bonds, its anion (oxalate) binds the calcium. This study investigated the production of a dilute oxalic acid solution by the fungus *Aspergillus niger* (*A. niger*) using whey permeate as a substrate. This study was based on the work by Strasser et al., which found that *A. niger* exclusively produces oxalic acid when fermenting a lactose carbon source. Whey permeate is a desired substrate due to its high lactose content, and because it can be viewed as a by-product of the dairy industry. Oxalic acid production was evaluated by independently incubating two strains of *A. niger*, ATCC 9029 and ATCC 6275, at two concentrations: 11% lactose whey permeate (no lactose added) or a 20% lactose whey permeate (lactose added), to see if either strain could produce the 1–1.5% oxalic acid solution necessary for struvite formation. Fungi were grown in two-liter vessels for 6 d at 30°C and a pH of 6. Samples were collected each day and analyzed for oxalic acid content. The first study compared oxalic production between the two strains when fermenting a 20% lactose whey permeate solution, and found that *A. niger* 9029 produced a 125mM oxalic acid solution and *A. niger* 6275 produced a 200mM oxalic acid solution over a period of 6 d. The production data were fitted with polynomial regression lines of $y = -5.0x^2+41.17x+37.95$ ($R^2 = 0.72$) and $y = -2.80x^2+36.88x+68.98$ ($R^2 = 0.89$), respectively. The second study compared oxalic production between the two strains when fermenting an 11% lactose whey permeate solution (no added lactose), and found that *A. niger* 9029 produced a 350mM oxalic acid solution and *A. niger* 6275 produced a 150mM oxalic acid solution over a period of 6 d. The data were fitted with polynomial regression lines of $y = -17.4x^2+147.7x+57.26$ ($R^2 = 0.85$) and $y = -6.85x^2+58.23x+28.81$ ($R^2 = 0.75$), respectively. These data indicate that *A. niger* can produce the necessary concentration of oxalic acid for struvite production when fermenting whey permeate with no added lactose.

Key Words: *Aspergillus niger*, oxalic acid, whey permeate

1208 Effects of pre- and postpartum supplementation of ruminally protected polyunsaturated fatty acids on reproductive performance of suckled beef cows.
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To evaluate the effects of a ruminally protected PUFA supplement (M-R, Church & Dwight Co., Princeton, NJ) on reproductive performance of suckled beef cows, 66 multiparous cows (621 ± 70 kg of BW) were used in a completely randomized design. Cows were stratified by breed, BCS and the previous year's calving date and assigned to 1 of 2 treatments: Control (CTRL; 0.91 kg·d^{-1} of corn gluten feed (CGF) + 0.23 kg·d^{-1} of Megalac-E) and treatment (MEGR; 0.91 kg·d^{-1} of CGF + 0.23 kg·d^{-1} of Megalac-R). The experiment was designed for cows to receive treatments from 30 d prepartum to 30 d postpartum (mean d fed prepartum = 29.66; mean days fed postpartum = 29.34). Treatments were provided individually 5 d per wk. All cows had ad libitum access to bermudagrass hay (*Cynodon dactylon*), water and mineral supplement during supplementation period. After completion of supplementation, all cows grazed a mixed winter forage pasture of rye (*Secale cereale*) and ryegrass (*Lolium multiflorum*) during for the remainder of the study. Cow and calf BW and cow BCS were assessed weekly. Postpartum concentrations of progesterone were determined on a weekly basis to access resumption of postpartum estrous cycles. Cows were exposed to a 7-d CO-Synch+CIDR estrus synchronization protocol and fixed timed artificial insemination (TAI) was performed 60 ± 6 h after $PGF_{2\alpha}$. Cows where then exposed to fertile cleanup bulls for 70 d. Ultrasonography was performed 35 d after AI when pregnancy status and embryo size was assessed. Pregnant cows were monitored until calving and calf birth weight and calving distribution were determined. Data were analyzed using the Mixed procedure of SAS with cow as the experimental unit and treatment as fixed effects. There was no difference between treatments for mean cow BW ($P = 0.97$) or BCS ($P = 0.20$). In addition, weaning weights of calves among treatments did not differ ($P = 0.16$) and the percentage of cows resuming estrous cycles by initiation of the breeding season did not differ ($P = 84$). There was no effect of treatment on pregnancy percentage at d 35 ($P = 0.13$) and at the end of the breading season ($P = 0.56$). At d 35 postbreeding, there were no differences ($P = 0.26$) between treatments on fetus crown-rump length and no effect of treatment on birth weight ($P = 0.31$) and calving distribution ($P = 0.91$). We conclude that Megalac-R supplementation failed to improve reproductive performance of suckled beef cows when compared with Megalac-E.

Key Words: Beef cows, polyunsaturated fatty acids, reproduction

1209 The effect of straw bedding on dry matter intake and residual feed intake ranking in yearling bulls. J. B. Hall[1,2], M. C. Roberts Lew[*3], and W. K. Smith[3], *[1]University of Idaho Nancy M. Cummings Research, Extension Education Center, Carmen, [2]Department of Animal & Veterinary Sciences, University of Idaho, Moscow, [3]UI Nancy M. Cummings Research, Extension & Education Center, Carmen, ID.*

The objective of this study was to examine the effect of straw bedding on dry matter intake (DMI) and residual feed intake (RFI) ranking in bulls. For animal care purposes, cattle are commonly bedded with straw when being housed in pens where snow and rain are frequent. Over 2 yr, residual feed intake (RFI) was analyzed on Angus and Shorthorn bulls (n = 188) using the GrowSafe® system. The bulls were fed a total mixed ration (TMR) with 14.2% protein and 68.7% TDN. These bulls were divided into four pens based on bull owner. Daily feed intake was measured for 80 d and 47 d in 2014 and 2015, respectively. Straw bedding was added twice a week. Dry matter intake (DMI, kg), average daily gain (ADG, kg/d), feed to gain ratio (F:G) and residual feed intake (RFI) were calculated. For F:G and RFI, bulls were ranked numerically then DMI was excluded from days where straw bedding was included and the bulls were ranked again. The individual bull DMI decreased ($P < 0.001$) on days were straw bedding was added (Bedding = 11.3 ± 0.1 kg, No bedding = 11.6 ± 0.1 kg). The pen DMI decreased ($P < 0.02$) when straw bedding was added as well (Bedding = 267.1 ± 2.2 kg, No bedding = 273.1 ± 1.4 kg). Year was not significant for both individual and pen DMI. The majority of the bulls did not maintain the previous ranking. 86.4% (159/184) and 77.7% (146/188) of the bulls changed rank for RFI and F:G, respectively. Of those bulls that changed rank, 76.7% (122/159) of the RFI and 56.9% (83/146) of the F:G changed by more than 2 rankings. The average change in rank for RFI and F:G was 4.63 and 1.86, respectively. It can be concluded that adding straw bedding to pens with cattle decreases DMI in a GrowSafe® system. Reduced intake due to bedding caused a change in RFI and F:G rankings within bulls. Bulls on a RFI test should be given minimal straw bedding and those days bedding is added should be left out of the RFI calculation.

Key Words: Bulls, feed efficiency, residual feed intake, bedding

1210 Management of dairy bull calves on U.S. dairy operations. C. B. Shivley[*1,2], N. Urie[1,2], and J. E. Lombard[1], *[1]USDA:APHIS:VS:Center for Epidemiology and Animal Health, National Animal Health Monitoring System, Fort Collins, CO, [2]Colorado State University, Fort Collins.*

The objective of this study was to evaluate management practices of dairy bull calves and compare these practices to those used for dairy heifer calves in the United States. This study was conducted as part of the National Animal Health Monitoring System's Dairy 2014 study, and included 36 operations in 8 states. Overall, 7.9% (SE 0.7) of bull calves were stillborn. Stillbirth percentage for all calves on the 36 operations was 6.0% (SE 0.6). Regarding colostrum management, 95.6% (SE 2.8) of bull calves received colostrum; 94.9% (SE 2.1) received colostrum by hand feeding only, 3.3% (SE 1.5) received colostrum by hand feeding and suckling, and 1.8% (SE 1.0) received colostrum by suckling only. No heifer calves received colostrum by suckling only. Bull calves received colostrum 4.6 h (SE 0.5) after birth, compared with 3.0 h (SE 0.5) after birth for heifer calves. At the first feeding, bull calves received 3.3 L (SE 0.1) of colostrum, plus 1.7 L (SE 0.3) in all subsequent feedings for a total of 5.0 L (SE 0.3) of colostrum in the first 24 h, compared with a total of 5.4 L (SE 0.4) of colostrum in the first 24 h for heifer calves. On average, 2.3% (SE 0.5) of bull calves died before leaving the operation. Most operations did not dehorn bull calves (77.8%). Of the 22.2% of operations that did dehorn bull calves, 62.5% of operations dehorned using hot irons at an average age of 21.0 d (SE 7.6). Only 12.5% of operations used analgesics/anesthetics when dehorning bull calves. Heifer calves were dehorned on 91.4% of operations, with hot iron being the most commonly used method. Anesthetics/analgesics were used when dehorning heifer calves on 28.0% of operations. Most operations did not castrate bull calves (71.4%). Of the 28.6% of operations that did castrate bull calves, 30.0% used a knife, with an average age of 14.7 d (SE 4.8); no operations used analgesics/anesthetics. Bands were used by 70.0% of operations at an average age of 6.3 d (SE 0.9 d); 9.8% of operations (n = 1) used analgesics/anesthetics. Bull calves on these operations were managed differently from heifer calves. These results highlight the need to administer the appropriate volume of quality colostrum in a timely manner, and the value of using analgesics or anesthetics for painful procedures in bull calves.

Key Words: dairy bull calves; colostrum quality; dehorning practices

1211 Assessment of different bedding systems for lactating cows in freestall housing. H. Su[*1], N. M. Esser[2], W. K. Coblentz[3], M. A. Borchardt[3], W. Jokela[3], and M. Akins[1], *[1]University of Wisconsin, Madison, [2]University of Wisconsin, Marshfield, [3]US Dairy Forage Research Center, Marshfield, WI.*

The objective of this study was to compare different bedding systems for lactating cows in freestall housing. Bedding systems included new sand (NS), recycled byproducts of manure separation (organic solids [OS] and recycled sand [RS]), and foam-core mattresses with a shallow layer of OS (MS). The experimental barn contained 128 freestalls that were divided into 4 equal quadrants with 1 bedding system for each quadrant. All animals included in this study were first lactation cows, randomly assigned to different quadrants as cows calved. This experiment was conducted between January 2014 and December 2015 with 2 periods (1 calendar year for each period). Bedding systems were changed the last week of the first period. Milk yield data was recorded daily and milk samples were collected monthly for milk composition and somatic cell count (SCC). Cow's behavior, hygiene, and hock score were collected monthly. Clinical mastitis and hoof trimming cases were summarized based on veterinary records. Quadrant (pen) was considered the experimental unit with all data averaged by quadrant before analysis. Results represent 2 yr of data collection, and are presented as means ± SD (Table 1); Therefore, yearly comparisons of means are numerical only, and do not imply statistical significance. The OS and NS groups had greater milk yield compared with RS and MS groups, and the same responses were observed for energy-corrected (ECM) and fat-corrected milk (FCM). The SCC and somatic cell score (SCS) were greatest for the OS group. Cows housed in NS stalls had the greatest cow comfort and stall usage indexes. Cows in OS, NS and RS stalls were cleaner (lower flank score) than cows in MS stall. Cows in MS stalls had the most severe hock lesions (greater hock score). Greater incidence (total cases over 2 yr) of clinical mastitis was observed for cows with OS freestalls. Cows housed in NS and RS stalls needed fewer hoof trimmings than cows housed in OS and MS stalls. Based on the data thus far, NS seems to be the best bedding material for lactating cows based on milk performance, behavior, hygiene, and health data.

Key Words: lactating cow, bedding, freestall housing

1212 Management practices related to the welfare of dairy heifer calves on U.S. dairy operations. C. B. Shivley[*1,2], N. Urie[1,2], and J. E. Lombard[1], *[1]USDA:APHIS:VS:Center for Epidemiology and Animal Health, National Animal Health Monitoring System, Fort Collins, CO, [2]Colorado State University, Fort Collins.*

Animal welfare is a growing concern among the general public. The objective of this study was to evaluate dairy heifer welfare based on the results of the calf component of the National Animal Health Monitoring System's Dairy 2014 study. The 18-mo longitudinal calf study focused on dairy heifer calves from birth to weaning, and included 104 dairy operations in 13 states. Data were collected on 2,545 calves. Major risk factors for poor calf welfare were identified. Regarding calving management, 43.7% of births were unattended and 21.2% of calves did not have their navels disinfected. Concerning colostrum management, 22.7% of calves received poor quality colostrum (IgG < 50 g/L), and 13.0% of calves had failure of passive transfer with serum IgG < 10 g/L. Colostrum was primarily obtained via sucking for 22.1% of calves, with no control over quantity or quality. While the average timing after birth to colostrum feeding was within the recommended 4 h at 2.8 h (SE 0.05), 14.9% of calves received colostrum after 4 h, with the maximum 20 h after birth. An inadequate volume of colostrum (< 5.7 L) was administered to 67.5% of calves within the first 24 h. Of the 52.3% of all calves that were dehorned during the preweaning period, only 27.8% received any anesthetics or analgesics. Regarding milk feeding, restrictive feeding practices were common, with 29.6% of calves receiving less than 4.7 L of milk per day, and the average volume of milk per day fed was 5.7 L (SE 0.03). This restriction was reflected in the average daily gain of calves, with 35.5% of calves gaining less than 0.63 kg/day. The average age at weaning was 9.4 wk (SE 0.05), which was slightly higher than the recommended 6 to 8 wk of age. The most commonly used weaning criterion was age; only 4.6% of calves were weaned based on starter intake. Only 13.4% of calves were housed in groups, which has been shown to increase cognitive development but has increased disease risk. Bedding is important for calves to remain clean and comfortable but 12.6% of calves were bedded with sand or no bedding. Overall, 5.0% of calves died during the preweaning period, and most of these deaths had no reported cause, identifying an area for further investigation. Identifying risk factors for calf welfare is the first step toward finding solutions.

Key Words: dairy heifer calves; animal welfare; colostrum management

1213 Performance and health of calves pre- and post-weaning when fed pasteurized whole milk and whole milk supplemented with differing milk replacer protein sources. D. Ziegler[*1], H. Chester-Jones[1], D. L. Cook[2], J. L. Olson[2], and S. M. McCusker[2], *[1]University of Minnesota Southern Research and Outreach Center, Waseca, [2]Milk Products, Chilton, WI.*

The objectives of this study were to compare calf pre- (d 1 to 49) and postweaning performance (d 50 to 56) when fed pasteurized waste milk (PWM) or a combination of 67% PWM with 33% milk replacers (MR) formulated with similar crude protein (CP) to PWM with varying protein sources. One hundred-eight (2 to 5 d old) individually fed Holstein heifer calves (38.4 ± 0.64 kg) were randomly assigned to 1 of 4 milk treatments. Milk treatments included 1) PWM fed at 0.34 kg DM 2× daily from d 1 to 42 and 1× daily from d 43 to weaning at d 49 **(**WM); 2) PWM (67%) fed with 33% all-milk protein MR as in treatment 1 **(**AM); 3) PWM (67%) fed with 33% MR containing 50% all-milk and 50% blend of soy protein concentrate/wheat protein as in treatments 1 and 2 (SWP); 4) PWM (67%) with 33% MR containing 50% all-milk and 50% blend of hydrolyzed vegetable proteins and autolyzed yeast fed as in treatments 1, 2, and 3 (PP). Calf starter (CS;18%CP) and water were fed free choice d 1 to 56. Waste milk was collected 2× wk and pasteurized before each feeding. Total milk DMI was similar for all calf groups, averaging 29.9 kg. Pre-weaning ADG tended to be greater ($P = 0.09$) for WM (0.76 kg/d) and AM (0.73 kg/d) calves vs. those fed SWP (0.69 kg/d) and PP (0.70 kg/d). There were no postweaning ADG differences ($P > 0.05$) in the nursery. Pre- and postweaning CS DMI, were similar ($P > 0.05$) across treatments, averaging 21.8 and 15.5 kg, respectively. Hip height gain d 1 to 56 averaged 12.7 cm. Preweaning and overall d 1 to 56 gain/feed was highest for WM calves ($P < 0.05$). There were no differences ($P > 0.05$) in number of scouring days and treatment costs. From d 57 to d 84 there were no differences in ADG ($P > 0.05$) across calf groups when all calves were on a common diet in group pens. Under conditions of this study calves fed WM tended to have better pre-weaning performance parameters vs. those fed 2/3 WM and 1/3 MR containing varying protein sources.

Key Words: calf performance, pasteurized waste milk, milk replacers.

1214 Performance and health of calves pre- and post-weaning when fed milk replacers formulated with alternative protein sources. H. Chester-Jones[*1], D. Ziegler[1], R. Blome[2], and D. Wood[2], *[1]University of Minnesota Southern Research and Outreach Center, Waseca, MN, [2]Animix, Juneau, WI.*

The objectives of this study were to compare pre- (d 1 to 42) and postweaning performances of calves (d 43 to 56) when fed milk replacers (MR) with differing protein sources. One-hundred thirty (2 to 5 d old) individually fed Holstein heifer calves (38.4 ± 0.71 kg) were randomly assigned to 1 of 5 non-medicated 24% CP: 20% fat MR treatments (trt): 1) MR containing all-milk protein fed at 0.34 kg DM with 2.39 L water 2× daily for 35 d and once daily from d 36 to weaning at d 42 **(**AM), 2) MR fed as in trt 1 with 16% of the CP replaced by Manildra GemPro 7700 wheat (MG)**,** 3) MR fed as in trt 1 and 2 with 16% of the CP replaced by MG and 16.8% by plasma (Nutrapro B; MGNB), 4) MR fed as in trt 1, 2, and 3 with 17.1% of the CP replaced by Chamtour Nutrior wheat (CN), and 5) MR fed as in trt 1, 2, 3, and 4 with 16.8% of the CP replaced by NB. All diets were formulated to contain standardized 2.4% lysine, 0.8% methionine and 1.6% threonine. Calf starter (CS;18% CP as-fed) and water were fed free choice d 1 to 56. There were no differences in pre- and postweaning ADG ($P > 0.05$) which averaged 0.68 and 1.07 kg, respectively. Overall d 1 to 56 ADG averaged 0.78 kg. All calf groups doubled their initial BW by 56 d with 12.24 cm of HH gain average. Total MR was 24.9 kg across calf groups. There were no differences ($P > 0.05$) in pre- and postweaning CS intake which averaged 48.9 kg for the 56 d. Pre- (0.67 kg), postweaning (0.48 kg), and overall (0.63 kg) gain/feed were similar ($P > 0.05$) across calf groups. Serum protein averaged 5.9 mg/dl. There were no trt differences in scouring d and trt costs. Under the conditions of this study replacing milk protein in milk replacers with 2 different sources of wheat (approx.17%) with or without plasma (16.8%) resulted in very acceptable calf performances. Calf performance was not compromised by inclusion of wheat proteins in the milk replacers fed for 42 d.

Key Words: calf performance, milk replacers, protein sources.

1215 Performance and health of calves pre- and post-weaning when fed milk replacer supplemented with algae. D. Schimek*[1], B. Ziegler[1], D. Ziegler[2], and H. Chester-Jones[2], *[1]Hubbard Feeds Inc., Mankato, MN, [2]University of Minnesota Southern Research and Outreach Center, Waseca.*

The objectives of this study were to compare calf pre- (d 1 to 42) and postweaning performance (d 43 to 56) when fed milk replacer (MR) supplemented with microalgae meal *(All-G Rich™ Schizochytrium limacinum* CCAP 4087/2; Alltech, Inc.) in a dose titration study from August through November, 2015. One hundred-eight (2 to 5 d old) individually fed Holstein heifer calves (38.6 ± 0.61 kg) were randomly assigned to 1 of 4 treatments (trt); 1) Milk replacer, 24% CP:20% fat fed at 0.34 kg in 2.39 L water ×2 daily for 35 d and ×1 daily from d 36 to weaning at d 42 (CON); 2) Milk replacer as in trt 1 plus 2 g algae/calf daily (2 gA); 3) Milk replacer as in trt 1 with 4 g algae/calf daily (4 gA); 4) Milk replacer fed as in trt 1 supplemented with 6 g algae/calf daily (6 gA).Texturized calf starter (CS; 18% CP) and water were fed free choice d 1 to 56.There were no differences in pre- and postweaning total BW and daily gain ($P > 0.05$). Calves fed 6 g algae tended to have numerically higher preweaning gain (linear effect, $P = 0.11$). Average BW and HH after 56 d for all calf groups, met the suggested guidelines of double their initial BW and at least 10.2 cm of HH gain. Total MR intake was similar ($P > 0.05$) among all calf groups, averaging 24.7 kg. There were no CS intake differences among calf groups ($P > 0.05$). There was a trend for a linear increase in gain/feed preweaning ($P = 0.08$) with increasing levels of algae in the MR compared to CON. This numerical trend was also observed from d 1 to 56. There were no differences in scouring d (fecal score ≥ 3). There was a linear decrease ($P = 0.06$) in the number of scouring d when the fecal scores = 4 from calves fed CON compared to those fed increasing MR algae levels. There were no differences in treatment costs. Under conditions of this study, supplementing algae in MR from 2 to 6 g/calf daily was not detrimental to pre- and postweaning calf performance. There was an indication of a positive trend for supplementing 6 g algae for feed efficiency especially preweaning.

Key Words: calf performance, milk replacers, algae

1216 Evaluation of the efficacy of a copper sodium hypochlorite footbath and a 5% copper sulfate footbath on the control of digital dermatitis lesions. B. A. Wadsworth*, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

Digital dermatitis (DD) may be prevented using a 5% copper sulfate footbath. One alternative solution is a copper sodium hypochlorite solution (treatment; 2.5% copper sulfate footbath with 1.4 L of sodium hypochlorite solution added; GEA Farm Technologies, Naperville, IL). The objective of this study was to compare the copper sodium hypochlorite solution to a 5% copper sulfate footbath (positive control) on the frequency and severity of DD. This study was conducted at the University of Kentucky Coldstream Dairy from May 11, 2015 to June 26, 2015. Holstein cows ($n = 66$) were housed in 2 freestall barns (A and B) and cows were balanced for parity and days in milk. Footbath solutions were administered through 2 poly footbaths (J&D Manufacturing, Eau Claire, WI) in separate locations, measuring 15.24 cm × 81.28 cm × 198.12 cm and holding 94.64 L of solution each. Cows in barn A passed through the positive control footbath 5 d a week, 2 times per day. Cows in barn B passed through the treatment footbath 5 d a week, 2 times per day. The positive control footbath was refreshed every other day and the treatment footbath was refreshed every day. Rear feet DD lesions were scored weekly using a M0 to M4 scoring system: M0 indicates no lesion (non-active lesion); M1 represents an early growth < 2 cm in size (active lesion); M2 indicates an ulcerative lesion > 2 cm in size (active lesion); M3 represents a healing growth (non-active lesion); and M4 designates a chronic growth (non -active lesion). The DD lesions were further separated into active lesions or non-active lesions for statistical analysis. The GENMOD procedure of SAS (SAS Institute, Inc., Cary, NC) was used to analyze the probability of having an active lesion with each treatment. The probability of having left rear active lesions was 1.53 times greater ($P = 0.28$) than non-active lesions for the positive control compared to the treatment. The probability of having right rear active lesions was 1.87 ($P = 0.10$) times greater than non-active lesions for the positive control compared to the treatment. In conclusion, no significant differences were observed between the two footbaths, highlighting that copper sodium hypochlorite solution might be a viable alternative footbathing solution.

Key Words: digital dermatitis, footbath, copper sulfate, sodium hypochlorite

1217 Comparison of DX613 copper sulfate acidifier to a 5% copper sulfate footbath for prevention of digital dermatitis lesions in dairy cattle. H. B. Reichenbach*, B. A. Wadsworth, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

Digital dermatitis (DD) is an infectious disease seriously plaguing the dairy industry. The gold standard for prevention is a copper sulfate footbath. Although this method is effective, the large quantities of product required and the negative environmental impacts of bath waste necessitates a search for alternatives. The objective of this study was to compare a 2.2% copper sulfate footbath with 325.31 mL of DX613 Acidifier (treatment; GEA Farm Technologies, Naperville, IL) to a 5% copper sulfate footbath (positive control) on the frequency and severity of DD. Footbaths were delivered via a split footbath (Intra Care Foot Bath, Diamond Hoof Care LTD Alberta, Canada), measuring 32.5 cm wide by 233 cm

long, allowing for 80 L of solution per side. A metal coil separated the 2 footbaths to prevent cross contamination of solutions and decrease organic matter contamination. The left side of the bath served as the positive control and the right side served as the treatment. Baths were refreshed every 2 to 3 milkings, twice weekly. The study was conducted at the University of Kentucky Coldstream Dairy from November 11, 2015 to January 20, 2016. Holstein (n = 59) cows were housed in 2 freestall barns and balanced for parity and days in milk. The cows were exposed to the solutions on leaving the parlor after morning and afternoon milkings, 5 times per week. The DD lesions were scored biweekly using a M0 to M4 scoring system. A M0 score indicated no lesion (non-active lesions); M1 indicated small lesions (active lesions); M2 indicated large and potentially severe lesions (active lesions); M3 represented healing lesions (non-active lesions); and M4 represented chronic lesions (non-active lesions). The DD lesions were further separated into active lesions or non-active lesions for statistical analysis. A Chi-Square test calculated using the FREQUENCY procedure of SAS (SAS Institute, Inc., Cary, NC) indicated no-significant difference between the two solutions (chi-square = 1.18, P = 0.56). Eleven percent of treatment cows had active lesions and 9% of positive control cows had active lesions. A McNemar's test indicated significant differences in the prevalence of lesions from the beginning to end of the study (treatment: $P < 0.05$, positive control: $P < 0.01$; Table 1). This concludes a comparable effectiveness of both solutions. Given the potential for reduced environmental impact, the DX613 Acidifier may be a viable alternative for dairy producers.

Key Words: digital dermatitis, footbath, copper sulfate, acidifier, hoof care

Table 1217.

Table 1: Prevalence of lesions from beginning to end of study

Item	Positive Control	Treatment
No lesion at baseline and no lesion at end	46	42
No lesion at baseline and lesion at end	1	13
Lesion at baseline and no lesion at end	11	4
Lesion at baseline and lesion at end	1	0

1218 ortheast dairy herd characteristics: transition cow management strategies, performance, culling, and health. A. B. Lawton*[1], W. S. Burhans[1], D. V. Nydam[2], M. Tetreault[3], and T. R. Overton[1], *[1]Cornell University, Department of Animal Science and PRO-DAIRY, Ithaca, NY, [2]Cornell University, Department of Population Medicine and Diagnostic Sciences, Ithaca, NY, [3]Poulin Grain Inc., Newport, VT.*

A cross-sectional field study was conducted to describe transition cow management strategies and herd performance characteristics in high-producing dairies. A convenience sample of commercial Holstein herds (n = 72) in New York and Vermont were enrolled between November 2012 and August 2015. Data reported represent annual data at herd enrollment. Herd size range was 345 to 2,900 milk cows (mean ± SD; 935 ± 486) with a Dairy Herd Improvement herd milk average of 12,283 ± 1,051 kg (n = 50) and herd average milk yield/cow of 37.8 ± 3.8 kg/d (n = 69). Within the 40% of herds using recombinant bovine somatotropin (rbST) an average of 78% of eligible cows received rbST. Primiparous and multiparous animals had similar average days dry (56.5 ± 5.6) and herd reported voluntary waiting period (58.3 ± 9.4). All farms moved cows as parturition approached; 28% of herds moved animals to a maternity pen 0 to 3 d before calving; the other 72% used a calving pen, defined as animals moving to a pen when showing signs of calving. Eighteen percent of herds used separate calving locations for nulliparous and parous animals. Farms used a 1-group (9.7%) or 2-group (90.3%) dry cow system and 1-group (6.9%) or 2-group (93.1%) early lactation system for parous animals. Far-off and prefresh pens were either freestall (92.7%, 82.5%, respectively) or bedded packs (7.3%, 17.5%, respectively). Pens housing prefresh animals had animals moving in 1×/wk (71.6%) whereas 23.2% had animals moving in multiple times per week. From dry off until calving, number of pen moves for parous animals was either 2× (19.4%), 3× (69.4%), or 4× (11.1%) (n = 72 herds). From 60 d before due date until calving, nulliparous animals were moved 1× (4.2%), 2× (50.7%), 3× (40.3%), or 4× (4.2%) (n = 72 herds). Herd mean cull and death rate for animals $\leq$ 60 d in milk (DIM) was 5.9 ± 4.5% for primiparous animals and 8.4 ± 4.3% for multiparous animals (n = 71). Herd mean (SD) cull and death rate for animals overall was 20.6% (7.8%) for primiparous animals and 35.7% (7.2%) for multiparous animals (n = 71). Incidence of herd identified post-partum health

events (n = 71) were as follows; stillborn heifers: 5.9 ± 1.8%, twinning: 4.1 ± 1.4% (n = 72), RP: 6.5 ± 3.8%, metritis ≤ 30 DIM: 6.4 ± 8.5%, DA ≤ 60 DIM: 2.0 ± 1.6%, and ketosis ≤ 30 DIM: 6.6 ± 8.9%. These results demonstrate the variability in current practices and health related outcomes in large, progressive dairies in the Northeast.

Key Words: Transition cow, management, health outcomes

1219 Facilities, management, and animal factors associated with heifer culls in New York State dairy farms. B. D. Scott* and J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY.*

Objectives were to evaluate the rate of heifers leaving herds from 151 to 600 d of age relative to facilities, management practices, and individual animal factors. A survey was conducted on 55 commercial dairy farms in 2014 to assess and define herd factors for the prior and subsequent year. Dairy records from the on farm herd management software were collected approximately 1 yr later to analyze data for calves born in 2013 and 2014. Cull rates (P[mortality, dairy sales, or slaughter]) were established for a 151 to 360 (EXIT360) and 361 to 600 (EXIT600) days of age risk period. Risk ratios of EXIT360 and EXIT600 were analyzed using Poisson regression with PROC GENMOD of SAS. The heifer was the experimental unit within farm, utilizing an exchangeable correlation matrix. Variables of interest for both EXIT360 and EXIT600 were birth season (BIRTHSSN; cold = September through February and warm = March to August) and year, pneumonia or diarrhea events for the first 150 (ILLNESS150), 151 to 360 (ILLNESS360), and 361 to 600 (ILLNESS600) days of age, colostrum and milk feeding factors (quantity and duration), wean transition (methodology, age, and duration), number of pen moves, bunk space access, relative stocking density (heifers per stall), number of feedings and pushups per day, bedding amount and type, herd growth mode, culling style of herd manager (forgiving, moderate, aggressive), and number of lactating cows in the herd. Mortality and dairy sales were reported as 50% and 26% of all EXIT360 (6.2% of 33,168 heifers). Mortality and dairy sales were reported as 31% and 11% of all EXIT600 (10.6% of 9465 heifers). Birth season, birth year, ILLNESS150, and ILLNESS360, were all associated with EXIT360 (Table 1). Birth season and ILLNESS600 were associated with EXIT600 (Table 1). When ILLNESS and BIRTHSSN are considered, no facility or management factors were associated (P > 0.10) with EXIT360 or EXIT600 across these herds and their diversity of facilities and management in 2013 to 2014. We conclude that birth season and year as well as pneumonia and diarrhea events are associated with the probability of dairy heifers leaving herds between 151 and 600 d of age.

Key Words: replacements, mortality, illness

1220 Facilities, management, and animal factors associated with primiparous cows postpartum herd exit risk in New York state dairy farms. B. D. Scott* and J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY.*

Objectives were to evaluate the rate of primiparous cows leaving herds in the first 60 DIM relative to facilities, management practices, and individual animal factors. A survey was conducted on 55 commercial dairy farms in 2014 to assess and define herd factors for the prior and subsequent year. Dairy records from the on farm herd management software were collected approximately 1 yr later to analyze data for cows entering first lactation in 2013 and 2014. Cull rates (P[mortality, dairy sales, or slaughter]) were established for a 60 d eligible risk period (EXIT60). Risk ratios of EXIT60 were analyzed using Poisson regression with PROC GENMOD of SAS. The cow was the experimental unit within farm, utilizing an exchangeable correlation matrix. Cow level variables of interest for EXIT60 were calving season, age at first calving (AFC), maximum energy corrected milk produced in the first 60 DIM (MECM60), and maximum somatic cell linear score in the first 60 DIM (LSFresh). Peripartum facility and management variables analyzed were bunk space access, relative stocking density (animals per stall), bedding depth, bedding type, commingling with multiparous cows, herd growth mode, culling style of the herd manager (forgiving, moderate, aggressive), years of experience of the herd manager, lactating cow herd size, and whether heifers were all raised on-farm or some purchased. Final EXIT60 included 54 farms with

Table 1219.

Table 1. Estimates of relative risk (RR) for EXIT360 and EXIT600 within 52 farms, 2013-2014

	EXIT360				EXIT600			
	RR	95% CI		Pr > |Z|	RR	95% CI		Pr > |Z|
Birth Season (Cold vs. Warm)	1.27	0.97	1.68	0.09	1.55	1.15	2.11	<0.001
Birth Year (2013 vs. 2014*)	0.48	0.39	0.58	<0.01	-	-	-	-
ILLNESS150	1.49	1.17	1.89	<0.01	-	-	-	-
ILLNESS360	1.99	1.30	3.05	<0.01	-	-	-	-
ILLNESS600	-	-	-	-	4.59	3.05	6.91	<0.01

*No heifers born in 2014 had yet reached 600 days of age for EXIT600 analysis

Table 1220.

Table 1. Estimates of relative risk of 30,145 primiparous cows exiting the herd within 60 days in milk on 54 farms in New York State in 2013 and 2014

	RR	95% CI		Pr > |Z|
Calving Season (Cold vs. Mild)	1.30	1.02	1.65	0.033
Calving Season (Hot vs. Mild)	0.73	0.54	0.98	0.039
AFC (≤21 Months vs. 21-24.5)	0.69	0.50	0.95	0.022
AFC (≥24.5 Months vs. 21-24.5)	1.48	1.25	1.75	<0.001
Heifer Purchasing (None vs. Some)	1.48	0.96	2.26	0.073
MECM60 (Per 1 Kg Increase)	0.89	0.88	0.90	<0.001
LSFresh (Moderate[a] vs. Low)	1.20	1.03	1.41	0.022
LSFresh (High[a] vs. Low)	1.82	1.52	2.17	<0.001

[a]Low<4.0, 4.0≤Moderate≤6.0, High>6.0

adequate records for analysis and 30,145 cows. Mortality and dairy sales were reported to be 20% and 16% of all EXIT60, respectively, which totaled 6.6% of all cows at-risk. Table 1 summarizes differences and parameter estimates. Calving season, AFC, MECM60, LSFresh, and purchasing cows were associated with EXIT60. Conversely, no facilities or management factors were associated ($P > 0.10$) with EXIT60 across these herds and their diversity of facilities and management. We conclude that in years 2013 and 2014 calving season, age at first calving, milk production, and linear score were associated with the probability of a primiparous exiting the herd in the first 60 DIM across these 54 dairies in New York.

Key Words: culling, primiparous cow, dairy

1221 Facilities, management, and animal factors associated with calf losses in New York state dairy farms. B. D. Scott* and J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY.*

Objectives were to evaluate the rate of calves leaving herds in the first 150 d of age relative to facilities, management practices, and individual animal factors. A survey was conducted on 55 commercial dairy farms in 2014 to assess and define herd factors for the prior and subsequent year. Dairy records from the on-farm dairy management software were collected approximately 1 yr later to analyze data for calves born in 2013 and 2014. Cull rates (P[mortality, dairy sales, or slaughter]) were established for calves with a 150 d of age eligible risk period (EXIT150). Risk ratios of EXIT150 were analyzed using Poisson regression with PROC GENMOD of SAS. The calf was the experimental unit within farm, utilizing an exchangeable correlation matrix. Variables of interest were birth season (BIRTHSSN) and year, first colostrum administration (liters, type, and timeline), liters of colostrum (total) on the day of birth, number of milk feedings in a day, type of milk solution fed and quantity, weaning approach, weaning age and duration of process, pre-wean housing type, growth mode of the dairy, reported culling style of manager, experience level of calving supervisor, hours of calving area supervision, post wean ration, age at first exposure to fermented feeds, recorded pneumonia and/or diarrhea (ILLNESS) events, and relative scale of the dairy operation. The final regression model for EXIT150 retained 53 herds (n = 55,108 calves) after losses for inadequate records. Overall, mean EXIT150 was 4.91% (range = 0.53 to 22.0%). Reported mortality and dairy sales represented 59.9 and 16.3% of all EXIT150, respectively. Birth year of 2014 had higher ($P < 0.01$) EXIT150 (7.68%, n = 26,807) than 2013 (2.29%, n = 28,301). Colder BIRTHSSN (September through February) was associated with increased ($P < 0.01$) EXIT150 (RR = 1.58, 95%CI = 1.33–1.88) relative to other seasons. Reported ILLNESS data were available from 38 herds with 11.2% of the total calves having reported ILLNESS. Calves with reported ILLNESS had higher ($P < 0.01$) EXIT150 (RR = 1.43, 95%CI = 1.16–1.76). All other factors tested had no association with EXIT150 ($P > 0.10$) across the dairies included in the study and within their diversity of facility and management practices. We conclude that events of pneumonia and diarrhea, birth season, and birth year were associated with heifers leaving the herd and mortality within the dairies surveyed in 2013 and 2014.

Key Words: culling, survey, risk ratio, mortality

1222 Seasonal effects on milk yield and somatic cell score in organic dairy farms from the Northeast United States. J. G. B. Galvão Jr.*[1], A. F. Brito[2], A. H. N. Rangel[3], and J. B. A. Silva[4], *[1]Federal Institute of Science, Education,and Technology of Rio Grande do Norte, Ipanguaçu, Brazil, [2]University of New Hampshire, Durham, NH, [3]Federal University of Rio Grande do Norte, Natal, Brazil, [4]Universidade Federal do Semiarido, Mossoro, Brazil.*

The objective of this study was to evaluate the seasonal milk performance of organically-certified dairy farms in the Northeast region of the United States. Dairy Herd Improvement (DHI) records from May 2012 to May 2015 were obtained monthly from 7 herds in the states of New Hampshire (n = 2), Maine (n = 3), Vermont (n = 1), and New York (n = 1).

Table 1222.

Table 1. Least square means and SEM for the effects of season on milk yield and composition, and somatic cell score in Northeastern organic dairy farms

Season	Milk yield, kg/d	Protein, %	Fat, %	SCS	n
Fall	20.7 ± 0.34[b]	3.43 ± 0.01[a]	4.41 ± 0.02[ab]	2.47 ± 0.03[ab]	2,725
Spring	22.0 ± 0.34[a]	3.22 ± 0.01[c]	4.24 ± 0.02[c]	2.46 ± 0.03[b]	2,894
Summer	21.7 ± 0.32[a]	3.24 ± 0.01[c]	3.97 ± 0.02[d]	2.58 ± 0.03[a]	2,988
Winter	21.5 ± 0.35[a]	3.34 ± 0.01[b]	4.46 ± 0.02[a]	2.51 ± 0.03[ab]	2,837

[a,b,c]Values in the same column with different superscripts are significantly different at $P < 0.05$.

A total of 11,444 observations including milk yield, concentrations of milk fat and protein, and somatic cell score (SCS) were obtained and tested against the effects of season using the PROC GLM procedure of SAS. The herds averaged (mean ± SD) 166 ± 107 DIM, 21.5 ± 8.21 kg/d milk yield, 3.31 ± 0.52% milk protein, 4.27 ± 0.98% milk fat, and 2.51 ± 1.71 SCS. The seasonal effects on selected milk variables are shown in Table 1. All milk variables analyzed herein were affected by season. Milk yield was lower ($P < 0.05$) in the fall (mean = 20.7 ± 8.03 kg/d) compared with spring (mean = 22.0 ± 8.35 kg/d), summer (mean = 21.7 ± 7.88 kg/d), and winter (mean = 21.5 ± 8.48 kg/d), which did not differ from each other. The observed decrease in milk yield during the fall may be explained by limited pasture biomass production and changing of diets as cows transition from pasture- to winter-based rations. Milk protein and fat concentrations showed an inverse relationship with milk yield, thus suggesting a dilution effect caused by increased or decreased milk volume. The SCS was greatest during the summer (2.58 ± 1.74), intermediate during the fall and winter, and lowest during the spring (2.46 ± 1.71). Cows are susceptible to heat stress and nuisance flies during the summer, which can depress their immune system and increase intramammary infections. Somatic cell score is positively correlated with poor udder heath and a SCS over 4.0 possibly indicates the presence of intramammary infections and associated reduction in milk yield. However, the SCS across the 7 organic dairies used in our study ranged from 2.46 to 2.58, suggesting adequate milking procedures and preventative mastitis program. The use of annual forage crops can extend the grazing season potentially helping farmers mitigate milk yield losses during late fall, while management tools to reduce fly pressure and heat stress are likely needed to reduce SCS during the summer.

Key Words: milk composition, organic dairies, somatic cell score

1223 Argentina Veterinarian preferences to devise a mastitis control plan: A conjoint analysis approach.

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The rationale applied for veterinarians to propose the most suitable udder health plan to farmers is not well understood in Argentina. Objective: to quantify the preference of different technical and economic criteria considered by veterinarians when a mastitis control plan (MCP) is being devised to apply on farm. Methodology: During an annual meeting of the Argentinian Milk Quality Association, 45 veterinarians with at least 5 yr of experience working on milk quality participated in a choice experiment (CE). Six interventions were considered in the design of MCP: milking machine maintenance, milking routine, clinical mastitis management, dry cow therapy, culling of cows with persistent infection, and environmental hygiene. Four attributes were defined for MCP: operational costs, efficacy over bulk milk somatic cell count (BMSCC) reduction, efficacy on clinical mastitis (CM) reduction, and specific level of technical support needed to implement the MCP. The cost attribute had 3 levels (50, 40, and 30 US$ /day), the efficacy on BMSCC reduction had two levels (300,000 to 500,000 cells/mL or < 300,000 cells/mL), the efficacy in reducing CM cases had 3 levels (10 to 20%, 5 to 10% and < 5%) and technical support had three levels (3, 6, and 16 US$/day). The CE was framed using a fractional factorial design combining MCP attributes ($n = 4$) and their level ($n = 12$) in an orthogonal matrix (IBM SPSS Conjoint 20). Ten cards were randomly chosen from the matrix (48 combinations) to perform the CE. Each card contained a MCP (A to I) with its attributes and its specific

Table 1223.

Table 1: Relative importance (%) of the mastitis control plan attributes for two choice scenarios

	Cost	Efficacy on BMSCC reduction	Efficacy in reducing CM cases	Technical support
Completely confined dairy herd	22.5	23.2	42.2	12.1
Confined plus grazing dairy herd	26	24.4	38.3	11.3

level. The CE was conducted considering that the MCP would be applied in a 100 milking cows herd with a BMSCC around 500,000 to 600,000 cells/mL, during the last 12 mo. The veterinarians had to evaluate two scenarios; a completely confined and a confined plus grazing dairy herd. Participants ranked the MCP list from the best to the worst, for both herd scenarios. Such arrange was used to estimate the average utility (U) taking into account the preferences of the participants. The model was as follows, U = u(a1)+u(a2)+…+u(a4), where, U = total utility of MCP; a = attribute; $u(a_i)$ = unit of change of U for u. Results: The model showed that efficacy criteria prevailed over economic criteria; while the technical support had marginal influence in the decision (Table 1). An inverse relationship between cost and utility was found, which means that less costly intervention is preferred. In contrast, we found a direct relationship between efficacy and utility.

Key Words: conjoint analysis, mastitis control, choice experiment

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1224 A model to estimate losses due to bovine mastitis for Argentinian dairy herds. M. Richardet[1,2], H. Solari[3,4], C. Vissio[*1,2], J. Bartolome[5], G. Bo[6], P. Turiello[2], C. Bogni[7], and A. Larriestra[2], *[1]CONICET, Rio Cuarto, Argentina, [2]Facultad de Agronomia y Veterinaria, UNRC, Rio Cuarto, Argentina, [3]CONICET, Buenos Aires, Argentina, [4]Facultad de Ciencias Exactas, Fisicas y Naturales, UBA, Buenos Aires, Argentina, [5]Facultad de Ciencias Veterinarias, UNLPam, General Pico, Argentina, [6]IAP Ciencias Basicas y Aplicadas, UNVM, Villa Maria, Argentina, [7]Facultad de Ciencias Exactas, Físico-Químicas y Naturales, UNRC, Rio Cuarto, Argentina.*

A comprehensive economic evaluation of disease control implies developing models to capture the complexity and dynamics of the production system, especially for diseases like mastitis, which has multiples effects such as milk losses, increased risk of culling or a higher likelihood of reproductive failure. Objective: to describe preliminary results of estimated clinical (CM) and subclinical mastitis (SCM) frequency caused by *S. aureus* and their milk associated losses by a stochastic simulation model. Methodology: The model simulates discrete events overtime mimicking a real Holstein herd in terms of production and reproduction. The system has been divided into compartments involving reproduction, production, disease, feeding and culling/mortality events and their respective costs overtime. The model has been written in C language and its parameters have been gathered through a literature review. The model starts with a user defined herd in terms of demography and health status. From that point, the system projects the whole dynamics of the herd for a specific time horizon (e.g., 12 mo). The model focuses on *S. aureus* infections and drives the infection within the herd considering transition probabilities among different cows (uninfected or subclinically or clinically infected). The system updates the whole herd and disease information every 2 wk. As an example, the model has been run 100 times in a 200-cow herd. Results: The annual projection showed a median gross CM prevalence of 3% (q1 = 2%; q3 = 4%) and a median gross SCM prevalence of 21% (q1 = 17%; q3 = 25%). Estimated milk losses due to CM and SCM were 2.87 and 1.40 l/cow/day, respectively. All results are consistent with observational data recently published in Argentina. The model evaluation and verification on relevant assumptions need to be done. The model runs satisfactorily and it can be customized for the user. Further development will involve the inclusion of multiples contagious and environmental microorganisms.

Key Words: stochastic model, milk loss, mastitis

1225 Effects of oral calcium formate supplementation in peripartum dairy cows. E. W. Carneiro[1], E. E. Ichikawa[2], D. M. V. F. Carneiro[3], and R. D. Almeida[*1], *[1]Universidade Federal do Paraná, Curitiba, Brazil, [2]Bayer HealthCare, São Paulo, Brazil, [3]Instituto Federal Catarinense, Araquari, Brazil.*

The objective of the study was to evaluate the effects of oral calcium formate supplementation on serum total calcium (tCa), ionic calcium (iCa), β-hydroxybutyrate (BHBA), total cholesterol, and cortisol in early-lactation dairy cows. In 2 commercial dairy farms in Castro county, Paraná State, Southern Brazil, 242 Holstein cows (150 multiparous and 92 primiparous) were blocked by herd, parity, and tCa status 6 h after calving. Blood samples were analyzed for group allocation (normal and hypocalcemia groups) using 8.9 mg/dL as the cutpoint (IDEXX VetTest® Chemistry Analyzer, Inc., Westbrook, ME). Within each block, fresh cows were randomly allocated to treatment (T) and control (C) groups, with treated -cows being supplemented twice, 6 and 31 h after parturition, with 350 mL of 14.3% (w/w) calcium as a 48.6% aqueous suspension of calcium formate (Calfon Oral®, Bayer HealthCare). Six blood samples from each animal were collected (6, 12, 31, 54, 78, and 102 h after calving) for determination of tCa and iCa. Blood samples for cortisol and cholesterol analysis were collected 6 h and 5 d after calving, while for BHBA analysis, blood samples were collected on Days 3, 5, and 7. Data was analyzed using MIXED procedure of SAS with a model containing the effects of block, treatment, time, and treatment*time interaction as fixed effects and cow within treatment as a random effect. Hypocalcemia incidence rates were 43% using on-farm tCa from VetTest ($\leq$ 8.9 mg/dL), 78% using tCa ($\leq$ 8.0 mg/dL) and 76% using iCa (concentration $\leq$ 4.0 mg/dL), with the lowest iCa values being observed at 12 h postpartum. Serum iCa values were higher (P = 0.04) in oral Ca formate-treated cows; 3.62 vs. 3.55 ± 0.02 mg/dL for the controls. Subclinical ketosis (serum BHBA $\geq$ 1.2 mmol/L) incidence rate was 21.5% (52/242). Estimates

of BHBA on Day 5 were lower ($P = 0.03$) for treated cows; 0.70 vs. 0.87 ± 0.06 mmol/L for the non-treated ones. No differences were detected ($P > 0.05$) for tCa, cholesterol, and cortisol concentrations between T and C animals. During the experimental period, both farms had shown very high levels of subclinical hypocalcemia. The oral calcium formate supplementation had shown modest, but beneficial effects in early-lactation dairy cows, increasing ionic Ca and reducing BHBA concentrations, important goals to control metabolic disorders in dairy farms.

Key Words: milk fever; ketosis; subclinical hypocalcemia

1226 Effect of prenatal and lactating cow trace mineral source on Angus and Brangus calf acute phase protein response to a weaning stressor.

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Trace mineral (TM) source provided to gestating and lactating Angus and Brangus cows and its subsequent effect on acute phase protein (APP) response in like breeds of calves at weaning was examined during 2 yr. Treatments were inorganic (salt sulfates) or organic (Se-yeast and proteinates) TM supplementation of Co, Cu, Fe, I, Mn, Mo, Se and Zn (3 d/wk, 0.4 kg·$^{-1}$454 kg BW·$^{-1}$d·cow^{-1}·d^{-1}). Delivery of TM to cows was initiated 88 ± 2 d pre-calving in year 1 and from conception to weaning of year 2. In both years, calves (year 1, $n = 28$/sex, 7/treatment×breed of bulls, heifers, steers; year 2, $n = 48$/sex, 24/treatment×breed of heifers, steers) were physically separated from dams at weaning (d 0) and maintained in dry-lot pens from d 0– 7, and on bahiagrass pastures from d 7–14. Calf blood samples were collected for analysis of APP including acid soluble protein (ASP), ceruloplasmin and haptoglobin on d 0, 1, 3, 7, and 14 relative to weaning. Calf was the experimental unit with PROC MIXED repeated measures within each year for analysis. Models included fixed effects of TM treatment, breed, calf sex, day relative to weaning, and interactions. Treatment did not affect any APP in year 1 ($P > 0.05$) or year 2 ($P > 0.05$). Day affected ($P \leq 0.05$) all APP values within a year. In year 1, peak concentrations of all APP occurred on d 3. In year 2, peak concentrations of ASP and haptoglobin occurred on d 3, while ceruloplasmin concentrations peaked on d 7. Within a year, ASP concentrations were greater ($P \leq 0.01$) in Brangus (year 1 = 83.4 ± 3.5; year 2 = 84.9 ± 2.6 mg/dL) than Angus (year 1 = 68.0 ± 3.5; year 2 = 61.7 ± 2.6 mg/dL) calves. Haptoglobin concentrations were greater ($P \leq 0.05$) in year 1 and year 2 in Angus (1.8 ± 0.1 units) than Brangus (1.5 ± 0.1 units) calves within each year. For ceruloplasmin, heifers had greater ($P \leq 0.05$) concentrations (15.2 ± 0.5 mg/dL) than steers (13.6 ± 0.5 mg/dL) and bulls (12.9 ± 0.5 mg/dL) in year 1; whereas in year 2, heifers (16.7 ± 0.4 mg/dL) had greater ($P \leq 0.05$) ceruloplasmin concentrations than steers (15.5 ± 0.4 mg/dL). In conclusion, calf breed and sex had greater effects on APP response to weaning than TM source.

Key Words: trace minerals, weaning, acute phase response

1227 Factors associated with average daily gain in dairy heifer calves on U.S. dairy operations.

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The objective of this study was to evaluate average daily gain (ADG) in U.S. dairy heifer calves based on different health, feeding, and management practices, as well as environmental factors. This study was conducted as part of the calf component of the National Animal Health Monitoring System's Dairy 2014 study, which included 104 dairy operations in 13 states. The calf component was an 18-mo longitudinal study focused on dairy heifer calves from birth to weaning. This analysis included data from 1,331 Holstein calves. The mean ADG was 0.75 kg/day (SE = 0.007), and calves were fed liquid diets an average of 63.8 d (SE = 0.4). Backward elimination model selection in Proc Mixed of SAS® was used after univariate screening ($P < 0.2$) to determine which environmental factors, diet, and management practices significantly impacted ADG. The final model included disease Y/N ($P < 0.001$), kg protein fed in the liquid diet per day ($P < 0.001$), the average temperature and humidity index for the preweaning period ($P < 0.001$), dam lactation number ($P < 0.001$), bedding type ($P < 0.001$), and singleton vs. twin birth ($P = 0.006$). After controlling for other independent variables in the model, calves with no disease events gained on average 0.05 kg/d more than calves with one or more disease events. Every 1 kg of protein fed per day equated to 0.1 kg/day of gain. Each 10-unit decrease in THI equated to 0.02 kg/day of gain. Calves from third or higher lactation dams had the highest gains (0.68 kg/d), followed by second lactation dams, and last first lactation dams (0.63 kg/d). Calves bedded with a combination of bedding materials gained the most (0.72 kg/d), followed by those bedded with shavings, then straw or hay, and lastly no bedding or sand (0.52 kg/d). Single calves gained 0.08 kg/day more than twins. These results highlight the importance of feeding an appropriate quantity and quality of a liquid diet, keeping calves healthy, and mitigating the effects of temperature and humidity on ADG.

Key Words: dairy heifers, average daily gain, calf nutrition

1228 Factors associated with morbidity in dairy heifer calves on U.S. dairy operations.

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The objective of this study was to evaluate morbidity in U.S. dairy heifer calves based on different health, feeding, and management practices, as well as environmental factors. This study was conducted as part of the calf component of the National Animal Health Monitoring System's Dairy 2014 study, which included 104 dairy operations in 13 states. The calf component was an 18-mo longitudinal study focused on dairy heifer calves from birth to weaning; data were collected on 2,545 calves. The morbidity rate for all calves enrolled in the study was 34%, with 7% of calves experiencing more than one disease event. It is likely that some sick calves were neither identified nor recorded and morbidity is underreported. The majority of clinical signs reported were digestive (56%) and respiratory (34%). Almost all sick calves (90%) received treatment, with 81% of treated calves receiving antimicrobials. Of calves treated with antimicrobials, the most commonly used classes were fluoroquinolones (28% of calves) and sulfonamides (25% of calves). The mortality rate for the study was 5.2%. The primary causes of death were reported as unknown (35% of calves), digestive (31%), and respiratory (16%). Backward elimination model selection in Proc Genmod of SAS® was used after univariate screening ($P < 0.2$) to determine which environmental factors and management practices significantly impacted morbidity. The final model included serum IgG ($P = 0.024$), gender of the primary caretaker ($P = 0.031$), and number of calves housed together ($P = 0.049$). Calves with an increased serum IgG were less likely to have a reported a disease event. Calves that had a female or male as the primary caretaker were 1.2 times more likely to have a reported disease event compared with calves that had a male and female as the primary caretaker. As group size increased, the risk of reported disease also increased. Practices that weren't significant in the final model included the use of vaccines, the addition of antibiotics, coccidiostats, or direct fed microbials to milk, and pasteurization of milk. These results highlight the continued importance of ensuring a high level of passive transfer of immunoglobulins in calves via colostrum, the importance of vigilant caretakers, and the possible morbidity risks of group housing.

Key Words: dairy heifers, morbidity, mortality

1229 Factors associated with *Cryptosporidium* and *Giardia* infection in preweaned dairy heifer calves.

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The objective of this study was to evaluate the presence of *Cryptosporidium* (*Crypto*) and *Giardia* in U.S. dairy heifer calves based on different management practices and environmental factors. This study was conducted as part of the calf component of the National Animal Health Monitoring System's Dairy 2014 study, which included 104 dairy operations in 13 states. The calf component was an 18-mo longitudinal study focused on dairy heifer calves from birth to weaning. Fecal samples were collected from 2,009 calves: 1,258 calves in the East region (IA, MI, MN, MO, NY, OH, PA, VT, VA, WI) and 751 calves in the West region (CA, CO, WA). Calves were sampled from 3 to 66 d of age, with a mean of 22 d (SE = 0.13). Calves were evenly sampled throughout the spring ($n = 491$), summer ($n = 539$), fall ($n = 536$), and winter ($n = 443$) seasons. Overall, 43.6% of calves were infected with *Crypto* and 30.0% of calves were infected with *Giardia*. Backward elimination model selection in Proc Genmod of SAS® was used after univariate screening ($P < 0.2$) to determine which environmental factors and management practices significantly impacted the presence of *Crypto* or *Giardia*. The final *Crypto* model included days of age at fecal collection ($P < 0.001$), herd size ($P = 0.03$), and season ($P = 0.04$). Calves £28 d of age were 1.24 times more likely to be infected with *Crypto* compared with calves > 28 d of age. Large herds (500+ cows) were 1.12 times more likely to be infected with *Crypto* compared with small herds (30 to 99 cows). Calves sampled in the fall were 1.1 times more likely to be to be infected with *Crypto* than calves sampled in the spring. The final *Giardia* model included season ($P < 0.001$), region ($P = 0.001$), liquid diet additives ($P = 0.002$), and average daily gain (ADG; $P = 0.003$). Calves sampled in spring, summer, or fall were 1.14 times more likely to be infected with *Giardia* than calves sampled in the winter. Calves in the East region were 1.15 times more likely to be positive for *Giardia* than calves in the West region. Calves fed additives other than antibiotics and direct fed microbials, such as larvicides and coccidiostats, in their liquid diet were 1.12 times more likely to be infected with *Giardia.* Additionally, ADG had a negative association with *Giardia*. These results highlight the factors associated with the presence of *Crypto* and *Giardia* in preweaned dairy heifer calves.

Key Words: dairy heifers, *Cryptosporidium*, *Giardia*

1230 Factors associated with colostrum quality and passive transfer status of dairy heifer calves on U.S. dairy operations. J. E. Lombard[*1], C. B. Shivley[1,2], and N. Urie[1,2], *[1]USDA:APHIS:VS:Center for Epidemiology and Animal Health, National Animal Health Monitoring System, Fort Collins, CO, [2]Colorado State University, Fort Collins.*

Passive transfer of immunity is essential for the short- and long-term health of dairy calves. The objective of this study was to evaluate colostrum quality and passive transfer status of U.S. dairy heifer calves. This study was conducted as part of the calf component of the National Animal Health Monitoring System's Dairy 2014 study, which included 104 dairy operations in 13 states. This longitudinal study focused on dairy heifer calves from birth to weaning and was conducted over an 18-mo period. Data analysis included 1,972 Holstein calves. The mean colostrum IgG was 74.4 g/L (SE 0.72), with 77.4% of samples having colostrum IgG levels above 50 g/L. The mean serum IgG was 21.6 g/L (SE 0.25), and 73.3% of calves had serum IgG levels above 15 g/L. Backward elimination model selection in Proc Mixed of SAS® was used to determine which factors were most important ($P < 0.05$) for determining colostrum IgG levels. The final model for colostrum IgG included the source of the colostrum ($P < 0.001$) and the temperature and humidity index (THI) for the month before calving ($P < 0.001$). Colostrum IgG was highest for third or higher lactation dams (84.2 g/L) and lowest for commercial colostrum replacers (39.5 g/L). For every 10-unit increase in THI, the colostrum IgG increased 1.4 g/L. Factors most important for predicting serum IgG levels were also evaluated using a backward elimination model selection in Proc Mixed after univariate screening ($P < 0.2$). The final model for serum IgG included source of the colostrum ($P < 0.001$), timing to the first feeding ($P < 0.001$), total amount of colostrum fed in 24 h ($P = 0.010$), the age of the calf at blood sampling ($P < 0.001$), colostrum IgG ($P < 0.001$), and THI for birth month ($P = 0.026$). Serum IgG was highest for calves from first lactation dams (23.4 g/L) and lowest for commercial colostrum replacer (14.5 g/L). For every hour following birth that colostrum was administered, serum IgG decreased 0.37 g/L. For every 1 L of colostrum administered in the first 24 h after birth, the serum IgG increased 0.56 g/L. For every 10 g/L increase in colostrum IgG, serum IgG increased 1.1 g/L. For every 10-unit increase in birth month THI, the serum IgG increased 0.32 g/L. These results indicate that prompt feeding of high-quality colostrum in appropriate amounts following birth and THI are crucial to the passive transfer status of dairy calves.

Key Words: dairy heifer calves; colostrum quality; passive transfer

1231 Risk factors for calf mortality on farms using automated feeders in the Midwest USA. M. Jorgensen* and M. I. Endres, *University of Minnesota, St. Paul.*

Use of automated calf feeding systems is increasing across the USA, yet information regarding health and mortality outcomes is limited. The objective of this study was to investigate the association of various farm management practices, housing, and environmental factors with mortality in preweaned dairy calves. Twenty-three Midwestern dairy farms were included in this mortality analysis. Farms were visited approximately every 60 d for 18 mo. Housing and environmental factors were measured at the time of each visit. Management practices were collected using a questionnaire and mortality events were gathered from producer-kept records. Relationships between categorical factors of interest and mortality rate were calculated using the mixed procedure of SAS. Pearson's correlation was used for continuous variables. Average mortality of calves on farms using automated feeders was 3.85 ± 3.70%/yr and 57% of farms (13/23) reported mortality rates below 3%/yr. The maximum recorded mortality rate was 13.41%/yr and the minimum was 0.24%/yr. Farm average serum total protein concentration of calves < 5 d old was negatively associated with farm annual mortality rate ($R = -0.50$, $P = 0.02$; mean sTP = 5.4 g/dL ± 0.74). Farms that disinfect the navels of newborn calves had a lower ($P = 0.03$) mortality rate (mean ± SE, 2.97 ± 0.80%; 78% of farms) than farms that do not disinfect (7.32 ± 1.59%; 22% of farms). Farms that use the drinking speed of calves as an alarm had a lower ($P < 0.001$) annual mortality rate (2.37 ± 0.83%; 74% of farms) than those that do not (6.57 ± 1.13%; 36% of farms). Farms that disinfect the calf pens between groups had a lower ($P = 0.04$) annual mortality rate (2.55 ± 0.94; 59% of farms) than those that do not disinfect (5.78 ± 2.55%, 41% of farms). Trends were detected in the correlations between mortality rate and bacteria counts (standard plate count) of milk collected from the feeder hose ($R = 0.37$, $P = 0.08$; median = 435,000 cfu/mL, IQR = 3764,375 cfu/mL), size of the dairy (number of calves on site; $R = -0.41$, $P = 0.08$; mean = 82.18 ± 84.26 calves) and age difference in calf groups ($R = 0.41$, $P = 0.06$; mean = 3.07 ± 2.03 wk). Basic calf-care practices remain vital to ensuring calf survival in automated feeding systems. These data indicate that farms using automated feeders are able to achieve a very low rate of death loss in preweaned calves, but a high variability in mortality among farms indicates continued room for improvement in calf death losses.

Key Words: automated calf feeding, mortality, management

1232 Impact of milk-feeding programs on fecal bacteria population and antimicrobial resistance genes in *Escherichia coli* isolated from feces in preweaned calves. G. Maynou[*1], L. Migura-Garcia[2], J. Subirats[3], H. Chester-Jones[4], D. Ziegler[4], A. Bach[1,5], and M. Terré[1], *[1]IRTA, Caldes de Montbui, Spain, [2]CRESA, Cerdanyola del Vallès, Spain, [3]ICRA, Girona, Spain, [4]University of Minnesota Southern Research and Outreach Center, Waseca, MN, [5]ICREA, Barcelona, Spain.*

The objectives of this study were to characterize fecal bacteria communities and evaluate the presence of antimicrobial resistance genes isolated from fecal *Escherichia coli* of dairy calves fed two different milk feeding programs. Fifteen Holstein newborn female calves (38.4 ± 3.21 kg BW) were fed pasteurized waste milk (pWM) with β-lactam antimicrobials residues, and 10 calves (39.2 ± 4.89 kg BW) were fed milk replacer (MR) with similar nutrient composition (27.5% CP, 32.1% fat) to waste milk (28.6% CP, 30.0% fat) from birth to weaning at 49 d of age. Fecal samples of 8 calves fed MR and 11 calves fed pWM were obtained on d 42 to profile fecal bacteria populations. The DNA was extracted and amplified for Eubacteria sequencing using Illumina Miseq platforms. Samples were filtered and assigned to a reference taxonomy using the SILVA reference database. A first analysis was made to assess differences in α and β diversity between the 2 milk-feeding sources using QIIME. An ANOVA was used to identify differences at order level between feeding practices. Furthermore, 25 *E. coli* isolates from fecal swabs of all calves at 35 d of age were used to identify resistance genes. A total of 10 resistance genes corresponding to aminoglycosides (*aadA*, *strA/strB* and *aac(3)IV*), β-lactam (*bla*CMY-2), tetracyclines (*tetA*, *tetB* and *tetC*) and sulfonamides (*sul1*, *sul2* and *sul3*) were examined by PCR and analyzed using a binary logistic regression to assess differences between feeding practices. Chao1 and Shannon α diversity indexes were similar in calves regardless of the feeding program followed. The prevalence of Clostridiales order was greater ($P < 0.05$) whereas Bacteroidales tended ($P = 0.07$) to be lower in pWM calves (0.58 ± 0.029 and 0.33 ± 0.032, respectively) than in those fed MR (0.44 ± 0.034 and 0.46 ± 0.038, respectively). A high prevalence of *sul1*, *sul2*, *tetA*, *aadA*, *strA/strB* and *aac(3)IV* were found in both treatments (0.43 ± 0.142, 0.62 ± 0.137, 0.50 ± 0.141, 043 ± 0.142, 0.63 ± 0.138, 0.43 ± 0.149, respectively) whereas the prevalence of CMY-2 in pWM calves (0.67 ± 0.122) was greater ($P < 0.05$) than in MR fed calves (0.10 ± 0.095). In conclusion, milk feeding practices can cause shifts in calf gut bacteria populations. High prevalence of extended spectrum β-lactamase resistance genes has been found in fecal *E. coli* isolates from pWM fed calf.

Key Words: calf feeding programs, fecal bacteria population, resistance genes.

1233 A survey of management practices and producers' perceptions regarding manual and automated milk feeding systems for dairy calves. C. Medrano-Galarza[*1,2], J. Rushen[3], A. M. de Passillé[3], A. Jones-Bitton[1], T. J. DeVries[4,5], S. J. LeBlanc[1], and D. B. Haley[1,2], *[1]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada, [2]Campbell Centre for the Study of Animal Welfare, University of Guelph, Guelph, ON, Canada, [3]Faculty of Land & Food Systems, University of British Columbia, Agassiz, BC, Canada, [4]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada, [5]University of Guelph, Guelph, ON, Canada.*

Dairy calves are commonly housed individually and fed by manual milk feeding (MMF) methods, with buckets or bottles. Automated milk feeders (AMF) allow for more natural milk feeding frequency and volume, with calves usually housed in groups. A national online survey was developed to determine management practices for the care of milk-fed calves in Canada, and factors that influence use of MMF or the switch to AMF. A total of 670 responses were received (5.7% of all dairy farms in Canada). Of respondents, 16% used AMF and 84% used MMF. Seventy percent of farms using AMF had free-stall barns compared to only 48% for those using MMF. Interestingly, 30% of AMF farms also had automatic milking systems (AMS), compared to 8% for MMF farms. Having a herd size > 80 milking cows (OR = 5.1; $P = 0.003$) and automated feed pushers (OR: 5.0; $P = 0.03$) were associated with having an AMF among tie-stall farms. For loose-housing farms (i.e., free-stall and bedded-pack), herd size > 80 milking cows (OR = 2.7; $P = 0.004$), having an AMS (OR = 2.4; $P = 0.01$), and use of cow-brushes (OR = 4.5; $P = 0.002$) were associated with having an AMF. Automated milk-fed calves were typically housed in groups of 10 to 15, while nearly 75% of the farms with MMF housed calves individually. Having group housing for milk-fed calves was associated with larger farms (> 80 milking cows; OR = 2.2; $P < 0.001$), having an AMS (OR = 1.8; $P = 0.03$), and having fewer personnel looking after the calves (1 vs. 2 people: OR = 1.8; $P = 0.009$; and 1 vs. ≥ 3 people: OR = 2.0: $P = 0.007$). Although both AMF and MMF farms fed similar amounts of milk the first week of life (a median of 6 L/d), the cumulative volume fed in the first 4 wk differed significantly ($P < 0.001$), with a median of 231 vs. 182 L, respectively. Median milk allowance for AMF also peaked higher than for MMF (10 vs. 8 L/d, respectively). The 4 most important producer-identified factors that motivated producers to switch to automation were to raise better calves, offer more milk to calves, reduce labor, and improve working conditions. For MMF farms, the investment in equipment and in group housing facilities, and farm size were the primary reasons given for maintaining manual feeding methods. To conclude, AMF farms were larger, provided more milk to calves, and use

more automation. These data provide insights into calf rearing practices across Canada, resulting in improved understanding of producers' uptake, and application of technology.

Key Words: calves, feeding practices, automation.

1234 Investigating the within-herd prevalence and risk factors of hyperketonemia of dairy cattle in Ontario as diagnosed by the test-day concentration of milk β-hydroxybutyrate.

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A large-scale observational study was conducted to estimate the within-herd prevalence and cow-level risk factors of hyperketonemia (HK) in dairy herds in Ontario that participate in a dairy herd improvement association (DHIA) program. Hyperketonemia was diagnosed as milk β-hydroxybutyrate ≥ 0.15 mmol/L (Ketoscreen test, MilkoScan FT600, Foss Analytical A/S, Hillerød, Denmark) at first DHIA test within the first 30 d in milk (DIM). Eight hundred and thirteen herds providing at least 61 first milk tests from June 2014 to December 2015 and were used to estimate the provincial within-herd prevalence with 95% confidence, 80% power and precision of 10%. All herds on DHIA in Ontario (n = 3,042) were used to construct multi-level logistic regression models to investigate the association of commonly measured variables with the odds of HK at first DHIA milk test at the cow-level. The overall HK prevalence in Ontario was 22% of cows at first test, with an average within-herd prevalence of 21% (SD = 10.6). The prevalence of HK had a distinct seasonality with the lowest prevalence occurring from July to November. Herds with automatic milking systems (AMS) (11%, n = 92) had higher within-herd prevalence than all other herds, as well as increased odds of HK in multiparous animals at first test (OR: 1.46; CI_{95}: 1.30 to 1.63). This association requires further study of causal factors. Both primiparous and multiparous Jersey cattle had 1.4 times higher odds of HK than Holstein cattle. After controlling for breed, a milk yield > 26 kg and milk fat > 4.8% at the last milk test of the previous lactation were associated with decreased odds of HK in the current lactation (OR_{yield}: 0.55; $OR_{fat\%}$: 0.83). Increased days dry and longer calving intervals, for multiparous animals, and older age at first calving for primiparous animals increased the odds of hyperketonemia at first test. This is the first report of associations of AMS, and milk yield and components late in the previous lactation with increased HK.

Key Words: prevalence hyperketonemia β-hydroxybutyrate

Table 1235.

Table 1. Effect of 8 wk milk replacer (kg) and calf starter (kg) intake on first-lactation 305-d milk, fat, and protein yield (kg) in all cows (n=2880).

Item	R^2	Variable	Estimate	SE	P-value
305-d milk	0.10	Milk Replacer	9.89	12.42	0.4261
		Calf Starter	8.21	2.53	0.0012
305-d fat	0.28	Milk Replacer	0.52	0.53	0.3332
		Calf Starter	0.36	0.10	0.0002
305-d protein	0.17	Milk Replacer	0.29	0.35	0.4115
		Calf Starter	0.33	0.07	<0.0001

1235 Relationships between early life milk replacer and starter intake and first lactation performance of Holstein dairy cows.

H. Chester-Jones*[1], B. J. Heins[2], D. Ziegler[1], D. Schimek[3], S. E. Schuling[3], B. Ziegler[3], M. B. De Ondarza[4], C. J. Sniffen[5], and N. Broadwater[6], *[1]University of Minnesota Southern Research and Outreach Center, Waseca, [2]University of Minnesota West Central Research and Outreach Center, Morris, [3]Hubbard Feeds Inc., Mankato, MN, [4]Paradox Nutrition, West Chazy, NY, [5]Fencrest, LLC, Holderness, NH, [6]University of Minnesota Extension, Rochester.*

The objective was to determine relationships between early life milk replacer and starter intake and first lactation performance of Holstein cows. Data were collected from birth yr of 2004 to 2012 for 2,880 Holstein animals. Calves were received from 3 commercial dairy farms and enrolled in 37 different calf research trials at SROC from 3 to 195 d. Upon trial completion, calves were returned to their respective farms. Milk replacer options included varying protein level and amounts fed but in the majority of studies calves were fed a 20% CP: 20% fat MR at 0.57 kg/calf daily. Most calves (93%) were weaned at 6 wk. Milk replacer DM intake, starter intake, ADG, and BW at 8 wk were (mean ± SD): 21.7 ± 2.5, 44.4 ± 12.0 kg, 0.63 ± 0.12 kg/d, and 75.8 ± 8.4 kg, respectively. Average age at first calving and first lactation 305-d milk yield were: 715 ± 46.5 d and 10,959 ± 1,527 kg, respectively. Mixed model analysis was conducted using the REML model fitting protocol of JMP (SAS) to determine the effect of 8 wk milk replacer and 8 wk calf starter intake on first-lactation 305-d milk, milk fat, and true protein yield. Birth season, calving season, calving yr, and calving yr nested within herd were included in the models with calf trial as a random effect. Eight-wk intake of calf starter had a significant positive effect on first lactation 305-d yield of milk and milk components (P < 0.01; Table 1). However, these improvements were modest and variation was high suggesting additional factors not accounted for in this analysis impact first lactation performance. Milk replacer intake, which varied very little in this dataset, had no effect on first

lactation 305-d yield of milk and milk components.

Key Words: calves, milk replacer, calf starter, first lactation.

1236 Feeding management strategies on large and smaller freestall dairy herds in Minnesota. L. Kloeckner* and M. I. Endres, *University of Minnesota, St. Paul.*

The objectives of this study were to evaluate feeding management practices on freestall dairy farms in Minnesota and compare practices between two dairy farm sizes. Eighty-two farms were randomly selected from a list provided by the Minnesota Department of Agriculture that included all dairies in the state. Farms were visited once between May and November to collect on farm measurements and observations and to inquire about management practices. Farms were blocked by size: large farms ($\geq$ 400 cows; n = 45) and smaller farms (> 150 and < 400 cows; n = 37). Data were analyzed using the MEANS, TTEST and FREQ procedures of SAS. Mean farm size for the large and smaller farms was 886 and 278 cows, respectively. Large farms had more separate lactating rations (mean ± SE, 2.98 ± 0.20) and non-lactating rations (1.71 ± 0.07) than smaller farms (1.81 ± 0.15 and 1.35 ± 0.08, respectively). Large farms had more frequent feed pushups (8.91 ± 0.63) and milkings (2.95 ± 0.05) per day than smaller farms (4.94 ± 0.45 and 2.36 ± 0.08, respectively). Bovine somatotropin was used on 75.6% of large farms vs. 43.2% of smaller farms (P = 0.004). The use of a feeding management software (57.8% vs. 2.7%, P < 0.001) and the use of other technologies (84.4% vs. 62.2%, P = 0.03) was greater on large farms compared to smaller farms. Large farms were more likely to use an on farm master mix (37.8% vs. 16.2%, P = 0.047) and less likely to use uprights silos (20.0% vs. 43.2%, P = 0.03) and Ag bags (17.8% vs. 43.2%, P = 0.02) than smaller farms. There were no differences in the usage of bulk bins, commodity bays, bunker silos, and forage piles between each farm size. There were no differences in the type of plastic used to cover forages. Other management practices where no differences were observed included number of feedings per day, target percent refusals, processing method of corn silage, own or hired chopping, corn silage hybrids, TMR mixer type, and an estimate of feed shrink. Results of the study indicate that some feeding management practices are influenced by farm size.

Key Words: feeding, herd size, management practices

1237 Evaluation of the CowVac for controlling flies on Minnesota organic dairy farms. M. A. Kienitz[1] and B. J. Heins*[2], [1]*University of Minnesota, Lakeville,* [2]*University of Minnesota West Central Research and Outreach Center, Morris.*

The objective of this study was to evaluate the efficacy of the CowVac (Spalding Laboratories, Reno, NV) in on-farm organic dairy production systems to control horn flies, stable flies, and face flies. The CowVac utilizes a chute apparatus and powerful vacuums to suction flies off the cows as they walk through the system. The study utilized eight organic dairy farms during the summer of 2015 in Minnesota, and herds ranged from 30 to 350 cows. The farms were divided into pairs by location and during the first period of the summer (June to July) the CowVac was set up on one farm and during the second period of the summer (August to September) the CowVac was sent to its paired farm. Farms were visited once per week to collect flies (or collect and count flies) from the CowVac, as well as count and record flies on cows. Bulk tank milk, fat, and protein production and SCC were collected on farms during the entire study period. Data were analyzed using the GLM procedure of SAS. Independent variables for analyses were the fixed effects of farm, CowVac presence, housing scenario, and period. Horn fly numbers on cows were reduced (P < 0.05) by 44% on farm in the presence of a CowVac (11.4 vs. 20.5 flies/side) compared to the absence of a CowVac. Stable fly (5.4 vs. 7.1 fly/leg) and face fly (1.0 vs. 1.0 fly/cow) numbers were similar (P > 0.05) on farm whether the CowVac was present or absent on farms, respectively. Milk production was similar (P > 0.05) for farms with the CowVac (15.5 kg/d) compared to without (15.3 kg/d) the CowVac. The presence of a CowVac on farm reduced (P < 0.05) horn fly population growth rates (−0.008 vs. 0.002 flies/d) compared to the absence of a CowVac. Cows on farms with no housing (100% pasture) tended (P = 0.07) to have reduced horn fly numbers (11.7 vs. 28.3 flies/side) in the presence of a CowVac compared to the absence of a CowVac on farm. Cows on farms with housing had similar (P > 0.60) horn fly numbers (11.2 vs. 14.8 flies/side) in the presence of a CowVac compared to the absence of a CowVac on farm. In summary, these results indicate the CowVac was effective in reducing horn fly numbers on cows and reduced horn fly growth rates during the pasture season in organic dairy production systems.

Key Words: organic, CowVac, fly control

Table 1239.

Table 1: Mean and variance components of DM content and particle size distribution in TMR (n=318)

Variable (%)*	Mean	Variance				
		Farm	Pen	Day	Feed bunk site	Sampling + analytical
DM	45.2	20.59	6.44	7.50	0.05	2.69
>19.0 mm	10.0	0.43	0.12	0.07	0.00	0.11
19.0 -8.0 mm	36.6	0.11	0.02	0.01	0.00	0.01
8.0-1.18 mm	36.6	0.02	0.01	0.01	0.00	0.01
<1.18 mm	11.0	0.32	0.03	0.07	0.00	0.06

*Variance estimates for particle size distribution were obtained from the logarithmically transformed variable

1238 Prediction of daily concentration of milk and milk components from single-milking values.
M. Duplessis[*1], L. Fadul-Pacheco[2], R. Lacroix[1], D. M. Lefebvre[1], D. E. Santschi[1], and D. Pellerin[3], *[1]Valacta, Ste-Anne-de-Bellevue, QC, Canada, [2]Département des sciences animales, Université Laval, Québec, QC, Canada, [3]Universite Laval, Quebec, QC, Canada.*

Alternate a.m.-p.m. milk testing has been introduced in many countries and is often used instead of collecting milk for 2 consecutive milkings. Models taking into account milking interval have been developed to predict 24-h yield and concentration from milk yield and fat concentration single-milking values. However, there is still a gap between the prediction and the reality. It has been hypothesized that feeding factors could help better estimating 24-h prediction. The purpose of this study was to evaluate feed-related management factors affecting a.m. and p.m. milk yield and milk fat, protein, lactose, urea, somatic cell count (SCC), and β-hydroxybutyrate (BHBA) concentrations as a single predictor of 24-h concentrations. Separate milk samples from a.m. and p.m. milkings were taken for each cow on 98 tiestall and 2 freestall barns. Milk samples were analyzed using Fourier transform infrared spectroscopy. Milk production weighted averages were calculated to obtain daily concentrations. Milking intervals, number of concentrate meals offered, feeding systems (conventional, individual concentrate feeding [ICF] and total mixed ration [TMR]), interval between milking and last concentrate meal were recorded and used as independent variables in the multiple regression analysis. Milk yield and component concentrations from a.m. or p.m. samples to calculated daily concentrations ratios were computed and considered as dependant variables. For analysis purposes, individual ratios were averaged by herd. Multiple regressions were performed with Proc GLMSELECT of SAS using stepwise selection and $P = 0.05$ as the cut-off point. Highest R-squares were obtained while predicting milk yield (a.m.: $r^2 = 0.63$; p.m.: $r^2 = 0.51$), followed by fat concentration (a.m.: $r^2 = 0.30$; p.m.: $r^2 = 0.26$), SCC (a.m.: $r^2 = 0.29$; p.m.: $r^2 = 0.26$), BHBA (a.m.: $r^2 = 0.15$; p.m.: $r^2 = 0.16$), protein (a.m.: $r^2 = 0.14$; p.m.: $r^2 = 0.10$), urea (a.m.: $r^2 = 0.13$; p.m.: $r^2 = 0.08$), and lactose (a.m.: $r^2 = 0.03$; p.m.: $r^2 = 0.00$). Milking interval affected daily prediction of a.m. and p.m. milk yield and a.m. and p.m. fat, SCC, and BHBA contents. Interval between milking and last concentrate meal affected 24-h prediction in all a.m. models except for BHBA. Feeding system had an impact on 24-h prediction of a.m. and p.m. protein and urea concentrations. Regarding lactose, results confirm that a.m. or p.m. concentrations without adjustment could predict 24-h lactose concentration as this component is relatively constant. In summary, feed-related management factors slightly improved 24-h prediction as compared with models adjusting only for milking interval as suggested by the low R-Square increment.

Key Words: single milking, milk yield, component

1239 Sources of variation in dry matter content and particle size distribution in total mixed rations in dairy farms in Argentina.
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Total mixed rations (TMR) composition variation has been associated with lower milk yield and higher health problems at herd level. Our objectives were to describe TMR DM percentage and particle size distribution, and to partition that variance into different sources of variation. Ten dairy farms in Southern Cordoba province, Argentina, were visited for 3 consecutive days during the summer. Fresh TMR offered in the morning to each lactating pen was sampled within 5 min after delivery, to assess DM percentage and particle size distribution with a

Penn State Particle Separator. Duplicate samples were taken at the beginning and at the end of the feed bunk (feed bunk site) in each pen. Number of pens ranged from 1 to 4. To estimate variances in physical and DM composition of TMR and to partition that variance into measurements components, random effects models including farm, pen within-farm, day within-pen and farm, place, and residual error, were fitted to the data (n = 318) using mixed procedures of InfoStat. Particles were assumed to be logarithmically normally distributed. Results are shown in Table 1. Mean DM content of TMR was 45.2% and it ranged from 22.8 to 56.9%. Particle retention on the top sieve (>19.0 mm) was higher than recommended (2 to 8%) for high producing cows. Because cows are expected to sort against large particles and that would change NDF and starch intake, it is important to follow the recommended proportion on the top sieve. Although mean particle percentage on the 19.0 to 8.0-mm sieve was according to the recommendation (30 to 50%), there is a wide range of values. More than 72% of the variation in particle size distribution and DM content was explained by farm and pen within-farm. Within-pen, daily variation accounted for half of the variation for particle size distribution (46 to 61%), which is demonstrating that procedures involved in ration preparation (including adjusting forage inclusion for moisture content) were not always the same. The rest of this variation was explained by sampling and analytical variance. For DM content, 73% of the within-pen variation was explained by day-to-day variation. Our data shows that day-to-day ration variation is an important source of variation within pen in a farm, particularly when DM content is determined, although attention should be paid to sampling and analytical effects to make appropriate decisions.

Key Words: variation, TMR, particle size distribution

1240 Growth measurements of crossbred dairy steers compared to Holstein dairy steers raised in an organic production system. H. N. Phillips* and B. J. Heins, *University of Minnesota West Central Research and Outreach Center, Morris.*

Bull calves (n = 30) were used to compare growth measurements of crossbred and Holstein dairy steers raised in an organic production system. Calves were born at the University of Minnesota West Central Research and Outreach Center organic dairy from March to May 2015 and assigned to 1 of 3 replicated breed groups at birth. Breed groups were: crossbreds comprised of Montbéliarde, Holstein, and Viking Red (MVH; n = 10), crossbreds comprised of Jersey, Normande, and Viking Red (NJV; n = 10), and purebred Holstein (HO; n = 10). Calves were group-housed by breed group (n = 5) and group-fed 6 L/d of 13% total solids organic milk once daily and were weaned when the group consumed an average of 0.91 kg of organic starter per calf per day for 3 consecutive days. Body measurements were recorded at birth, weekly during the pre-weaning period, at weaning, and monthly thereafter. After weaning, steer groups were fed a diet of organic corn, corn silage, alfalfa haylage and minerals. Diets were recorded daily with herd management software. Analysis was performed using PROC MIXED of SAS, independent variables for statistical analysis were the fixed effects of breed group, and replicate was a random effect. Analysis of variables was on a pen basis. Birth weight for calves was: HO: 40.2 kg, MVH: 46.4 kg, and NJV: 39.3 kg ($P > 0.05$). Weaning age was: HO: 69.1 d, MVH: 68.4 d, and NJV: 78.8 d; weaning weight was: HO: 91.7 kg, MVH: 106.0 kg, and NJV: 100.6 kg; and gain per day was: HO: 0.74 kg/d, MVH: 0.86 kg/d, NJV: 0.77 kg/d. Breed groups were not different ($P > 0.05$) for weaning age and weaning weight. However, the MVH calves tended ($P < 0.10$) to have greater gain per day than the HO calves. For the first 9 mo of age, gain per day for steers was: HO: 1.07 kg/d, MVH: 1.01 kg/d, and NJV: 0.98 kg/d ($P > 0.05$). Hip height (cm) (HO: 95.9; MVH: 97.8, and NJV: 94.9) and heart girth (cm) (HO: 107.7, MVH: 112.4, and NJV: 112.1) at weaning was not different ($P > 0.05$) for breed groups. In summary, no significant differences in growth measurements were found between breed groups for dairy steers in this organic production system.

Key Words: organic; dairy steers; growth; breeds

1241 Accuracy and precision of diets for high-producing dairy cows and their impacts on production and milk composition. J. H. Carneiro[1,2], J. F. Santos[2], P. Schmidt[1], T. J. DeVries[3], and R. D. Almeida*[1], *[1]Universidade Federal do Paraná, Curitiba, Brazil, [2]Castrolanda Cooperativa Agroindustrial, Castro, Brazil, [3]Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada.*

The goal of this study was evaluate associated feeding management and nutritional accuracy with milk production and composition on commercial herds. Twenty high-producing dairy farms from Campos Gerais county, Paraná State, Southern Brazil, were visited for 3 consecutive days in the 2015 fall season. Feeding management and TMR preparation related variables, and the physical and chemical characteristics of the offered diets and orts were collected. Production performance and milk composition from the high-production group of cows were obtained from regular milk testing, performed on average 1 ± 5d before or after the data collection period. Pearson correlations were estimated among the management and diet variables with production, milk composition, and feed sorting estimates. Using the Penn State Particle Separator, the offered diets had on average 14.9, 41.8, 32.8, and 10.5% (DM) of long, medium, short, and fine particles, respectively. Long particles showed a daily refusal rate of 9.0%, whereas short and medium particles were preferentially consumed at 1.1 and 1.7%, respectively. A high proportion of long particles in the forage (78.2% of haylage and hay) was

associated with reduction in milk fat % (%MF) ($r = -0.50$; $P < 0.05$), and an increased proportion of cows with fat:protein ratio lower than 1 (FPR < 1) ($r = 0.50$; $P < 0.05$). Errors associated with loading an excess of concentrate ingredients in the TMR wagon were negatively associated with %MF ($r = -0.52$; $P = 0.05$) and milk production ($r = -0.47$; $P < 0.05$). By comparing the formulated diet with the one delivered to the cows, we noted, on a DM basis, a decrease in CP (−3.1%), fat (−7.0%), and ash contents (−10.5%), and an increase in NDF (+10.3%). The accuracy observed between formulated and delivered diets was not associated with the performance of the cows. However, daily variation of the DM content of the diet was associated with a greater proportion of cows with FPR < 1, and reduced FPR ($r = 0.40$; $P = 0.09$ and $r = -0.43$; $P = 0.07$, respectively). Low homogeneity (across 3 d) of the % of long particles in the diet was associated with greater selection against these particles ($r = -0.64$; $P < 0.05$), which showed a curvilinear association with %MF. These results demonstrated that the addition of more concentrate ingredients than expected, as well as the inconsistent intake of different particle sizes throughout the day, had a negative impact on milk production and composition of the studied herds.

Key Words: feed management, feed sorting, total mixed ration

1242 Health treatment costs of pure Holsteins in 8 high-performance Minnesota dairies. M. R. Donnelly*[1], A. R. Hazel[1], B. J. Heins[2], and L. B. Hansen[1], *[1]University of Minnesota, St. Paul, [2]University of Minnesota West Central Research and Outreach Center, Morris.*

Health treatment costs of pure Holstein cows (n = 4,997) were evaluated in 8 high-performance dairy herds in Minnesota. Cows calved from March 2008 to September 2015, and 17 types of health treatments were defined uniformly across herds. The cost for treatment of retained placenta, metritis, cystic ovary, miscellaneous reproduction, ketosis, displaced abomasum, milk fever, lameness, mastitis, digestive, respiratory, injury, California Mastitis Test/milk culture, and other treatments were summed within 6 stages of lactation for parities 1 to 5. Excluded from analysis were hoof trimming, palpation, and reproductive aid. The 6 stages of lactation were defined based on days in milk. The first 4 stages were 60 d each, stage 5 started on Day 241 and was variable in length and continued until the dry date, and stage 6 included the dry period only. Treatment costs were the mean cost of treatment protocols defined by the veterinarians used by the herds in addition to a fixed labor cost of $18/h reported by producers. Labor costs were applied based on time per treatment from a producer survey. Cows were grouped into 2 year-blocks of calving and year-blocks were defined as 2008 to 2010 and 2011 to 2015. Statistical analyses were conducted separately for each parity, and independent variables were the fixed effects of herd, year-block of calving, interaction of herd and year-block, stage of lactation, and interaction of stage of lactation and year-block. Year-blocks were combined for parities 3 to 5 because cows left the herds as they aged. For this reason, only the fixed effects of herd and stage of lactation were considered for parities 3 to 5. For all 5 parities, herd and stage of lactation were highly significant ($P < 0.01$). For parities 1 and 2, year-block and its interactions were highly significant ($P < 0.01$). As expected, treatment costs were largest during the first 60 d in milk, which is usually when cows experience high treatment costs for transition disorders. Least squares means of treatment costs (Table 1) for parities 1 and 2 decreased as year-block increased for most stages of lactation. The most dramatic decrease in treatment cost by year-block occurred within the first 60 d in milk, perhaps indicating an improvement in transition cow management among the herds during the years of the study.

Key Words: treatment costs, management, health

1243 Relationships between early life growth and first lactation performance of Holstein dairy cows. B. J. Heins*[1], H. Chester-Jones[2], D. Ziegler[2], M. B. De Ondarza[3], S. E. Schuling[4], B. Ziegler[4], D. Schimek[4], N. Broadwater[5], and C. J. Sniffen[6], *[1]University of Minnesota West Central Research and Outreach Center, Morris, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]Paradox Nutrition, West Chazy, NY, [4]Hubbard Feeds Inc., Mankato, MN, [5]University of Minnesota Extension, Rochester, [6]Fencrest, LLC, Holderness, NH.*

The objective was to determine relationships between early life ADG and BW and first lactation performance of Holstein

Table 1243.

Table 1. Effect of 6 wk BW (kg) and ADG (kg/d on first-lactation 305-d milk, fat, and protein yield (kg; n=2,880).

Item	Variable	R^2	Estimate	SE	P-value
305-d milk	6 wk BW	0.11	20.11	4.41	< 0.0001
	6 wk ADG	0.10	543.71	248.80	0.0290
305-d fat	6 wk BW	0.28	0.84	0.17	< 0.0001
	6 wk ADG	0.28	21.04	9.46	0.0262
305-d protein	6 wk BW	0.17	0.70	0.12	< 0.0001
	6 wk ADG	0.16	22.98	6.70	0.0006

cows. Data were collected from birth yr of 2004 to 2012 for 2,880 Holstein animals. Calves were received from 3 commercial dairy farms and enrolled in 37 different calf research trials at SROC from 3 to 195 d. Upon trial completion, calves were returned to their respective farms. Milk replacer options included varying protein level and amounts fed but in the majority of studies calves were fed a 20% CP: 20% fat MR at 0.57 kg/calf daily. Most calves (93%) were weaned at 6 wk. Milk replacer DM intake, starter intake, ADG, and BW at 6 wk were: 21.5 ± 2.2 kg, 17.3 ± 7.3 kg, 0.53 ± 0.13 kg/d, and 62.4 ± 6.8 kg, respectively. Average age at first calving and first lactation 305-d milk yield were: 715 ± 46.5 d and 10959 ± 1527 kg, respectively. Separate mixed model analyses were conducted using the REML model fitting protocol of JMP (SAS) to determine the effect of 6 wk BW or ADG on first-lactation 305-d milk, fat, and true protein yield. Birth season and calving season, yr, and yr nested within herd were included in the models with calf trial as a random effect. Early life BW and ADG positively affected first-lactation 305-d yield of milk and components ($P < 0.03$; Table 1). Six-week ADG class (< 0.23, 0.23 to 0.33, 0.34 to 0.44, 0.45 to 0.56, 0.57 to 0.67, 0.68 to 0.80, and > 0.80 kg/d) also affected 305-d yield of milk and components ($P < 0.02$). Greater BW and ADG at 6 wk resulted in increased first lactation milk and milk component yields. However, these improvements were modest and variation was high suggesting additional factors not accounted for in this analysis impact first lactation performance.

Key Words: calves, early life, growth, first lactation

1244 Relationships between birth season versus early life starter intake and growth and first lactation performance of Holstein dairy cows.

B. J. Heins*[1], D. Ziegler[2], D. Schimek[3], S. E. Schuling[3], B. Ziegler[3], H. Chester-Jones[2], M. B. De Ondarza[4], C. J. Sniffen[5], and N. Broadwater[6], *[1]University of Minnesota West Central Research and Outreach Center, Morris, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]Hubbard Feeds Inc., Mankato, MN, [4]Paradox Nutrition, West Chazy, NY, [5]Fencrest, LLC, Holderness, NH, [6]University of Minnesota Extension, Rochester.*

The objective was to determine the effect of birth season on early life starter intake, growth, and on first lactation performance of Holstein cows. Data was collected from birth yr of 2004 to 2012 for 2,880 Holstein cattle. Calves were received from 3 commercial dairy farms and enrolled in 37 different calf research trials at SROC from 3 to 195 d. Upon trial completion, calves were returned to their respective farms. Milk replacer options included varying protein level and amounts fed but in the majority of studies calves were fed a 20% CP: 20% fat MR at 0.57 kg/calf daily. Most calves (93%) were weaned at 6 wk. Milk replacer DM intake, starter DM intake, ADG, and BW at 8 wk were: 21.7 ± 2.5, 44.4 ± 12.0 kg, 0.63 ± 0.12 kg/d, and 75.8 ± 8.4 kg, respectively. Average age at first calving and first lactation 305-d milk yield were: 715 ± 46.5 d and 10,959 ± 1,527 kg, respectively. Separate mixed model analyses were conducted using the REML model fitting protocol of JMP (SAS) to determine the effect of birth season on 8 wk starter intake, BW, and ADG, and on first-lactation 305-d milk, milk fat, and true protein yield. Birth season, calving season, calving yr, and calving yr nested within herd were included in the models with calf trial as a random effect. Eight wk ADG and 8 wk ADG x birth season were also included when evaluating first-lactation performance. Calves born in fall and winter had greater ($P < 0.05$) starter intake (48.3 vs. 42.8 kg), BW (77.5 vs. 75.1 kg), and ADG (0.66 vs. 0.63 kg/d) at 8 wk. However, calves born in summer produced more 305-d milk during their first lactation than those born in the fall and winter ($P < 0.05$). There was no interaction between birth season and 8 wk ADG on first lactation performance.

Key Words: birth season, early life growth, first lactation

1245 ADSA®-EAAP Speaker Exchange Presentation: Comparing milk yield between cows with different dry period lengths over multiple lactations.

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To assess economic and environmental consequences of shortening the dry period (DP), we need to be able to compare milk yields of cows with different DP lengths, and to estimate effects on yield over multiple lactations. Milk yield is generally

Table 1244.

Table 1. Effect of birth season on first-lactation 305-d milk, fat, and protein yield.

Item	Birth season P-value	Spring	Summer	Fall	Winter
305-d milk (kg)	0.0206	11,033[ab]	11,145[a]	10,875[b]	10,863[b]
305-d fat (kg)	0.0508	401[ab]	409[a]	401[ab]	397[b]
305-d protein (kg)	0.0343	336[ab]	340[a]	333[ab]	332[b]

[ab]Values in the same row with different superscripts are different ($P < 0.05$)

compared using 305-d yields. This measure, however, does not account for additional yield before calving and potentially shorter calving intervals in case the DP is shortened. First, we aimed to develop a measure to compare milk yields between cows with different DP lengths. We defined an 'effective lactation yield' as kg of fat-and-protein-corrected milk (FPCM) per cow per day from 60 d before calving to 60 d before next calving. We applied this measure to 817 cows with a standard (49d to 90d), short (20d to 40d), or no DP before second calving, using first parity 305-d yield as a covariate. Compared with cows with a standard DP, 305-d yields were reduced by 2.3 kg FPCM d^{-1} for cows with a short DP ($P < 0.05$) and by 7.0 kg FPCM d^{-1} for cows with no DP ($P < 0.05$). Compared with cows with a standard DP, effective lactation yields were similar for cows with a short DP and reduced by 3.1 kg FPCM d^{-1} for cows with no DP ($P < 0.05$). Second, we aimed to assess the impact of shortening the DP over multiple lactations on effective lactation yield. Lactation data (2007 to 2015) of cows of 16 Dutch dairy farms that apply no or short DP were selected if effective lactation yield, current DP, and previous DP were known. Dry period categories were: no (0 to 2 wk), short (3 to 5 wk), standard (6 to 8 wk), and long (9 to 12 wk). A long, short, or no current DP reduced effective lactation yield, compared with a standard DP. Previous DP, however, did not affect effective lactation yield over multiple lactations. In conclusion, the effective yield enables comparison of yield when DP length and calving interval vary. Moreover, cows can be managed with short or no DP over multiple lactations without increasing yield losses.

Key Words: dairy cow, dry period length, long-term effects

1246 Economic impact of introducing automatic milking system on Canadian dairy farms.

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Adoption of automatic milking system (AMS) increased exponentially over the last years around the world. In 2014, 5% of Canadian dairy farms owned an AMS. The objective of this study was to evaluate the economic impact following AMS introduction in Canadian dairy herds. Data were first collected during a phone interview on 213 Canadian dairy farms having shifted to AMS (British-Colombia, $n = 8$; Alberta, $n = 42$; Saskatchewan, $n = 6$; Manitoba, $n = 12$; Ontario, $n = 73$; Québec, $n = 65$; and Atlantic provinces [New-Brunswick, Nova-Scotia, Prince-Edward-Island], $n = 7$). Second, 151 farms out of 213 have answered a more detailed online survey. After AMS adoption, herd size, milk production, and number of robots per herd averaged 100.2 ± 64.3 cows, 10,764 ± 1,663 kg, and 1.94 ± 1.36 robots, respectively. Milk production, reproduction, and culling data were provided by Valacta and CanWest DHI. Partial budgets were computed using an Excel spreadsheet; surveyed data were completed with literature data. Results of the partial budgets were divided by the respective number of cows after the AMS introduction to allow comparison regardless of herd size. Average parameter values were calculated for herds below percentile 25 and above percentile 75 for the net margin per cow and were compared with either a *t* test or a Wilcoxon signed-rank test. On average, after AMS introduction, herd size, milk production and culling rate were increased by 7.3 cows, 741.6 kg/cow/yr and 1.5%, respectively, and calving interval and labor requirement were decreased by 6.8 d and 15.1 h/cow/yr, respectively. Net margin per cow following AMS adoption was negative and averaged CAN $-1,204.41 ± 1,080.06. Introducing AMS resulted in increased costs of CAN $2,277.45 ± 1,362.21/cow mainly due to robot, barn construction or modifications and cow purchase amortizations (41.9% of total increased costs) and interest (27.8%). Increase in income averaging CAN $1,073.04 ± 1,739.10/cow was explained by milk production increase (55.1% of total increased income) and labor requirement decrease (29.8%). Highest net margin herds (P75) were characterized by having higher increased income (P75, CAN $2,331.76 and P25, CAN $-315.81; $P < 0.0001$) as compared with P25 herds. No difference was noted for increased costs ($P = 0.82$) between P25 and P75 herds. Difference in profitability between P75 and P25 herds was mainly due to milk production increase (CAN $524.47/cow; $P = 0.0004$). In summary, only 6% of dairy producers shifting to AMS have an expected payback less than 12 yr, which is the theoretical milking robot useful life.

Key Words: milking robot, partial budget, dairy

1247 Potential economic returns associated with weekly body condition scoring.

C. M. Truman* and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this study was to estimate the potential economic returns from weekly recordings of body condition score (BCS) using a farm-level decision support tool. The feasibility of weekly BCS increases with the availability of automated BCS systems. To fully benefit from frequent BCS, the information must be used to make BCS-related cow, group, or herd management changes. These decisions may alter BCS distributions which can positively impact disease incidence, reproduction parameters, and feed efficiency. User inputs for the decision support tool included farm-specific herd demographics, financial data, disease incidences, and herd BCS distribution at calving. Differences between the current and goal BCS distributions were used to evaluate the economic returns from a potential improvement. The reported current disease incidences of metritis, milk fever, and ketosis were compared with the newly predicted disease incidences estimated from published odds ratios for effects of BCS on the

disease occurrence. Reproductive improvements were evaluated from a change in days open estimated from odd ratios describing BCS effects on conception rate. The lactation BCS curve was estimated using average herd BCS at calving and a sixth order polynomial regression equation. The average herd BCS before and after implementing regular scoring were used to compare differences in net energy costs across each lactation to compare the effects of BCS on feed efficiency. In an example scenario, input assumptions were sourced from 2015 DairyMetrics (DRMS, Raleigh, NC), USDA National Agriculture Statistics Service, and peer-reviewed literature. The inputs for current and herd BCS distributions are shown in Table 1. The increased revenue from improvements in disease incidence, reproduction, and feed efficiency estimated from this investment were $1,961.95/yr for a herd size of 183 cows. When the herd size was increased to 500 cows, with all other inputs held constant, financial improvements resulted in $3,692.12. Results from improvements in BCS are highly dependent on herd size, prior herd BCS, disease occurrence, and reproduction. This model can be used as a decision support tool to estimate farm-specific economic returns from improving BCS, potentially resulting from an investment in an automated BCS technology.

Key Words: body condition score, economics

1248 The influence of genetic potential on lactation curve and survival response of commercial dairy cattle to early lactation non-steroidal antiinflammatory (NSAID) drug administration.

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Previous research has indicated that the attenuation of inflammation in early lactation through the use of NSAID has a beneficial effect on whole-lactation milk production. Multiparous dairy cattle were blocked by breed, dystocia, and twin births, and assigned to 1 of 3 treatments at 12 to 36 h post-parturition (n = 153). Treatments were 1 placebo bolus on the first day of treatment and 3 consecutive daily drenches of sodium salicylate (125 g/cow/d; SAL); 1 bolus of meloxicam (675 mg/cow) and 3 drenches of an equal volume of water (MEL); and 1 placebo bolus and 3 daily drenches of water (CON). Daily milk production was averaged by week of lactation for statistical analysis. As reported previously, there was a significant increase in daily milk production and whole-lactation milk yield following NSAID administration, and a tendency for fewer cows receiving MEL to leave the herd up to 300 d in milk compared to CON. For all cows with at least 8 weekly milk observations reported (n = 130), lactation curves were fit to the MilkBot® model (DairySight LLC, Argyle, NY) to estimate decay, persistence, ramp, and scale. In brief, "decay" describes the rate of decline in daily milk production following peak, and it is used to mathematically derive persistence; "ramp" describes the rate of incline in daily milk production up to peak; and "scale" is a factor that is used to adjust the magnitude of the lactation curve without altering its shape. As a main effect, NSAID did not influence any of these parameters ($P \geq 0.15$); however, there was a significant interaction between the predicted transmitting ability for milk production (milk PTA) and NSAID treatment for decay of the lactation curve (P = 0.02; n = 121). A significant milk PTA and NSAID interaction was also detected for survival ($P < 0.01$). While milk PTA itself had a significant effect on risk of leaving the herd, such that lower milk PTA was associated with increased risk of leaving (P = 0.02), there was no evidence of this relationship in cows who had received either NSAID treatment. In conclusion, NSAID administration protected cattle with lower genetic potential from removal from the herd, possibly through an interaction with persistency of milk production in later lactation.

Key Words: lactation, persistence, inflammation, risk

Table 1247.

Table 1. Body condition score distributions in the before and after example scenario

BCS Score	Before	After
1.00 to 1.75	2.10%	1.20%
2.00 to 2.25	7.40%	4.80%
2.50 to 2.75	29.40%	38.00%
3.00 to 3.25	44.20%	48.00%
3.50 to 3.75	12.40%	6.80%
4.00 to 4.25	3.80%	1.20%
4.50 to 5.00	0.70%	0.00%

1249 Management practices and dietary physically effective fiber are related to bulk tank milk de novo fatty acid concentration on Holstein dairy farms. M. E. Woolpert*[1,2], H. M. Dann[1], K. W. Cotanch[1], C. Melilli[3], L. E. Chase[3], R. J. Grant[1], and D. M. Barbano[4], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]University of Vermont, Burlington, [3]Cornell University, Ithaca, NY, [4]Cornell University, Department of Food Science, Northeast Dairy Foods Research Center, Ithaca, NY.*

This study investigated the relationship of management and diet with de novo fatty acid (FA) concentration in bulk tank milk from commercial Holstein dairy farms. De novo FA are synthesized primarily from rumen fermentation products acetate and butyrate. It was hypothesized that farms with higher de novo FA concentrations would prioritize management that optimizes rumen conditions and cow comfort. Farms (n = 39) located in Vermont and northern New York were selected based on high (HDN; 24.5 ± 0.8 g/100 g FA; mean ± SD) or low (LDN; 22.9 ± 0.9 g/100 g FA) bulk tank de novo FA from the previous 6 mo. Milk FA were analyzed using mid infrared spectroscopy chemometric prediction models. Management was assessed during one visit per farm (February to April 2015). Total mixed ration samples were collected and analyzed for chemical composition using near infrared spectroscopy and for particle size distribution using a Penn State Particle Separator modified to include a 4-mm screen. Data were analyzed using the GLIMMIX procedure of SAS with de novo group as the fixed effect and farm as the random effect. In addition, data were categorized as above or below a defined threshold and odds ratios (OR) were calculated using a binary distribution with GLIMMIX. Milk fat (4.0 vs. 3.8%, SE < 0.1, P < 0.01), true protein (3.2 vs. 3.1%, SE < 0.1, P < 0.01), de novo FA concentration (26.0 vs. 23.8 g/100 g FA, SE = 0.2, P < 0.01) and de novo FA yield (315.6 vs. 276.2 g/d, SE = 9.5, P < 0.01) were greater for HDN than LDN farms. Milk (31.9 ± 4.1 kg/d; mean ± SD), fat (1.2 ± 0.2 kg/d), and true protein (1.0 ± 0.1 kg/d) yields and days in milk (173 ± 30 d) were not different (P > 0.25). Bunkspace (50.0 vs. 39.8 cm/cow; SE = 3.7, P = 0.06) tended to be greater for HDN than LDN freestalls. High de novo freestalls tended to be more likely to feed twice per day (OR = 5.0, 95% CL = 0.9 to 28.0, P = 0.07), have a stocking density ≤ 1.1 cows/stall (OR = 4.7, 95% CL = 0.8 to 27.2), P = 0.08) and ≥ 46 cm bunkspace per cow (OR = 10.1, 95% CL = 0.9 to 112.4, P = 0.06). Dry matter (42.6 ± 4.8%), crude protein (15.8 ± 1.5%), neutral detergent fiber (36.4 ± 4.0%), and starch (23.4 ± 4.5%) were not different (P > 0.20) between groups. Ether extract was lower (3.7 vs. 4.0%, SE = 0.1, P < 0.01) and physically effective neutral detergent fiber was higher (26.8 vs. 21.4%, SE = 1.1, P < 0.01) for HDN diets. Overcrowded freestalls, reduced feeding frequency, greater dietary ether extract and lower physically effective fiber were associated with lower milk fat, protein, and de novo FA content on commercial Holstein dairy farms.

Key Words: feed management, milk fat composition, stocking density

1250 Estimating the benefit:cost ratio of monensin supplementation. K. A. Dolecheck* and J. M. Bewley, *University of Kentucky, Lexington.*

The economic benefits of monensin supplementation have not been well documented. The objective of this study was to estimate the benefit:cost ratio of monensin supplementation. A deterministic, partial-budget model was used to estimate the effect of monensin supplementation in the lactating and dry cow rations of a dairy herd. Feed costs for lactating, far-off dry, and close-up dry rations were set at $227 per ton dry matter, $2.50 per cow per day, and $3.50 per cow per day, respectively. The non-supplemented herd level incidence rate of clinical mastitis, displaced abomasum, and clinical ketosis were set at 19.7%, 3.6%, and 6.3%, respectively. Milk price was determined using 5-yr (2011 to 2015) means of Federal Milk Marking Order product prices for butterfat ($4.50/kg), protein ($6.76/kg), and other solids ($0.73/kg). Monensin supplementation costs per cow per day were set at $0.050 and $0.035 in lactating and dry rations, respectively. The average response to monensin supplementation across lactation was established by a 2008 meta-analysis (2% decrease in dry matter intake, 2% increase in milk yield, 3% decrease in milk fat percentage, 1% decrease in milk protein percentage, decreased risk of ketosis [risk ratio = 0.75], decreased risk of displaced abomasum [risk ratio = 0.75], and decreased risk of mastitis [risk ratio = 0.91]). The model was run under 3 scenarios to estimate the sensitivity of monensin supplementation to pre-supplemented herd milk yield, milk fat percentage, and milk protein percentage. In scenario 1, milk yield was 31.8 kg/cow/d with 4.1% milk fat and 3.2% milk protein. In scenario 2, milk yield was 36.3 kg/cow/d with 3.8% milk fat and 3.1% milk protein. In scenario 3, milk yield was 40.8 kg/cow/d with 3.5% milk fat and 3.0% milk protein. All scenarios increased income over feed cost per cow per day ($0.29, $0.35, and $0.42, respectively) and resulted in a positive benefit:cost ratio (5.6:1, 6.8:1, and 8.0:1, respectively). The biggest factor influencing returns from monensin supplementation in all scenarios was increased income from milk sales ($5.63, $7.11, and $8.69 per cow per month, respectively). Other factors contributing to the positive benefit:cost ratio of monensin supplementation were reduced total feed costs (-$1.53,-$1.70, and-$1.85 per cow per month, respectively) and reduced losses from disease (-$0.95,-$0.99, and-$1.02 per cow per month, respectively). Future stochastic models should consider how variation in other factors affect the monensin supplementation benefit:cost ratio.

Key Words: monensin, benefit:cost, economic model

1251 TMR versus grazing supplemented with TMR out or into the grazing plot: Productive response. D. A. Mattiauda*[1], J. P. Marchelli[2], and P. Chilibroste[1], [1]*Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay,* [2]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay.*

An experiment was performed to study the effect of three contrasting feeding strategies involving TMR and grazing, during the first 60 d in milk of Holstein dairy cows. Thirty six multiparous dairy cows were blocked according to parity, expected calving date, body condition score (BCS; 2.9 ± 0.37) and BW (641 ± 49.2 kg) before calving, and were randomly allocated to follow one of three feeding treatments: TMR = total mix ratio (corn silage/concentrate mix 40/60; respectively), GR-one = one grazing session (AM: 0800 to 1400 h) supplemented with 50% of TMR out of the grazing plot and GR-two = two grazing sessions (AM: 0800 to 1400 h; PM: 1800 to 0400 h) supplemented with 50% of the TMR into the grazing plot. The three treatments were based on the same offer of energy (50 Mcal ENL/cow/d), differing in the source of feed (TMR vs. grazing plus TMR) and the synchrony or not between the access to pasture and to TMR (GR-one vs. GR-two). The cows were milked twice a day (04:30 and 15:00 h). Milk production was registered daily, milk composition weekly (samples from two consecutive milking) and BCS every 2 wk (scale 1 to 5). A fresh daily strip of a fescue based pasture (3,270 ± 758 kgDM/ha) was open to each grazing treatment with an herbage allowance (above 4 cm) enough to reach 25 Mcal ENL per cow/d. A mix model was used (Glimmix procedure, SAS 9.2, 2010) to analyze the results with treatment, week and their interaction as fix effects and block as a random effect. A first order autoregressive heterogeneous (AR1) covariance structure was selected. TMR cows produced more milk, energy, protein and lactose (Table 1) than grazing cows. Daily fat production was not different between treatments, since TMR cows produced milk with less ($P < 0.05$) or tendency for less ($P < 0.1$) fat content than GR-two and GR-one treatments, respectively. Grazing treatments did not differ except on the tendency ($P < 0.1$) for a higher milk fat content in GR-two than GR-one cows (Table 1). A reverse trend ($P < 0.1$) was observed for BCS (2.9 vs. 2.7 for GR-one and GR-two, respectively). The potential of GR-two cows to select a better mix of TMR and herbage than GR-one cows was not expressed in this trial. The long distance to the grazing plots (1.7 km) might have masked the potential benefits of GR-two feeding strategy.

Key Words: grazing, TMR, early lactation dairy cows, synchronizing

1252 Shearing during milking increases milk yield in dairy ewes. A. Elhadi[1], G. Caja*[2], A. A. K. Salama[1,3], X. Such[1], and E. Albanell[1], [1]*Universitat Autonoma de Barcelona, Bellaterra, Spain,* [2]*Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain,* [3]*Animal Production Research Institut, Giza, Egypt.*

The effect of shearing during lactation was investigated in 48 dairy ewes of 2 breeds (Manchega, MN; Lacaune, LC); 32 were multiparous (MN, n = 16, 69.5 ± 1.7 kg BW; LC, n = 16, 69.1 ± 1.9 kg BW) and 16 were primiparous (MN, n = 8, 59.4 ± 2.0 kg BW; LC, n = 8, 57.4 ± 2.4 kg BW). Ewes were permanently sheltered indoors and allocated in 4 groups by breed to which treatments were randomly applied in duplicate. Treatments were: US (unshorn) and SH (shorn) during mid lactation at mild winter conditions. Diets consisted of alfalfa hay ad-libitum and concentrate rationed individually at milking according to breed and requirements (MN, 0.45 kg/d; LC, 0.65 kg/d). Ewes were in straw-wood chips bedded pens and the ambient temperatures were mild before (12.6 ± 0.9°C) and after (13.0 ± 0.3°C) shearing. Fleece weight was greater in shorn MN than LC (1.04 ± 0.10 vs. 0.75 ± 0.09 kg/ewe). As a result of shearing, rectal temperature decreased in the MN-SH ewes, when compared to the MN-US (38.51 ± 0.11 vs. 38.88 ± 0.12°C, respectively), but did no vary in the LC ewes (38.57 ± 0.08°C). No differences were detected in the fill value of

Table 1251.

Table 1. Effect of feeding strategies on milk production and composition

Variables	TMR	GR-one	GR-two	SED	T	W	T*W
Milk yield (L/d)	35.9^{a}	30.8^{b}	29.7^{b}	0.816	P<0.01	P<0.01	P<0.01
Fat (%)	3.25^{b}	3.67^{ab}	3.72^{a}	0.175	P<0.05	P<0.05	NS
Fat yield (kg/d)	1.24	1.13	1.13	0.078	NS	NS	NS
Protein (%)	3.24	3.40	3.35	0.079	NS	P<0.001	NS
Protein yield (kg/d)	1.27^{a}	1.06^{b}	1.02^{b}	0.055	P<0.01	NS	NS
Lactose (%)	4.80	4.75	4.78	0.041	NS	P<0.01	P<0.01
Lactose yield (kg/d)	1.87^{a}	1.52^{b}	1.45^{b}	0.080	P<0.01	NS	NS
Energy (Mcal/d)	25.7^{a}	21.8^{b}	22.0^{b}	1.20	P<0.01	NS	NS

Mean within a row with different superscript differ (Tukey; $p < 0,05$)
TMR= No grazing; GR-one= one grazing session; GR-two= two grazing sessions; SED= SE of the difference; T= treatment; W= week; T*W= interaction T*W.
Energy= energy in milk: (0.0929*Fat (kg/d) + 0.0547*Protein (kg/d) + 0.0395*Lactose (kg/d)) * 100.

the alfalfa hay, expressed as French sheep fill units (SFU), between sheep breeds (0.97 ± 0.03 SFU/kg DM). Lactational responses to shearing during milking varied according to breed, the results in LC being more marked than in MN ewes. Feed intake increased 5% in the LC-SH, when compared to LC-US, but did not vary in the MN ewes. Moreover, the LC-SH ewes yielded 10% more milk than LC-US ewes, but no differences were detected in the MN ewes. There were no differences in milk composition between US and SH ewes in both breeds. The milk protein and lactose yields were higher for LC-SH than LC-US ewes (20% and 17%, respectively) agreeing with the milk yield increase. No effects of shearing were detected on metabolic (glucose, NEFA) and hormonal (cortisol, insulin) plasma values, as well as on BW and BCS changes. In conclusion, shearing lactating ewes during winter, under moderate cold conditions, is a suitable management option for improving feed intake and milk production of high-yielding dairy ewes, without deleterious effects neither on physiological indicators nor milk composition regardless their production level.

Key Words: dairy sheep, shearing, lactation, milk yield, milk composition

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1253 Evaluation of different synchronization and early pregnancy diagnosis methods in postpartum Holstein cows. A. H. Shahzad*[1], A. Sattar[2], I. Ahmad[3], A. Y. Qamar[3], and N. Ahmad[3], *[1]University of Veterinary and Animal Sciences, Lahore, LAHORE, Pakistan, [2]Department of Theriogenology, University of Veterinary and Animal Sciences, Lahore, Pakistan, [3]University of Veterinary and Animal Sciences, LAHORE, Pakistan.*

Objectives were to appraise the pregnancy rate (PR) after G7G-Ovsynch and Ovsynch protocol as well as accuracy of Pregnancy Associated Glycoproteins (PAGs) in milk, plasma, and plasma P4 in comparison with ultrasonography as gold standard pregnancy diagnosis (PD) method. In experiment 1, Holstein cows (n = 37) were bred by G7G-Ovsynch protocol (n = 19) or MG7G-Ovsynch (PG-8h-PG in Ovsynch). Pregnancy was evaluated by ultrasonography (US) at Days 31, 59, and 87 after breeding. Blood plasma and Milk samples were collected on Day 3 after insemination and at weekly intervals either 1) through Day 59 PTAI in open cows on d31 or 2) through Day 87 if the cow was found pregnant. The PAGs were measured by using ELISA and P4 by RIA. These PAGs classified samples either open or pregnant. In experiment 2, Lactating cows (n = 212) were bred by TAI following G7G-Ovsynch protocol (n = 110) or standard Ovsynch. Cows were subjected to PD on Day 30, 60, and 90 PTAI. Subset (n = 15 in each group) was subjected to blood plasma and milk samples on Day 30, 45, 60, 75, and 90 for PAGs and P4 profile. Pregnancy rate was compared by chi square. Effect of treatment on BCS, Plasma PAGs and P4 profiles were calculated by GLM procedures of SAS. Association of P4 with Plasma Milk PAGs was calculated using REG procedures of SAS (P < 0.05). In experiment 1, PR was 47% compared with 53% for G7G-Ovsynch versus MG7G-Ovsynch, respectively on d 31 post-TAI. On d 59 and 87, PR was recorded as 37% in G7G-Ovsynch group in comparison with MG7G-Ovsynch group (33%). In experiment 2, PR was 52% versus 42% (P = 0.159) on d 30,45% versus 37% (P = 0.226) on d 60, and 44% versus 36% on d 90 with overall pregnancy loss of 16% and 14% in G7G-Ovsynch and Ovsynch, respectively. In milk PAGs method sensitivity was 100%. Positive predictive value (PPV) was 92%. Negative predictive value (NPV) was 100% (P < 0.05). Sensitivity of plasma PAGs was recorded as 98% with 92% PPV and 83% NPV. Sensitivity of plasma P4 was 98% with 98% PPV and 89% NPV. There was positive correlation among P4 profile and PAGs concentration in both milk and plasma.Other parameters including BCS, cyclicity, and parity did not show any impact on pregnancy neither independently nor in interaction with treatment. In conclusion, although non-significant, increase in PR in G7G-Ovsynch makes it a protocol of choice in postpartum cows and PAGs as PD tool either in milk or plasma is as feasible as ultrasonography.

Key Words: G7G-Ovsynch, Pregnancy Associated Glycoproteins, milk sample, blood plasma, ultrasonography, pregnancy rate

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1254 WS Effects of octacosanol on non-seasonal spermatogenesis in ovine. J. W. Dickison*, *Angelo State University, San Angelo, TX.*

This study was conducted to understand the benefits of utilizing octacosanol as an additive to increase fertility of rams during the non-seasonal time of the year. Rams of Suffolk and Rambouillet influence were placed on a 60-d trial to determine the value of octocasanol as a feed supplement to promote semen production through the summer months. Rams were randomly divided into 2 groups of mixed breeds. Treatment group was fed a balanced ration containing 0.25% octocasanol per ton, while control rams were fed identical ration with no added octocasanol. Rams were fed at the rate of 6 lbs a day with alfalfa hay supplementation 3 times a week. Final collection was June 27 when ambient stress is generally at its highest point. Semen characteristics such as scrotal circumference, volume, concentration, and motility were used in the evaluation of the success of the product. Scrotal circumference (SC) measurements taken at onset of project to final showed no significant differences among control or treatment (P = 0.21) respectively although, the treatment group saw a larger increase in SC when compared to control (0.81 ± .01, 0.31 ± .01), respectively. Volume of ejaculate of both treatment and control also showed no significant difference from initial to final collection (P = 0.13) although as SC in the middle of summer the treatment group did show some increase when compared to control (0.32 ± .01, −0.60 ± .01 respectively). The same progressions were observed with concentration and motility of ejaculates

from beginning to final collection although again there was no significance ($P = 0.51$, $P = 0.34$ respectively). Concentration of ejaculate from treatment, again showed some increase from the control rams (2.32×10^9, -1.28×10^9 respectively). Like the previous measurements, motility also showed an increase from the treatment group when compared to the control rams (0.31×10^9, -0.27×10^9 respectively). Rams fed octacosanol for 60 d tended to have larger scrotal circumference, produced larger ejaculates with greater volume and sperm concentrations than control rams during the harshest period of the year for these parameters.

Key Words: Octacosanol, spermatogenesis, ovine

1255 WS Winter grazing or confinement feeding heifer development strategies differ in energetics as measured by 24 h heart rate and activity.

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The ability of a heifer to thrive is partially due to traits including behavioral/metabolic adaption and genetic background. Type of weaning and development program implemented creates an environment replacement heifers must adapt to flourish. This study was designed to determine if heifers developed in confinement or grazing native range use different adaption and coping processes by measuring activity such as distance traveled and percent resting time in 24 h along with resting heart rate and average heart rate per day. Spring-born, crossbred heifers were stratified to 1 of 2 treatments at weaning (start of Period 1): (1) fence-line weaning on native range (NR) with self-fed salt-mineral protein supplement ($n = 118$) and after weaning received a hand fed daily energy supplement or a self fed protein supplement, or (2) weaned into a dry lot (DL) and fed a corn silage diet formulated to gain 0.68 kg/d ($n = 53$). Ad libitum grass hay was made available in mid-December due to snow coverage resulting in range forage inaccessibility. Heifer BW were taken every 28 d from initiation of weaning. Each month (except February and June) a cohort of 7 heifers from each treatment were fitted with equine heart rate monitors (Polar Equine RS800CX) and QSTARZ CR-Q1100P GPS tracking recorder. Data were recorded for 48 h. On April 9, 2014 (Period 2) the two supplement groups grazing NR and DL heifers were combined into a common pasture. Heifers receiving DL had greater ($P < 0.01$) BW throughout the entire study. Resting heart rate was influenced ($P < 0.01$) by an interaction of period and weaning/development management. The rankings of resting heart rate were reversed from period 1 to period 2. Resting heart rate was also shown to influence BW. Resting heart rate relationship with BW was negative suggesting that lower resting heart rate is related greater BW. The analysis suggests that for every 2.2 decline in resting HR there is an additional 0.45 kg of BW. This study indicates that resting heart is negatively related to BW implying that animals with lower resting heart rate may have a production advantage.

Key Words: beef heifers, heart rate, heifer development

1256 WS Effects of dietary phytoestrogens on testicular growth and semen quality characteristics in developing Angus bulls.

S. C. Yurrita*, *Angelo State University, San Angelo, TX.*

This study investigated the impact of scrotal growth and semen quality parameters of bulls consuming dietary phytoestrogens versus bulls that are not exposed to phytoestrogen-containing diet ingredients. Angus bulls born in consecutive years were used in 2 independent trials. Bulls born in the spring of 2014 ($n = 39$) and 2015 ($n = 24$) were stratified by weaning weight, age of dam (AOD), and sire into a soybean meal diet group (SBMTRT) or a cottonseed meal diet group (CSMCON). At weaning (d −42), bulls were assigned to treatment and adapted to concentrate diets. At d 0, 21, 54, and 86 scrotal circumference measures were collected with semen collection and assessment also being conducted at d 86. Differences in scrotal circumference were detected due to the diet × day (year) interaction. On d 54 and 86, SBMTRT in 2014 exhibited larger scrotal measures than SBMTRT in 2015 ($P \leq 0.05$). At d 54, SBMTRT scrotal measures were also greater than the CSMCON scrotal measures in 2015 ($P = 0.05$). Scrotal growth from d 0 to 21 was greater for SBMTRT across both years ($P < 0.0001$). This pattern of larger teste growth was also observed from d 54 to d 86 ($P = 0.05$), and from d 0 through d 86 ($P < 0.0001$). Variation in semen concentration was due to the diet × AOD (year) interaction. The SBMTRT, produced from 2-yr old females, expelled higher concentrated semen samples in 2014 ($P = 0.026$) and 2015 ($P = 0.0006$), and this was inconsistent with the 2015 CSMCON out of 5+ year old cows who were higher for semen concentration ($P < 0.0001$). The diet × AOD (year) interaction was also a source of variation for motility. The 2014 bulls from 2 and 5+ year old cows ranked higher than the CSMCON cohorts of like aged cows ($P < .0001$). This trend was not evident in 2015 however, as the CSMCON mean was greater than the SBMTRT from 3 yr old cows only ($P = 0.0129$). Variation from the effect of diet for motility was also observed as well, as SBMTRT scored higher than CSMCON ($P = 0.0308$). These data suggest that dietary phytoestrogens at 10% soybean meal diet inclusion improves scrotal growth and semen quality and this is particularly evident in bulls produced by 2-yr old, first calf females.

Key Words: bull development, phytoestrogen, semen quality

1257 Reproductive performance of lactating dairy cows managed for first service with the Double-Ovsynch or Presynch-Ovsynch protocol and different duration of the voluntary waiting period.
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Our objective was to investigate time to pregnancy of dairy cows during lactation after submission for first AI service with three different treatments. Holstein cows (522 primiparous and 870 multiparous) from a commercial farm were stratified by parity and total milk production in their previous lactation (multiparous only) and randomly allocated to receive timed AI (TAI) after the Double-Ovsynch protocol (DO; GnRH-7d-P-GF-3d-GnRH-7d-GnRH-7d-PGF-56h-GnRH-16h-TAI) at 60 ± 3 DIM (DO60 = 476), TAI after DO at 88 ± 3 DIM (DO88 = 431), or a combination of insemination after detected estrus and TAI with the Presynch-Ovsynch protocol (PGF-14d-P-GF-12d-GnRH-7d-PGF-56h-GnRH-16h-TAI; PSOv = 485). Cows in the PSOv group received AI to estrus (AIE) after the second PGF treatment given at 50 ± 3 DIM or TAI at 72 ± 3 DIM. Subsequent AI services occurred through AIE or TAI after the Ovsynch protocol (32 ± 3 d after AI-GnRH-7d-PGF-56h-GnRH-16h-TAI). Pregnancy outcomes were determined using transrectal ultrasonography at 35 ± 3 and 94 ± 3 d after AI. Time to pregnancy up to 350 DIM was analyzed using Cox's regression whereas pregnancies per AI, pregnancy loss, and cows nonpregnant at 350 DIM were analyzed by logistic regression. Hazard of pregnancy was greater ($P < 0.01$) for DO60 [HR = 1.50 (95%CI = 1.29 to 1.74)] and PSOv [HR = 1.37 (95%CI = 1.18 to 1.59)] than for DO88 but it was similar ($P > 0.10$) for DO60 and PSOv [HR = 1.10 (95%CI = 0.95 to 1.26)]. Median days to pregnancy were 97, 117, and 98 for DO60, DO88, and PSOv, respectively. Hazard of pregnancy was greater ($P < 0.01$) for primiparous than multiparous cows [HR = 1.44 (95%CI = 1.27 to 1.62)]. The percentage of cows nonpregnant at 350 DIM was similar ($P = 0.16$) for the 3 groups (9.9, 13.8, and 12.6% for DO60, DO88, and PSOv). First service pregnancies per AI were similar ($P = 0.24$) for the 3 groups (DO60 = 41.4% [$n = 454$], DO88 = 44.1% [$n = 397$], PSOv = 38.2%; [$n = 461$]) but greater ($P < 0.01$) for cows that received TAI (45.2% [$n = 188$]) than AIE (33.3% [$n = 273$]) in the PSOv group. Pregnancy loss was similar ($P = 0.80$) among groups (DO60 = 5.9%, DO88 = 7.4%, and PSOv = 7.4%). We conclude that time to pregnancy was reduced when cows received TAI at 60 DIM after the Double-Ovsynch protocol or a combination of AIE after 50 DIM and TAI at 72 DIM with the Presynch-Ovsynch protocol than when cows received TAI at 88 DIM after the Double-Ovsynch protocol. Despite differences in time to pregnancy, the percentage of cows nonpregnant at 350 DIM was similar for the 3 groups. Supported by New York Farm Viability Institute project AOR13006.

Key Words: Double-Ovsynch, Presynch-Ovsynch, dairy cow

1258 Estrus detection intensity and accuracy, and optimal timing of insemination with automated activity monitors for dairy cows.
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The objectives were to assess: the ability of automated activity monitoring (AAM) to detect estrus for first insemination; the accuracy of detection; and the optimum interval from the onset of estrus to insemination. Four commercial farms were studied over 1 yr; 2 employed the AfiAct (Afikim) system and 2 the Heatime HR (SCR Inc.) system. Cows were inseminated between 55 and 80 DIM based on AAM only, then supplemented with timed AI (TAI). Blood progesterone was measured in 1,014 cows at weeks 5, 7, and 9 postpartum; purulent vaginal discharge (PVD) was assessed at week 5 and lameness and BCS at week 7. Overall, AAM detected 83% of cows in estrus by 80 DIM. Cows that had 3 serum P4 < 1 ng/mL, had PVD, or were both lame and had BCS $\leq$ 2.5 were less likely to be detected in estrus by 80 DIM (62, 68, 53%, respectively). Blood samples were collected on the day of 445 AI based on AAM and 323 TAI. The proportion of cows not in estrus (P4 > 1 ng/ml) on the day of AI was similar ($P = 0.35$) between AAM (4 ± 1.8%) and TAI (3 ± 1.2%). Activity data were extracted from AAM software for 1454 AI. Onset of estrus was calculated using the same (AfiAct) or similar (for the proprietary SCR algorithm) criteria as the AAM system. Producers recorded the time of AI. The interval from onset of estrus to AI was categorized as 0 to 8, 8 to 16, or > 16 h. There was no effect of AAM system on the probability of pregnancy per AI, but there was an interaction of interval with parity. For multiparous cows, the probability of pregnancy per AI was 31%, which did not differ ($P = 0.7$) with the interval to AI. For primiparous cows, the odds of pregnancy were greater if AI occurred 0 to 8 h (49%) than 8 to 16 h (36%) or > 16 h (31%) after the onset of estrus. AAM can detect estrus for first AI in just over the length of 1 estrus cycle for over 80% of cows, but the remainder would likely require intervention. For multiparous cows, performing AI based on AAM once per day would not affect pregnancy per AI, but for primiparous cows AI within 8 h of the onset of estrus may be advantageous.

Key Words: reproduction, management

1259 Beta-hydroxybutyrate concentration influences conception date in young beef cows in Tennessee.

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Selection for increased maternal traits like milk production in beef cattle may decrease reproductive efficiency due to increased metabolic load of lactation resulting in metabolic dysfunction. Therefore, our objective was to analyze the association of milk production, serum metabolites, cow BW change, and calf performance with time of conception in 183 spring-calving beef cows. Cows were classified by conception date as cows conceiving by timed-AI (TAI) or natural breeding (NAT). In addition, cows were grouped by age to represent young (3-and 4-yr-old), mature (5- and 6-yr-old), and old (7- to 9-yr-old) cows. Starting approximately d 30 postpartum, cow BW and BCS were recorded and blood samples were collected weekly through the end of breeding. Serum samples were aliquoted into pre-breeding and breeding composites then analyzed for metabolites. Cow BW and BCS did not influence ($P > 0.40$) conception date. Similarly, calf performance did not influence ($P > 0.30$) conception date. An age group × treatment interaction ($P < 0.01$) occurred for serum β-hydroxybutyrate (BHB). Serum BHB concentrations for mature and old cows were similar ($P > 0.05$) regardless of conception date. However, serum BHB concentrations for young NAT cows were greater ($P < 0.01$) than young cows conceiving at timed-AI. Serum non-esterified fatty acids (NEFA) exhibited ($P < 0.05$) a conception date × sampling period interaction. Pre-breeding serum NEFA concentrations were greater ($P < 0.05$) for NAT cows than TAI cows. Contrarily, serum NEFA concentrations during breeding were similar ($P > 0.05$) regardless of conception date. Serum glucose and urea N concentrations were not different ($P > 0.23$) between cows conceiving by timed-AI or natural service. Results from this study indicate that only the young, postpartum beef cows during early lactation were susceptible to metabolic dysfunctions and elevated blood BHB concentrations causing a delayed time to conception.

Key Words: beef cattle, β-hydroxybutyrate, conception time

1260 Heifer development using stockpiled, dormant native forages delays gain without altering reproductive performance.

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Winter grazing utilizing stockpiled forages is an economical alternative to feeding harvested feedstuffs during heifer development. However, development on stockpiled forages may have a negative impact on productivity due to restricted growth during a key physiological period. Therefore, our objective was to determine growth rate, nutritional status and reproductive performance of yearling heifers grazing differing stockpiled forages. Spring-born, crossbred heifers ($n = 155$) were stratified by BW at weaning to 1 of 3 stockpiled forage types: 1) endophyte-infected tall fescue (TF; 7.51% CP and 65.82% NDF, DM basis) 2) big bluestem and indiangrass combination (BI; 4.54% CP and 69.74% NDF, DM basis), or 3) switchgrass (SG; 4.23% CP and 75.77% NDF, DM basis). Each year, grazing began in January and was terminated in April at the onset of a 60-d breeding season. Heifers were fed twice per week at a rate of 0.18 kg·heifer^{-1}·d^{-1} of CP and were managed together before and after the grazing period. Heifer BW was obtained monthly from initiation of grazing until breeding and again at overall pregnancy diagnosis in September. Blood samples were collected 10 d prior and the day of timed-AI for serum metabolite analysis. Initial BW was not different ($P = 0.72$) among forage types. However, ADG from January to March was lower ($P < 0.01$) in heifers grazing BI and SG pastures. From March to April, ADG was not different ($P = 0.56$) among forage types. However, from April until September, heifers grazing both BI and SG pastures compensated and outgained ($P < 0.01$) heifers developed on stockpiled tall fescue pastures. Overall, heifers developed on TF pastures did have greater ($P < 0.01$) BW at final pregnancy detection. Circulating serum glucose concentration did not differ ($P = 0.19$) irrespective of forage type. Forage type × year interactions ($P < 0.05$) were exhibited for circulating NEFA and serum urea N concentrations. Serum β-hydroxybutyrate concentrations did not differ ($P = 0.15$) among forage types. Although BI and SG heifers exhibited restricted growth early in development, timed-AI pregnancy rates were 66, 51, and 59% for TF, BI, and SG heifers ($P = 0.40$), respectively. In addition, final pregnancy rates were 93, 92, and 87% for TF, BI, and SG heifers ($P = 0.56$), respectively. These results indicate that stockpiling native warm-season forages for winter grazing during heifer development delayed gain without reducing reproductive competence.

Key Words: beef heifers, heifer development, stockpiled forages

1261 Effect of pre- and postnatal trace mineral (TM) source on Angus and Brangus heifer growth and body composition. D. M. Price*[1], M. M. O'Neil[1], W. B. Watson III[1], R. West[2], D. O. Rae[2], D. M. Irsik[2], M. J. Hersom[1], and J. V. Yelich[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]College of Veterinary Medicine, University of Florida, Gainesville.*

A 2 by 2 factorial design evaluated growth and body composition in Angus (n = 40) and Brangus (n = 40) heifers born to cows supplemented with either inorganic (n = 40, 20/breed) or organic (n = 40, 20/breed) TM sources. The TM was initiated 82 ± 2 d pre-calving and resultant calves were weaned, and blocked by maternal TM source, age, sire, and weaning BW, and randomly assigned to 10 pens (5 pens/TM) for a 168 d development period. The TM supplement was pen fed 3 d/wk at 0.4 kg·454 kg BW-^{1}·heifer-^{1}·d-^{1}. Heifer BW and BCS (scale 1 to 9) were collected every 28 d. Ultrasound LM area (LMA), 12th rib back fat thickness (FAT), and LM intramuscular fat percentage (IMF) were recorded every 84 d. Statistical analysis used heifer as the experimental unit and repeated measures PROC MIXED to analyze BW, BCS, and ultrasound measurements. Fixed effects included TM, breed, day, and interactions. Results are presented as LSM ± pooled SE. At trial start, BW did not differ (P > 0.05) by TM or breed in inorganic, organic, Angus or Brangus (217, 224, 218, 223 ± 3 kg, respectively) heifers; however, organic and Brangus heifers had greater ($P \leq 0.01$; 4.6 ± 0.04) BCS than inorganic and Angus (4.4 ± 0.04). On d 84, organic (276 ± 4 kg) had greater ($P \leq 0.05$) BW than inorganic (261 ± 4 kg) heifers, while Angus and Brangus BW did not differ (P > 0.05). The BCS did not differ (P > 0.05) by TM or breed on d 84 (4.9 ± 0.04) and d 168 (5.4 ± 0.1). On d 168, BW did not differ (P > 0.05) by TM or breed in inorganic, organic, Angus, or Brangus (328, 338, 329, 337 ± 5 kg, respectively) heifers. No TM, breed, or interaction affected (P > 0.05) the 168 d ADG. The TM had no effect (P > 0.05) on IMF, FAT, or LMA. Breed did not affect (P > 0.05) FAT. Angus had greater ($P \leq 0.05$) IMF, but lesser LMA ($P \leq 0.01$) than Brangus (4.80 vs. 3.44 ± 0.12% and 43.99 vs. 49.67 ± 0.89 cm^2, respectively) when pooled across days. The TM source administered to cows during the last 1/3 of gestation did not affect heifer BW, BCS, or body composition over a 168 d post-weaning development period.

Key Words: heifers, trace minerals, performance, ultrasound

1262 Effect of pre- and postnatal trace mineral (TM) source on Angus and Brangus heifer growth and reproductive performance. D. M. Price*[1], M. M. O'Neil[1], W. B. Watson III[1], R. West[2], D. O. Rae[2], D. M. Irsik[2], M. J. Hersom[1], and J. V. Yelich[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]College of Veterinary Medicine, University of Florida, Gainesville.*

A 2 by 2 factorial design evaluated reproductive performance in Angus (n = 40) and Brangus (n = 40) heifers born to cows supplemented with either inorganic (n = 40, 20/breed) or organic (n = 40, 20/breed) TM sources. The TM was initiated 82 ± 2 d pre-calving and resultant calves were weaned, and blocked by maternal TM source, age, sire, and weaning BW, and randomly assigned to 10 pens (5 pens/TM) for a 168 d development period. On d 161 and 168, blood samples were collected to determine pubertal status (puberty = progesterone $\geq$ 1.5 ng/mL at one of two samples). A BW, BCS (Scale 1 to 9), and reproductive tract score (RTS, 1 to 5) were recorded and heifers were sorted by breed and TM source into 4 pastures (1 pasture/TM × breed) on d 168 for a 72 d natural service breeding season. Pregnancy was determined by ultrasound on d 51 of breeding season and 28 d after bull removal. The TM supplement was pen fed 3 d/wk at 0.4 kg·454 kg BW^{-1}·heifer^{-1}·d^{-1} as a pellet during development and as loose mineral during breeding (88.8 g·heifer^{-1}·d^{-1}). Heifer was the experimental unit and analysis utilized PROC MIXED for BW, BCS, and RTS data and PROC GLIMMIX for pregnancy and pubertal status. Fixed effects included TM, breed, and interaction. On d 168, inorganic (328 ± 5 kg) and organic (339 ± 5 kg) did not differ (P > 0.05) in BW or BCS (5.4 ± 0.1). Heifer RTS tended (P = 0.10) to be greater for organic (3.3 ± 0.1) than inorganic (3.0 ± 0.1) and greater ($P \leq 0.01$) in Brangus (3.4 ± 0.1) than Angus (2.9 ± 0.1) on d 168. Pubertal status did not differ (P > 0.05) on d 168 for TM (Inorganic, 20% = 4/20; Organic, 20% = 4/20) and breed (Angus, 20% = 4/20; Brangus, 20% = 4/20). On d 51 of breeding, pregnancy rates did not differ (P > 0.05) between inorganic (45% = 18/40) and organic (63% = 25/40) but were greater ($P \leq 0.05$) in Brangus (65% = 26/40) than Angus (43% = 17/40). Final breeding season pregnancy rates did not differ (P > 0.05) between inorganic (87.5% = 35/40) and organic (95% = 38/40), or between Angus (93% = 37/40) and Brangus (90% = 36/40). The TM source affected RTS but not pubertal status at the start of breeding season in yearling Angus and Brangus heifers. Additionally, TM source did not influence pregnancy rates to a natural breeding.

Key Words: trace minerals, heifers, pregnancy rate

1263 Impacts of zinc, manganese, and copper source on mature bull trace mineral status and spermatozoa characteristics. A. L. Zezeski*[1], M. Van Emon[2], R. C. Waterman[3], B. Eik[1], J. S. Heldt[4], and T. W. Geary[5], *[1]USDA-ARS Fort Keogh LARRL, Miles City, MT, [2]Montana State University, Bozeman, MT, [3]USDA-ARS Fort Keogh Livestock and Range Research Laboratory, Miles City, MT, [4]Micronutrients, Indianapolis, IN, [5]USDA ARS Fort Keogh, Miles City, MT.*

Our objective was to measure impacts of trace mineral source on liver mineral status and spermatozoa characteristics in mature bulls. Thirty-seven bulls (682 ± 147 kg) of mixed breeds, 2 to 4 yr of age were used in a 71 d trial. Bulls were blocked by length of time without trace mineral supplementation and stratified by initial liver Cu status to one of three dietary treatments (4 pens/treatment): 1) Supplement without Cu, Zn, and Mn; 2) Supplement with Cu, Zn, and Mn sulfate (sulfate); and 3) Supplement with basic Cu chloride, Zn and Mn hydroxychloride (hydroxy). Liver biopsies were collected on d −73, −24, and 71 to determine trace mineral status. Supplements containing Cu, Zn, and Mn were fed at 75% of NRC requirements as top dressing to a feedlot (corn silage) diet. Semen collection and scrotal circumference measurements were collected on d 0, 36, and 70. Ejaculates were evaluated for spermatozoa concentration, motility, and morphology as part of a standard breeding soundness examination. Acrosome integrity, sperm viability, and mitochondrial membrane potential were evaluated via flow cytometry counting at least 5,000 sperm per ejaculate. The mixed procedure of SAS was used for statistical analysis. On d 71, liver Cu concentrations of bulls receiving hydroxy minerals were greater ($P = 0.008$) than bulls receiving no mineral supplement or sulfate minerals. Liver Zn concentrations tended to be greater ($P = 0.08$) in bulls receiving hydroxy minerals compared to sulfate minerals. All other trace minerals (Co, Mn, Mo, and Fe) were not different ($P \geq 0.16$) due to dietary treatments. Liver concentration of Cu increased ($P = 0.04$) from the d −24 to 71 biopsy in bulls receiving hydroxy mineral. No differences ($P \geq 0.17$) were observed in any other trace mineral concentrations between treatments from the d −24 to 71 liver biopsies. Bulls with greater liver Zn concentrations on d 71 were correlated ($r = -0.39$, $P = 0.02$) with less acrosome damaged spermatozoa and tended to be correlated with greater spermatozoa concentrations ($r = 0.31$, $P = 0.06$). We conclude that basic Cu chloride and Zn hydroxychloride is more bioavailable and more readily stored in the liver compared with Cu and Zn sulfate. Increased liver Zn concentrations may also improve acrosome integrity of bull spermatozoa. However, diets deficient in trace mineral for > 170 d had no other detrimental effects on semen quality of mature bulls.

Key Words: trace mineral, bull, spermatozoa

1264 WS Effects of early or conventional weaning on beef cow and calf performance in pasture and drylot environments. G. W. Preedy*[1], J. R. Jaeger[2], J. W. Waggoner[3], and K. C. Olson[1], *[1]Kansas State University, Manhattan, [2]Western Kansas Agricultural Research Center, Kansas State University, Hays, [3]Western Kansas Agricultural Research Center, Kansas State University, Garden City.*

Spring-calving beef cows (initial BW = 599 ± 54.5 kg; initial BCS = 5.5 ± 0.54) and calves (initial BW = 204 ± 26.7 kg; 153 ± 15 d of age) were assigned randomly to 1 of 4 weaning treatments: weaning at 153 d of age followed by 56 d of limit feeding in confinement (E-D), confinement of cow and calf together for a 56-d period of limit feeding followed by weaning at 209 d of age (C-D), weaning at 153 d of age followed by a 56-d grazing period (E-P), and a 56-d grazing period with cow and calf together followed by weaning at 209 d of age (C-P). Calves assigned to E-D and C-D were fed a concentrate-based diet at 2.5% of BW, whereas cows assigned to E-D were fed a forage-based diet at 1.6% of BW. Cows assigned to C-D were offered the diet fed to E-D cows at 2.0% of BW. All cows and calves were limit fed common diets for 7 d at the end of our study to equalize gut fill. Calves ADG were influenced by diet and weaning treatments ($P \leq 0.03$). In general, calves managed in confinement and fed concentrate-based diets (i.e., E-D and C-D) had greater ADG than unsupplemented calves maintained on pasture (i.e., E-P and C-P). Cow BW and BCS change (d 0 to 63) were influenced by diet and weaning status ($P \leq 0.05$). Non-lactating cows maintained on pasture had lesser BW loss than other treatments, whereas non-lactating cows fed in confinement had lesser BCS on d 63 and greater BCS loss from d 0 to 63 than other treatments. Conversely, rump-fat depth on d 63 was greater ($P < 0.01$) for non-lactating cows maintained on pasture than for lactating cows in either pasture or drylot environments. Similarly, change in rump-fat depth was greatest ($P < 0.01$) for non-lactating cows on pasture and least for lactating cows in both pasture and drylot environments. Results were interpreted to indicate that weaning at 153 d of calf age spared cow BW and rump fat compared to weaning at 209 d of calf age. Performance of cows appeared to be similar when either limit-fed under drylot conditions or pastured without supplement. Conversely, calf performance was greater in confinement than on pasture.

Key Words: beef cows, concentrate, early weaning, pasture

1265 Association between management practices and reproductive performance of lactating dairy cows.
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It is common to observe great variation in reproductive performance among dairy herds; which ultimately impacts profitability. The objective was to assess the association of pre- and post-partum management practices with the annual average 21-d pregnancy rate (PR) in lactating dairy cows. A survey instrument was developed to collect information on herd demographics (e.g., breed, size, facilities), management practices for replacements and cows (e.g., housing, feeding, criteria to initiate breeding), reproductive program and performance (e.g., PR), health management (e.g., written protocols), and personnel (e.g., training, frequency, turnover). Multivariable regression and CORR models were performed using SAS. Information was collected from approximately 17,008 lactating dairy cows distributed in 41 herds in Argentina. The most predominant breed of cows was Holstein (> 85%) with an average herd size of 414 cows (ranged from 78 to 2,300). The average PR was 17% (ranged from 5 to 31.5%) and the voluntary waiting period (VWP) was 54 d (ranged from 40 to 70 d). The reproductive programs utilized (estrus detection, timed-AI, or bull) were not significantly associated with PR. The 21-d PR was positively correlated with prevention of hypocalcemia in prepartum cows (r = 0.36, P = 0.03), personnel training (primarily on reproductive program and AI technique; r = 0.57, P = 0.0006), an established VWP $\geq$ 50 d (r = 0.59, P = 0.0001), defined criteria (body weight, age, and reproductive tract score) to initiate breeding in replacement heifers (r = 0.47, P = 0.002), and availability of written protocols at the farm (yes vs. no; r = 0.37, P = 0.01). These management practices accounted for more than 52% of the observed variation in PR. There was considerable variation in PR (about 26.5% points) that could be attributed, at least in part, to pre- and post-partum management practices among herds. The most important reasons for increased annual PR were associated with a program for replacement heifers (4.6% points increase), prevention of metabolic diseases early in lactation (4.2% points increase), and training of dairy personnel responsible for breeding cows (5.6% points increase).

Key Words: dairy, management, reproduction

1266 Association between management practices and dairy herd performance.
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It is common to observe large variation in milk yield among herds; which ultimately impacts profitability. The objective was to assess the association of pre- and post-partum management practices with average milk yield (kg/cow/d) of 41 dairy herds in Argentina. A survey instrument was developed to collect information on herd demographics (e.g., breed, size, facilities), management practices for replacements and lactating cows (e.g., housing, feeding, milking frequency), reproductive management of replacements and lactating cows (e.g., breeding methods, criteria to initiate breeding), herd performance (e.g., milk yield) and health management (e.g., written protocols), and personnel (e.g., training, turnover). Multivariable regression and CORR models were performed using SAS. Information from approximately 17,008 lactating dairy cows distributed in 41 herds was collected. The most predominant breed of cows was Holstein (> 85%) with an average herd size of 414 cows (ranged from 78 to 2,300). The average milk yield per cow was 29.5 kg/d (ranged from 12.6 to 33.8 kg/d). The average daily milk yield was positively correlated with housing (confinement vs. grazing) for lactating cows (r = 0.46, P = 0.02), milking frequency (2 vs. 3 times per d; r = 0.67, P = 0.0003), availability of written protocols at the farm (yes vs. no; r = 0.52, P = 0.008), personnel training (yes vs. no; r = 0.54, P = 0.006), water analysis (yes vs. no; r = 0.68, P = 0.0002), and defined criteria (body weight, age, and reproductive tract score) to initiate breeding in replacement heifers (r = 0.50, P = 0.01). These management practices accounted for more than 54% of the observed variation in the average daily milk yield of lactating cows. There was a considerable variation in milk yield (about 21.2 kg/cow/d) that could be attributed to different diets and management practices among herds. The most important reasons for increased milk production were associated with training of dairy personnel (primarily on TMR and feed bunk management; ~5.5 kg/cow/d) and defined criteria (~5.4 kg/cow/d) to initiate breeding in replacement heifers.

Key Words: dairy, management, milk yield

1267 Impacts of early lactation hyperketonemia on reproduction and 305-d milk production.
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Hyperketonemia is a common early lactation disorder. Analysis of β-hydroxybutyrate (BHBA) by Fourier transform infrared spectroscopy in DHI milk samples provides a rapid and low-cost herd-level monitoring tool to evaluate the prevalence of hyperketonemia. The objective of this study was to evaluate the impact of elevated BHBA concentrations in early lactation DHI samples on reproduction and 305-d milk and component yields. Test-day and lactation records from 220,939 Holstein cows (114,267 primiparous and 106,672 multiparous) were used. All cows in the dataset had BHBA concentration on first test-day between 5 and 35 DIM. The following thresholds were used to classify cows based on milk BHBA concentration in early lactation: < 0.15 mmol/L = Negative (NEG); 0.15 to 0.19 mmol/L = Suspect (SUSP); and ≥ 0.20 mmol/L = Positive (POS), based on a previously published trial comparing milk and blood BHB concentrations. The MIXED procedure of SAS was used to evaluate the impact of BHBA classification on reproduction and production outcome. Cows with high BHBA concentration in early lactation had longer calving to first service and first service to conception intervals, increased days open, more services per conception, and lower 56d nonreturn rate. Cows with high BHBA concentration in early lactation produced higher 305-d milk and fat yields, but lower 305-d protein yields. Overall, trends were similar for primiparous and multiparous cows. Results indicate that hyperketonemia negatively impacts reproduction, but suggest higher producing cows are more affected. Monitoring and prevention strategies to reduce the prevalence of hyperketonemia in early lactation could result in improved reproduction and potential benefits on lactation milk yield.

Key Words: BHB, DHI, Reproduction

1268 Reproductive performance and culling dynamics of lactating dairy cows with detected pregnancy loss.
R. Wijma*, M. L. Stangaferro, and J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY.*

Our objective was to evaluate the reproductive performance and culling dynamics of dairy cows that lose their pregnancy after an initial pregnancy examination. Individual cow records (AI dates, AI outcomes, and date of sale or death) were collected from five commercial farms. In all farms cows received AI after detected estrus and timed AI. Pregnancy outcomes after AI were determined using transrectal ultrasonography or rectal palpation at 32 ± 3 (*n* = 3 farms) or 39 ± 3 d (*n* = 2 farms) after AI. Pregnancy reconfirmation was conducted at 63 ± 3 (*n* = 1 farm), 90 ± 3 (*n* = 3 farms), or 100 ± 3 d (*n* = 1 farm) after AI. Cows with at least one pregnancy loss (PL) event were included in the PL group (PLG; *n* = 893) and cows with no PL recorded were included in the no PL group (NoPLG; *n* = 7856). Pregnancies per AI (P/AI) and PL were determined for inseminations preceded (*n* = 627) or not (*n* = 14,619) by a PL event for cows in the PLG and NoPLG combined. Dichotomous and time to event outcomes were analyzed using logistic regression and Cox's regression, respectively. Only cows that reached 150 d of gestation were considered pregnant for the analysis of time to pregnancy and P/AI. Hazard of pregnancy until 400 DIM was greater ($P < 0.001$) for NoPLG than PLG (HR = 4.2; 95%CI = 3.8 to 4.6). Median time to pregnancy was 114 and 324 d for NoPLG and PLG, respectively. Hazard of pregnancy was also greater ($P < 0.001$) for primiparous than multiparous cows (HR = 1.3; 95%CI = 1.2 to 1.4). The percentage of cows pregnant by 400 DIM was greater ($P < 0.001$) for the NoPLG (72.3%) than PLG (47.6%) and for primiparous (79.5%) than multiparous (64.3%) cows ($P < 0.001$). Pregnancies per AI were greater ($P < 0.001$) for AI services preceded (35.6%) than not preceded by PL (29.1%). Nevertheless, more cows ($P < 0.001$) underwent PL for AI services preceded (21.9%) than not preceded by PL (11.6%). Hazard of leaving the herd tended to be greater ($P = 0.08$) for the PLG than NoPLG (HR = 1.1; 95%CI = 0.9 to 1.2). More cows left the herd ($P < 0.001$) by 400 DIM for the PLG (39.5%) than NoPLG (30.9%) and the multiparous (46.7%) than the primiparous (20.5%) group ($P < 0.001$). We conclude that cows that underwent PL had delayed time to pregnancy and were more likely to leave the herd. Also, P/AI and PL for AI services preceded by PL were greater than for AI services not preceded by PL. Supported by USDA NIFA Multistate project NYC-127813.

Key Words: Pregnancy loss, reproductive performance, culling dynamics

1269 Profitability of dairy cows receiving first service timed artificial insemination after the Double-Ovsynch protocol with a voluntary waiting period of 60 or 88 d.
M. L. Stangaferro*, R. Wijma, M. Masello, G. E. Granados, and J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY.*

Our objective was to evaluate the profitability of dairy cows receiving first service timed artificial insemination (TAI) after a voluntary waiting period (VWP) of 60 or 88 d. Holstein cows from 3 commercial farms received TAI after the Double-Ovsynch protocol (GnRH-7d-PGF-3d-GnRH-7d-GnRH-7d-PGF-56h-GnRH-16h-TAI) at 60 ± 3 (SVWP = 1,365) or 88 ± 3 DIM (LVWP = 1275). Subsequent AI services were conducted after detected estrus or TAI (32 ± 3 d after AI-GnRH-7d-PGF-56h-GnRH-16h-TAI). Individual cow production and reproduction data was collected for an 18 mo period

(18MP) after calving. Only cows that calved ≥ 18 mo before the day of data collection for the current analysis were included in the 18MP evaluation (SVWP = 523 and LVWP = 520). Total profitability (TPROF; $/cow) for the experimental lactation (EL) and the 18MP was the aggregation of: income over feed cost (IOFC), reproductive cost (RPRC; EL only), replacement cost (REPLC), calf value (CF; 18MP only), and fixed cost (FXC). Time to pregnancy was analyzed using Cox's regression, whereas continuous and binomial outcomes were analyzed by linear or logistic regression, respectively. Hazard of pregnancy up to 350 DIM for the EL was greater ($P < 0.01$) for SVWP than for LVWP [HR = 1.35 (95%CI = 1.24 to 1.48)] with median days to pregnancy of 102 and 128 for SVWP and LVWP, respectively. During the EL, lactation length was greater ($P < 0.01$) for LVWP (308 ± 3 d) than for SVWP (297 ± 2 d) and the same proportion ($P = 0.14$) of cows were culled (SWVP = 29% vs. LVWP = 32%). During the EL, similar TPROF (SVWP = $1,982 ± 36 vs. LVWP = $2,051 ± 38; $P = 0.12$) and profitability per day of lactation (SVWP = $5.5 ± 0.2 vs. LVWP = $5.3 ± 0.2; $P = 0.71$) was observed. Specifically, IOFC was greater ($P = 0.01$) for LVWP ($3,146 ± 37) than SVWP ($3,033 ± 35), FXC was greater ($P < 0.01$) for LVWP ($770 ± 7) than SVWP ($743 ± 6). Conversely, RPRC was greater ($P < 0.01$) for SVWP ($66.1 ± 0.9) than LVWP ($61.6 ± 0.9) and REPLC was similar ($P = 0.25$) for SVWP ($242 ± 12) and LVWP ($270 ± 13). For the 18MP, similar TPROF (SVWP = $2,885 ± 77 vs. LVWP = $2,764 ± 78; $P = 0.31$) and profitability per day (SVWP = $5.4 ± 0.2 vs. LVWP = $5.1 ± 0.3; $P = 0.45$) was observed. Specifically, no differences were observed for IOFC ($4,353 ± 76 vs. $4,227 ± 79; $P = 0.26$), REPLC ($373 ± 23 vs. $408 ± 24; $P = 0.45$), CF ($81.6 ± 2.8 vs. $80.8 ± 2.8; $P = 0.96$), and FXC ($1,112 ± 16 vs. $1,073 ± 17; $P = 0.16$). Percentage of cows culled during the 18MP was similar ($P = 0.57$) for SVWP (48%) and LVWP (50%). We conclude that despite differences in reproductive performance and individual factors that affect profitability, there were no differences in profitability during the EL or an 18 mo period after calving for cows that received TAI after a VWP of 60 or 88 d.

Key Words: Profitability, Double-Ovsynch, dairy cow

1270 Profitability of dairy cows managed for first service with the Double-Ovsynch or Presynch-Ovsynch protocol and different duration of the voluntary waiting period. M. L. Stangaferro*, R. Wijma, M. Masello, G. E. Granados, and J. O. Giordano, *Department of Animal Science, Cornell University, Ithaca, NY.*

Our objective was to evaluate the profitability of dairy cows managed with 3 different strategies for first service. Holstein cows from a commercial farm were randomly allocated to receive timed AI (TAI) after the Double-Ovsynch protocol (DO; GnRH-7d-PGF-3d-GnRH-7d-GnRH-7d-PGF-56h-GnRH-16h-TAI) at 60 ± 3 DIM (DO60 = 476), TAI after DO at 88 ± 3 DIM (DO88 = 431), or a combination of insemination after detected estrus (starting at 50 DIM) and TAI with the Presynch-Ovsynch protocol (PGF-14d-PGF-12d-GnRH-7d-PGF-56h-GnRH-16h-TAI;PSOv = 485). Subsequent AI services were conducted after detected estrus or TAI (32 ± 3 d after AI-GnRH-7d-PGF-56h-GnRH-16h-TAI). Data was collected for an 18 mo period (18MP) after calving. Only cows that calved ≥ 18 mo before the day of data collection for the current data analysis were included for the 18MP evaluation (DO60 = 218, DO88 = 208 and PSOv = 217). Total profitability (TPROF; $/cow) for the experimental lactation (EL; all cows included) and the 18MP was the aggregation of: income over feed cost (IOFC), reproductive cost (RPRC; EL only), replacement cost (REPLC), calf value (CF; 18MP only), and fixed cost (FXC). Time to pregnancy was analyzed using Cox's regression, whereas continuous and binomial outcomes were analyzed by linear or logistic regression, respectively. Hazard of pregnancy up to 350 DIM was greater ($P < 0.01$) for DO60 [HR = 1.50 (95%CI = 1.29 to 1.74)] and PSOv [HR = 1.37 (95%CI = 1.18 to 1.59)] than for DO88. Median days to pregnancy were 97, 117, and 98 for DO60, DO88, and PSOv, respectively. During the EL, lactation length was greater ($P = 0.03$) for DO88 (302 ± 4 d) than for DO60 (293 ± 5 d) and PSOv (289 ± 4 d). During the EL, similar TPROF (DO60 = $1,884 ± 55, DO88 = $1,893 ± 59 and PSOv = $1,860 ± 56; $P = 0.78$) and profitability per day (DO60 = $5.5 ± 0.3, DO88 = $5.1 ± 0.3 and PSOv = $5.5 ± 0.2; $P = 0.58$) was observed. Specifically, RPRC was greater ($P < 0.01$) for DO60 ($64.2 ± 1.4) and DO88 ($61.4 ± 1.5) than for PSOv ($55.3 ± 1.3), whereas FXC was greater ($P = 0.03$) for DO88 ($756 ± 11) than for DO60 ($733 ± 9) and PSOv ($723 ± 10). No differences were observed for IOFC (DO60 = $2,905 ± 53, DO88 = $2,989 ± 59 and PSOv = $2,926 ± 52; $P = 0.31$) and REPLC cost (DO60 = $225 ± 18, DO88 = $279 ± 20 and PSOv = $288 ± 22; $P = 0.11$). For the 18MP, similar TPROF (DO60 = $2,925 ± 119, DO88 = $2,627 ± 123 and PSOv = $2,708 ± 125; $P = 0.28$) and profitability per day (DO60 = $5.3 ± 0.4, DO88 = $6.1 ± 0.4 and PSOv = $5.1 ± 0.3; $P = 0.49$) was observed. Specifically, no differences were observed for IOFC (DO60 = $4,363 ± 117, DO88 = $4,073 ± 126 and PSOv = $4,175 ± 122; $P = 0.31$), REPLC (DO60 = $373 ± 31, DO88 = $408 ± 35 and PSOv = $417 ± 38; $P = 0.18$), CF (DO60 = $88.1 ± 4.3, DO88 = $81.3 ± 4.8 PSOv = $83.4 ± 4.8; $P = 0.69$), and FXC (DO60 = $1,136 ± 24 DO88 = $1,062 ± 27 and PSOv = 1078 ± 26; $P = 0.17$). We conclude that despite differences in reproductive performance and individual factors that affect profitability, there were no differences in profitability during the experimental lactation or an 18 mo period after calving.

Key Words: Profitability, Double-Ovsynch, Presynch-Ovsynch, dairy cow

1271 Economic evaluation of a milk test for pregnancy confirmation in dairy cows. E. M. Wynands[*1], M. von Massow[2], S. J. LeBlanc[1], and D. F. Kelton[1], [1]*Department of Population Medicine, Ontario Veterinary College, University of Guelph, Guelph, ON, Canada,* [2]*School of Hospitality, Food & Tourism Management, University of Guelph, Guelph, ON, Canada.*

Timely diagnosis of pregnancy and pregnancy loss is economically important. A commercially available pregnancy-associated glycoprotein milk assay is offered through routine Dairy Herd Improvement (DHI) testing for diagnosis of pregnancy. The objective was to complete a cost-benefit analysis of the milk pregnancy test for confirmation of pregnancy. The test can be used to complement, or as an alternative to, veterinary diagnosis by palpation or ultrasound. CanWest DHI currently recommends using the test for confirmation of pregnancy $\geq$ 60 d in gestation. Therefore, for this analysis it was assumed cows had been previously diagnosed pregnant. The model included 4 simulated pregnancy confirmation strategies: 1) no confirmatory testing, 2) confirmation by milk PAG test, 3) confirmatory examination by a veterinarian, and 4) confirmation using a combination of the milk test and veterinary exam. The analysis was done by simulations of economic outcomes using a cow-level stochastic model (with @Risk for Excel) with uniform distributions for additional days open due to testing frequency. Model assumptions were that cows became eligible for testing at 60 d in gestation, the herd had biweekly veterinary visits, and was enrolled in DHI milk recording with a milk test every 5 wk. Data from the current literature were used to model input variables associated with losses due to days open (for cows eligible to be re-inseminated after pregnancy loss) and culling after pregnancy loss for cows too late in lactation to re-inseminate. The base cost of veterinary exam was $2 and the milk test was $6. For each scenario, 1,000 simulations were run generating a minimum, maximum, and mean value. The most costly option was no confirmatory testing. The benefit of confirmatory testing compared to no confirmatory testing was between $11.80 and $17.90 per cow. On average, the milk test was $6.10 more costly per cow tested than veterinary confirmation. Under the assumed inputs, milk testing would have to cost < $1.00 or occur weekly to have a lower cost than veterinary confirmation. Sensitivity analysis indicated that the models were most sensitive to the proportion of cows found open and the proportion of open cows eligible to re-inseminate. Models were found to be less sensitive to the cost of a day open, additional days open due to testing frequency, and the cost of the test. Pregnancy loss is a costly event but the cost can be limited by pregnancy confirmation testing.

Key Words: pregnancy confirmation, economics

1272 Effect of synchronizing, access to supplement, and grazing session on grazing behavior of early lactating dairy cows. P. Chilibroste[1], J. P. Marchelli[2], and D. A. Mattiauda[*1], [1]*Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay,* [2]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay.*

An experiment was performed to study the effect of two contrasting feeding strategies involving TMR and grazing, during the first 60 d in milk of Holstein dairy cows. Twenty four multiparous dairy cows were blocked according to parity, expected calving date, body condition score (BCS; 3.2 ± 0.35) and BW (688 ± 60.7 kg) before calving, and were randomly allocated to follow 1 of 2 feeding strategies: GR-one = 1 grazing session (AM: 800 to 1400 h) supplemented with a total mixed ratio (TMR corn silage/concentrate mix 40/60; respectively) out of the grazing plot orGR-two = 2 grazing sessions (AM: 0800 to 1400 h; PM: 1800 to 400 h) supplemented with TMR into the grazing plot. The 2 treatments were based on the same offer of energy (50 Mcal ENL/cow/d), differing in the synchrony or not between the access to pasture and to TMR (50% each of the total energy on offer). In both treatments TMR supplementation was offered once a day at 1700 h on feed troughs (0.6 m lineal access per cow). On Days 10, 13, 30, and 33 of the experiment the number of cows grazing or idling were determined every 15 min during the first 4 h of the AM and 3 h of the PM grazing session. The PROC GLIMMIX of SAS (SAS 9.2, 2010) with a binomial response distribution and with Logit as a link function was used to determine the probability of the different events. A first order autoregressive heterogeneous (AR1) covariance structure was selected. The probability of cows grazing (approximately 0.5) during the AM grazing session was not different between treatments. There was a significant effect of time with higher probability of grazing during the first hour than in the following ones (0.84^{a}, 0.32^{b}, 0.36^{b} and 0.41^{b} for the first, second, third and fourth h, respectively; $p < 0.01$). A significant interaction between treatment and time was detected: GR-one cows grazed longer than GR-two cows during the first h (0.89 vs. 0.75; $p < 0.05$) but shorter during the third hour (0.26 vs. 0.47; $p < 0.05$) of the grazing session. During the PM grazing session the GR-two cows expended a large proportion of time either around the feed troughs (0.83, 0.57 and 0.50) or idling (0.10, 0.19 and 0.17) during the first, second and 3rdh, respectively. The changes observed on grazing behavior were no reflected on productive performance (companion abstract).

Key Words: early lactation dairy cows, grazing behavior, grazing, TMR

1273 Profitability of reproductive management strategies for second and greater artificial insemination service in dairy cows.

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Our objective was to evaluate the profitability of dairy cows managed with two different resynchronization protocols. Individual cow production and reproduction data was collected for an 18 mo period after calving for cows that completed a study aimed at evaluating two management strategies for second and greater AI services (Giordano et al., 2015; J Dairy Sci. 98:2488–2501). Briefly, cows enrolled in the control group (CON; n = 634) received insemination based on increased physical activity (AIACT) any time after a previous AI and timed AI (TAI) after the Ovsynch protocol (GnRH-7d-PGF2α-56h-GnRH-16h-TAI) initiated 32 ± 3 d after AI. Cows enrolled in the treatment group (TRT; n = 616) diagnosed non-pregnant 32 ± 3 d after AI with a corpus luteum (CL) ≥ 20 mm received a PGF2α treatment to induce estrus. Cows not AIACT within 9 d of the PGF2α received TAI after a 5d-CIDR-Ovsynch protocol (GnRH+CIDR-5d-PGF2α+CIDR-removal-24h-PGF2α-32h-GnRH-16h-TAI). Cows in TRT with no CL received a GnRH treatment for presynchronization and if not AIACT within 7 d were enrolled in the 5d-CIDR-Ovsynch protocol to receive TAI. Total profitability (TPROF; $/cow) during the 18 mo period of evaluation was the aggregation of: income over feed cost (IOFC) during lactation and the dry period, reproductive program cost (RPRC), replacement cost (REPLC), calf value (CF), and fixed cost per day (FXC). Time to pregnancy was analyzed using Cox's regression whereas, continuous and binomial outcomes were analyzed by linear or logistic regression, respectively. The hazard of pregnancy up to 270 DIM was similar for cows in the CON and TRT group (HR = 1.07; 95%CI = 0.95 to 1.21) with median days to pregnancy of 111 and 110 d for the CON and TRT group, respectively. Total days in lactation were similar (P = 0.57) for CON (417 ± 5 d) and TRT (420 ± 6 d) and the same proportion (P = 0.79) of cows were culled for both groups (CON = 57% vs. TRT = 55%). Similar TPROF (CON = $3,563 ± 71 vs. TRT = $3,498 ± 69; P = 0.71) and profitability per day of lactation (CON = $8.2 ± 0.2 vs. TRT = $8.1 ± 0.2; P = 0.89) was observed. Among individual factors used to calculate profitability, there were no differences between groups for IOFC (CON = $4,771 ± 68 vs. TRT = $4,724 ± 66; P = 0.80), FXC (CON = $1,041 ± 14 vs. TRT = 1049 ± 14; P = 0.57), REPLC (CON = $468 ± 19 vs. TRT = $449 ± 18; P = 0.82), and CF (CON = 86.2 ± 2.6 vs. TRT = 85.2 ± 2.7). Conversely, RPRC was greater (P < 0.01) for TRT ($68.8 ± 2.1) than for CON ($59.4 ± 1.7). We conclude that despite a greater reproductive program cost for TRT than CON, overall profitability for an 18 mo period after calving was similar for both strategies.

Key Words: profitability, resynchronization, dairy cow

1274 Pre-weaning injections of bovine somatotropin enhanced puberty attainment of bos indicus-influenced beef heifers.

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A 2-yr study evaluated the effects of three pre-weaning 14-d apart injections of bovine somatotropin (bST) on growth and puberty of beef heifers. On d 0 of each yr, Angus × Brangus heifers (n = 15 heifers/treatment/yr; BW = 153 ± 21 kg; age = 135 ± 12 d) were stratified by BW and age, and randomly assigned to receive s.c. injections of saline (SAL; 5 mL; 0.9% saline) or half-dose of bST (250 mg of sometribove zinc; Posilac, Elanco, Greenfield, IN) on d 0, 14, and 28. Cow-calf pairs were allocated to 4 bahiagrass (*Paspalum notatum*) pastures (7 to 8 pairs/pasture/yr) from d 0 until weaning (d 127). Unshrunk BW and blood samples were collected on d 0, 14, 28, and 127. From d 127 to 346, heifers were pooled by treatment and allocated to bahiagrass pastures (1 pasture/treatment/yr) and fed blackstrap molasses-based concentrate at 1.1% BW (DM basis). Unshrunk post-weaning BW was obtained every 28 d, and blood samples every 9 to 10 d to determine plasma progesterone (P4) concentrations. Heifers were considered pubertal when 2 consecutive plasma samples had P4 ≥ 1.5 ng/mL. Each group of heifers was placed with 1 Brangus bull from d 282 to 346. Effects of treatment × yr and treatment × yr × time were not detected for any variable measured in the study (P ≥ 0.11). During pre-weaning phase, bST heifers had greater mean plasma IGF-1 concentrations (115 vs. 102 ± 3.8 ng/mL; P = 0.02) and ADG from d 0 to 42 (1.17 vs. 1.06 ± 0.035 kg/d; P = 0.01), but tended to have less ADG from d 42 to 127 than SAL heifers (0.77 vs. 0.84 ± 0.029 kg/d; P ≥ 0.06). Hence, BW at weaning did not differ between bST and SAL heifers (267 vs. 270 ± 1.70 kg, respectively; P = 0.58). During post-weaning phase, bST heifers had similar ADG from d 127 to 347 (0.17 vs. 0.12 ± 0.07 kg/d; P = 0.11), BW and age at puberty (290 vs. 291 ± 6.9 kg and 395 vs. 419 ± 14 d, respectively; P ≥ 0.15), but greater puberty achievement at start of breeding season (63 vs. 44 ± 7.9%; P = 0.02) than SAL heifers. Hence, three half-dose injections of bST administered to suckling beef heifers at 14-d intervals may be a feasible management practice to enhance puberty attainment at the start of the breeding season.

Key Words: somatotropin, heifers, puberty

1275 Effects of temperament on physiological and reproductive responses of Bos Indicus beef cows.

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This experiment evaluated the effects of temperament on physiological and reproductive responses of *Bos indicus* cows. A total of 954 lactating, multiparous, non-pregnant Nelore cows (age = 99 ± 1.6 mo; days post-partum = 51.4 ± 0.3 d; BCS = 5.34 ± 0.04; BW = 430 ± 2 kg), allocated into 8 groups of approximately 120 cows each, were utilized. Groups were assigned to an estrus synchronization + timed-AI protocol from d 0 to 11. On 11, cows were inseminated, blood samples were collected, and cow temperament was evaluated via chute score and exit velocity. Individual exit score was calculated by dividing exit velocity results into quintiles and assigning cows with a score from 1 to 5 (exit score: 1 = slowest; 5 = fastest cow). Temperament scores were calculated by averaging cow chute score and exit score, and cow temperament type was defined according to temperament score (≤ 3 = adequate temperament, ADQ, > 3 = excitable temperament, EXC). Pregnancy status was verified 30 d after timed-AI via transrectal ultrasonography. Cows not pregnant to AI were assigned to a second timed-AI protocol. Cows that still remained non-pregnant were exposed to natural breeding for 60 d. Cow age, BW, BCS, and days post-partum on d 0 were similar ($P \geq 0.27$) between ADQ and EXC cows. On d 11, EXC had greater ($P < 0.01$) plasma cortisol but similar ($P = 0.89$) plasma haptoglobin concentrations compared with ADQ cows (48.9 vs. 38.4 ng/mL of cortisol, SEM = 1.0). Pregnancy rate to the first timed-AI tended ($P = 0.10$) to be less in EXC vs. ADQ cows (41.0 vs. 47.2%; SEM = 3.5), whereas pregnancy rates to the second timed-AI, natural breeding, and final pregnancy rates (AI + natural breeding) were similar ($P \geq 0.23$) between ADQ and EXC cows. However, calving rate was less ($P = 0.02$) in EXC vs. ADQ cows (66.9 vs. 74.9%; SEM = 2.5), which can be associated with the greater ($P = 0.04$) pregnancy loss (based on final pregnancy status and actual calving) detected in EXC vs. ADQ cows (11.3 vs. 6.4%; SEM = 1.6). Results from this experiment indicate that *B. indicus* cows with excitable temperament have impaired reproductive performance during a breeding season based on timed-AI + natural breeding compared to cohorts with adequate temperament.

Key Words: beef cows, reproduction, temperament

1276 Carcass quality of primiparous cows managed under a single-calf heifer model combined with use of sexed semen and early weaning.

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The single-calf heifer model (SCHM) harvests females after early-weaning their first calf, reducing average age and maintenance requirements of the herd, hence increasing biological efficiency of beef production. However, pregnancy estrogens accelerate bone ossification, which might affect carcass value of SCHM females. This study evaluated: overall maturity (OM), bone maturity (BM), lean maturity (LE), marbling (MA), Warner-Bratzler (WBSF) and slice shear force (SSF), and cooking loss (CL) of carcasses of SCHM females. Fifty-three Angus-based yearling heifers (BW = 353 ± 38.8 kg) and a second set of 58 (BW = 307 ± 29.9 kg), were synchronized and inseminated with sexed semen during first and second year of the project, respectively, to calve at approximately 24 mo of age. At weaning, average age of calves was 106 ± 22 and 120 ± 21 d, and first-calf heifers (43 each year) were fed for 88 and 90 d at a feedlot, for years 1 and 2, respectively. At harvest, carcasses were scored for LE, BM, and MA (slight = 300, small = 400, and modest = 500); OM was estimated from BM and LE (A^{00}, $B^{00}$and C^{00} maturities corresponded to scores of 100, 200, and 300, respectively). One LM sample was removed for SSF, WBSF and CL measurements. Carcasses were sorted by OM as < 300 or $\geq$ 300, and the resulting means for carcass traits were compared with a *t* test. Data were combined across years, since same significant differences ($P < 0.05$) between OM groups were obtained for both years. Means ± SD for the 66% of the carcasses classified as < 300 OM were: 192 ± 39.3 OM, 211 ± 53 BM, 165 ± 29 LE, 446 ± 84 MA, 25.4 ± 8.6 kg SSF, 4.94 ± 1.19 kg WBSF, and 25.4 ± 4.1% CL. Remaining carcasses ($\geq$ 300 OM) were 305 ± 18 OM, 346 ± 46 BM, 167 ± 27 LE, 462 ± 78 MA, 27.6 ± 9.1 kg SSF, 4.96 ± 0.84 kg WBSF, and 26.1 ± 4.2% CL. Significant differences between the 2 OM groups were found for BM ($P < 0.001$). However, no differences were detected for LE ($P = 0.81$), MA ($P = 0.39$), WBSF ($P = 0.96$), SSF ($P = 0.29$) or CL ($P = 0.47$). Therefore, differences in OM and BM did not affect palatability characteristics of carcasses of primiparous SCHM females approximately 30 mo of age.

Key Words: bone ossification, shear force

1277 Milk metabolomics of dairy goats with mammary inflammation under heat stress conditions.
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The objective was to test whether mammary gland response to bacterial endotoxin could be conditioned by heat stress, and to detect biomarkers for heat stress and inflammation in milk. Eight multiparous Murciano-Granadina dairy (2.2 ± 0.1 L/d; 100 ± 5 DIM, 42 ± 2 kg BW) goats were maintained under 2 environmental conditions varying in temperature, relative humidity (RH) and temperature humidity index (THI): 1) 4 goats under thermoneutral (TN; 15 to 20°C, RH = 50 ± 5%, THI = 59 to 65), and 2) 4 goats under heat stress conditions (HS; 35°C from 0900 to 2100 and 28°C from 2100 to 0900, RH = 45 ± 5%, THI = 75 to 83). Adaptation of 11 d to the experimental treatments was allowed. On d 12 each animal had 1 udder half infused with 10 µg *E. Coli* lipopolysaccharide (LPS) and the other udder half as the control with 0.9% saline (CON). This resulted in 4 treatment combination: TN-CON, TN-LPS, HS-CON, and HS-LPS. Milk samples (0, 4, 6, 12, and 24 h) were collected and analyzed by ^{1}H NMR spectroscopy operating at 600 MHz. Data were processed by the ChemoSpec package of R program and further analyzed by the web-based MetaboAnalyst program. Principal component analysis and partial least square–discriminant analysis were used to identify possible metabolite markers in milk. Citrate, glucose-1-phosphate, pyruvate and malonic acid increased in milk of HS goats. The increment in milk citrate might explain the previously observed deteriorated coagulation properties during the cheese making from the milk of heat-stressed animals. On the other hand, the LPS challenge resulted in an increment in milk lactate, acetate, butyrate, and capric acid. In conclusion, the metabolomic profile of milk was dramatically affected by environmental temperature and udder health status. Milk citrate and lactate were detected as good markers for heat stress and udder inflammation, respectively. Acknowledgment: Project AGL-2013–44061-R (Plan Nacional, MINECO, Spain).

Key Words: metabolomics, mastitis, heat stress, dairy goats

1278 Winter climate variables and their effect on feed intake in *Bos taurus* bulls.
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In beef cattle, there are numerous factors that influence feed intake such as breed composition, ration formulation, and body size. Additionally, an animal's intake could be influenced by many different environmental factors such as weather and climate factors. It is hypothesized that animal intake is influenced by weather events, specifically daily temperature difference (TDIFF) and average daily wind speed (WSPD), experienced prior and up to a feeding event, however there is limited research on the affects of these variables on feed intake. Therefore the objective of this study was to determine if average daily pen DMI (ADMI) were significantly influenced by changes in weather during winter months. Feed intake observations were collected from a total of 158 *Bos taurus* bulls from 3 different sources that were separated into pens ($n = 5$), with pen allocation based on source and BW. Feed intake observations were collected for approximately 70 d from December through February. Climate and feed intake data were obtained from the Colorado State University Agricultural Research, Development and Education Center. The distance between the weather station and the feed intake unit was approximately 5 km. The independent variable TDIFF was defined as the difference between the daily maximum temperature and minimum temperature. The effects of pen, WSPD, and TDIFF were evaluated for their influence on ADMI using a generalized linear model. This regression was performed for the intake observation day (d0), as well as every day up to 4 d before d0. Pen was included in the model to account for differences in cattle's breed, size and pen location. The model results suggested that TDIFF was significant ($P < 0.0001$) on d0, as well as 1, 2, and 3 d before d0. WSPD was shown to be significant 2 ($P < 0.0003$) and 4 ($P < 0.0001$) days before d0. Model R2 was shown to be the greatest 2 d before d0 (0.55). These results suggest that differences in a bull's DMI are influenced by weather changes occurring 2 d before the intake day during winter months. Better understanding of climate variables effect on feed intake in beef cattle could potentially lead to more accurate evaluations of differences of feed efficiency in beef cattle in the future.

Key Words: beef cattle, feed intake, winter climate

1279 Maternal heat stress reduces body and organ growth in calves: relationship to immune tissue development.
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Maternal heat stress (HT) not only reduces fetal growth but also influences postnatal performance and immune function of the offspring. The objective was to evaluate the effect of in utero HT on overall fetal growth and organ development, particularly those associated with immune function. Dams were dried off 45 d before expected calving and randomly assigned to one of two treatments: HT or cooling (CL). During the dry period, all cows were housed under shade in a freestall barn, where the pen for CL cows was equipped with active cooling including water soakers and fans whereas the pen for HT cows had no soakers and fans. Based on rectal temperature (RT) and

respiration rate (RR), heat stress was severe. Average RT in HT cows was 39.3°C compared with 38.9°C for CL cows, and HT cows had 66.7 breath/min respiration rate and 43.2 for CL cows. After birth all bull calves were immediately separated from their dams and weighed. Bull calves (n = 30) were sacrificed at birth without colostrum feeding (5/trt) and 1 and 2 d of age (DOA, following colostrum feeding, 5/trt). Pooled colostrum (3.8 L) was fed within 4 h after birth to bulls slaughtered on 1 and 2 DOA. After slaughter, the small intestine was removed, weighed (1.0 to 1.4 kg), and dissected into duodenal, jejunal and ileal segments, and tissue samples from each section were fixed in 4% neutral formalin and then transferred to 70% ethanol for immunohistochemistry. Bull birth weight from HT dams was lower than bulls from CL dams (HT: 39.3; CL: 43.8 SEM = 1.1 kg; $P < 0.01$). The thymus, spleen, and heart weight of HT bulls was lower compared with the CL bulls (Thymus, HT: 107.7; CL: 138.0, SEM = 14.4 g; $P = 0.02$; Spleen, HT: 75.5; CL: 93.7, SEM = 6.9 g; $P < 0.01$; Heart, HT: 292.4; CL: 329.4, SEM = 19.6 g; $P = 0.03$). The liver weight of HT bulls tended to be lower compared with the CL bulls (HT: 811.4; CL: 914.0, SEM = 70.4 g; $P = 0.09$). We conclude that the acute difference in heat strain on HT and CL cows during the dry period has significant impact on general fetal growth and on immune tissue development, which may be associated with reduced immune function in early life.

Key Words: heat stress, bull, immune tissue

1280 Liver proteomic analysis of cows exposed to heat stress or cooling conditions during the dry period.

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Heat stress negatively impacts cow performance, compromises immune function and increases susceptibility to metabolic disorders, particularly during the transition period. Metabolic adaptations of the liver are critical for successful transition from gestation to lactation, yet it is unclear how heat stress impacts metabolic pathways within the liver at the molecular level. The objective of this study was to investigate the liver proteome of cooled and heat stressed dry cows to gain insight into how molecular pathways are altered by heat stress and may contribute to poor performance and transition-related disorders. The experiment was conducted at the University of Florida Dairy Unit. During the dry period, cows were either housed in shaded barns with fans and soakers (cooled group [CL]; n = 5) or in shaded barns lacking these cooling devices (heat stressed group [HT]; n = 5). Liver biopsies were collected +2 d relative to calving. Proteins were analyzed by quantitative shotgun proteomics at the Weizmann Institute of Science (Rehovot, Israel). Proteins were extracted and subjected to in-solution tryptic digestion followed by nanoflow liquid chromatography coupled to high-resolution tandem mass spectrometry. Quantitative data was extracted using the Genedata Expressionist data analysis package and proteins identified using the Mascot search engine. Proteomics data, after logarithmic transformation, were analyzed by t test to examine effect of treatment (CL vs. HT). Proteins were regarded as differential at $P \leq 0.05$ and fold change ± 1.2. Differentially expressed proteins were analyzed by Ingenuity Pathway Analysis. A total of 3270 proteins were identified, 65 of which were differentially expressed between treatments. The most relevant pathways identified were hepatic oxidative phosphorylation and mitochondrial dysfunction. The abundance of several proteins related to these pathways was lower in the liver of HT cows relative to CL cows, including cytochrome c oxidase subunit 4 isoform 1(COX4I1, $P < 0.04$), NADH dehydrogenase 1 α subcomplex subunits 10, 11, and 12 (NDUFA10, $P < 0.002$; NDUFA11, $P < 0.01$; NDUFA12, $P < 0.04$), and thioredoxin-dependent peroxide reductase (PRDX3, $P < 0.04$). NADH dehydrogenase and cytochrome c oxidase are 2 of the 4 enzyme complexes in the inner mitochondrial membrane involved in the redox reactions that create the proton gradient necessary to power ATP synthesis. Thioredoxin-dependent peroxide reductase is an antioxidant and as such protects enzymes from oxidative damage. These results suggest that cooling late gestation cows improves liver function during early lactation.

Key Words: oxidative phosphorylation, heat stress, mitochondrial dysfunction

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1281 A rumen bolus is a useful tool to monitor core body temperature in lactating dairy cows in a sub-tropical summer.

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The ability to vary body temperature is a common thermoregulatory response in mammals and rumen boluses may allow frequent monitoring of such variations during heat stress episodes. Twenty four Holstein Friesian lactating dairy cows were fed either a total mixed ration plus wheat (TMRW), TMR plus Bioprotect, a starch binding agent (TMRB), or TMR plus Corn (TMRC). The only difference between diets was the type of grain contained in the TMR. Cows had ad libitum access to water and feed in shaded pens at the University of Queensland, Gatton Campus, Dairy research facilities, 27.4986°S, 153.0155°E, 89 m elevation during 29 d in summer 2015. Rumen temperature (RuT) was recorded over 15 d at 20 min interval using transponder rumen boluses (RFID

transmitters; Smartstock, USA) placed in the ventral sac of the rumen. Rectal temperature (RT) was measured once every 4 d in the morning (0700 to 1000 h) and the temperature humidity index (THI) was calculated from an on-site weather station. Data were analyzed using the restricted maximum likelihood (REML) and Pearson correlation analysis procedure for GenStat V15. Treatment groups were considered statistically different at $P \leq 0.05$. Average THI during the experimental days was 72.4 ± 2.0 (mean ± SD) with 76% of the days having THI $\geq$ 72 which is the critical THI threshold for dairy cows. TMRC fed cows had lower RT than TMRW and TMRB (38.8 vs. 39.1 and 39.1°C respectively; $P < 0.001$) and RT was directly correlated to THI and RuT in all diets ($P < 0.001$). Diet had no significant effect on RuT (39.6, 39.7, 39.5°C for cows fed TMRB, TMRC and TMRW respectively; $P > 0.05$). Cows had large variations in RuT during the day that weren't associated with THI. For example, RuT was higher overnight (2000 to 0500 h) than during the day with the maximum occurring between 2100 and 0300 h. The minimum RuT occurred around the AM feeding (0600 to 1000 h) after which RuT gradually increased during the day. There was a positive association between RuT and mean daily THI during the bolus data collection period ($P < 0.001$). The data obtained from our study demonstrated that the variation in RuT follows daily THI and that the association between RT and RuT is positive. Therefore, RuT enables a sensitive prediction of RT when cows are exposed to high ambient temperatures.

Key Words: dairy cows, heat stress, rumen temperature

1282 Activity and rumination in an organic vs. a conventional grazing herd.

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The objectives of this study were to evaluate activity and rumination of organic and conventional Holstein and crossbred cows during the grazing and winter months and to investigate the correlation between ambient air temperature and daily rumination and activity. The study was conducted for 2 yr (March 2014 to March 2016) at the University of Minnesota West Central Research and Outreach Center, Morris grazing dairy. During the grazing season (May to October) organic cows were on pasture and supplemented with 2.72 kg of corn per cow per day whereas conventional cows were supplemented with a TMR of corn silage, alfalfa haylage, corn, soybean meal, and minerals. During the winter season, both organic cows and conventional cows were supplemented with a TMR. Activity and rumination time (daily and 2-h periods) were monitored electronically using HR-LD Tags (SCR Engineers Ltd., Netanya, Israel) for the 2-yr period. Activity is reported in "activity units" from SCR DataFlow II software. The PROC MIXED of SAS was used for statistical analysis, and independent variables were herd (conventional or organic), month (January to December), year and their interactions, and date was a random effect. Daily activity was greater ($P < 0.05$) for the organic herd compared to the conventional herd (544 vs. 533), respectively. Daily rumination (min/d) was also greater ($P < 0.05$) for the organic herd (553 min/d) compared to the conventional (538 min/d) herd. Daily activity was greatest ($P < 0.05$) during July (791) and least during January (334) for the organic herd, and greatest ($P < 0.05$) during July (752) and least during January (289) for the conventional herd. Daily rumination was greater ($P < 0.05$) during December (592 min/d) compared to July (482 min/d) for the organic herd, and was greater ($P < 0.05$) during December (563 min/d) compared to March (496 min/d) for the conventional herd. Greater daily rumination of cows on a herd basis was negatively correlated (−0.39) with increased ($P < 0.01$) ambient air temperature in the organic herd, and there was a slight negative correlation (−0.10, $P < 0.01$) of daily rumination and air temperature in the conventional herd. In summary, organic cows had greater daily activity, and greater daily rumination compared to conventional grazing cows. Monthly activity and rumination patterns of grazing organic and conventional dairy cattle in this study were influenced by the weather.

Key Words: rumination, organic, activity

1283 Understanding behavior patterns of cattle adaptation to heat stress.

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Changes in climate may have negative effect on livestock that will have to adapt to more extreme environment in the near future. Therefore understanding how different breeds developed mechanisms to thrive under extreme conditions may help livestock production. This research compared the movement, ruminating time and weight gain between 2 breeds, Nellore (indicine, n = 24, 210 ± 15 kg) and Angus (taurine, n = 24, 227 ± 25kg) aging 10 mo and kept for 80 d at pasture during tropical spring (average temperature 26°C, maximum 32.2°C, minimum 21.5°C). Animals were sons of the same bull (Nellore or Angus) to minimize genetic variation. Concentrate supplement was provided twice a day (1.5% LW/day), netted shade was available (80% sun block, 10 m^2/animal). Animal motility (using an accelerometer, measured

relative movement-RM) and rumination time (minutes/day, using a sound sensitive sensor) were evaluated through a collar-sensor (SCR, Systems Heat time) by radio telemetry. Live weight (kg) was measured with a chute scale every 15 d. Data were compared by unpaired *t* test, two-way ANOVA and Pearson correlation analysis. We observed that Angus remained under the netted shade during daytime and grazed after sunset, Nellore on the other hand stayed on the sun despite the available shade. Nellore (781 ± 16 RM) moved less ($P < 0.001$) than Angus (919 ± 17 RM) but ruminated for longer periods ($P < 0.0001$; Nellore: 496 ± 9 min/day) compared to Angus (370 ± 8 min/day). Nellore (268 ± 27 kg) were lighter ($P = 0.0003$) than Angus 303 ± 24 kg) at the end of the 80 d period, average daily gain was lower ($P = 0.029$) in Nellore (0.65 ± 0.04 kg/day) compared to Angus (0.85 ± 0.05 kg/day). In summary Nellore moved less and ruminated more compared to Angus. It is possible that a reduction on movement is part of the Nellore adaptation to heat stress. By being less active Nellore produces a lower amount of heat to be dispersed but to move less, it selects the grass ingested in a worst way. The consequence is a need to ruminate more that can be done without much muscle activity and less heat production. Despite of moving more and ruminating less, Angus animals were more efficient than Nellore considering average daily gain. Samples from blood, muscle, skin, liver and semen were collected to be evaluated for metabolic, gene expression and epigenetic modifications induced by heat stress.

Key Words: Nellore, Angus, time ruminating

1284 Plasma insulin and glucose concentrations of feedlot cattle during summer.

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Periods of heat stress are typically associated with an increase in basal insulin (INS) concentration and a decrease in basal glucose (GLU) concentration, thereby altering energy metabolism. The purpose of this study was to investigate circulating INS and GLU of shaded and un-shaded *Bos indicus* and *Bos taurus* feedlot cattle during summer. Thirty-six steers (12 Angus, Charolais and Brahman) with an initial BW of 318.5 ± 6.7 kg were used in a 180 d feedlot study with 2 treatments: un-shaded and shaded (3 m^2/animal; 90% solar block shade cloth). There were 6 steers (2/breed) per pen (162 m^2) and 3 pens/treatment. Blood samples were collected via jugular venepuncture on 5 occasions (period 1 to period 5). Plasma concentrations of INS and GLU were analyzed using a repeated measures model (PROC MIXED; SAS Inst. Inc. Cary, NC). Plasma INS were highly variable across breed × treatment groups, therefore concentrations were Log_{10} transformed analysis. The model included breed ($P = 0.03$; $P = 0.03$), treatment ($P = 0.81$; $P = 0.97$), period ($P < 0.0001$; $P = 0.0003$), treatment × breed ($P = 0.38$; $P = 0.39$), treatment × period ($P = 0.06$; $P = 0.09$), breed × period ($P = 0.03$; $P < 0.0001$) and treatment × breed × period ($P = 0.50$; $P = 0.48$) as fixed effects for Log_{10} INS and GLU (mmol/L), repectively. Pen nested within treatment and treatment × breed × animal ID nested within pen were included as random effects. Overall the Brahmans had higher plasma GLU than Angus, particularly during periods 1 ($P < 0.0001$) and 2 ($P = 0.003$). However as days on feed increased, the variability of GLU on a breed × treatment group basis decreased. There was a trend for increasing INS and GLU over time, which can be partly explained by the high starch, high energy diet that was fed. In other species, feeding diets with a high glycaemic index is known to be associated with insulin resistance characterized by persistent hyperglycemia despite increased insulin secretion. In the current study, plasma GLU concentrations increased but GLU homeostasis was maintained but with a marked increase in circulating INS. Together these results may indicate the development of insulin sensitivity in feedlot cattle during summer on a diet designed for weight gain and fat deposition.

Key Words: feedlot cattle, glucose, heat stress, insulin

1285 Impact of heat stress on immune status of sheep.

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The objective of this study was to examine the effects of heat stress on sheep physiology. Australian Merino wethers (n = 144; 44.02 ± 0.32 kg) were randomly allocated to treatment in a climate controlled facility (CCF: 4 rooms; 3 pens/room; 6 sheep/pen; pen = 2.32 m^2). The treatments were: hot (HOT) and thermoneutral (TN). Treatment were replicated 4 times and each replication ran for 29 d. Dry bulb temperature (DBT) and relative humidity was obtained every 10 min. From these data a temperature humidity index (THI) was calculated: THI = DBT– {(0.31– 0.31× RH/100) × (DBT– 14.4)}. During HOT means for DBT, RH and THI were: 32.5 ± 0.40°C, 62.5 ± 7.22% and 30.5 ± 0.55, respectively. During TN the values were 19.7 ± 0.40°C, 79.9 ± 7.22% and 19.4 ± 0.55. Respiration rate (RR) were obtained 3 hly between 0800 and 1700 h. Rumen temperature (TRUM) was recorded at 10 min intervals using RFID rumen temperature boluses. Blood (2 × 10 mL) was collected by jugular venipuncture on entry and then every 7 d. Plasma concentrations of interleukin-1β (IL-1β), interferon-γ, tumor necrosis factor α, lipopolysaccharides (LPS), haptoglobin, alkaline phosphate (ALP), γ-glutamyl transpeptidase (GGT), creatine kinase (CK) and creatinine were determined. The MIXED procedure (SAS Inst. Inc. Cary, NC) was used. The model fitted included terms for replicate and treatment, a term for collection and a collection × treatment interaction. Mean RR of HOT was greater ($P < 0.01$)

at 140.0 ± 3.55 breaths per minute (bpm) compared with TN at 74.9 ± 3.55 bpm. The HOT group had a greater ($P < 0.05$) TRUM (40.4 ± 0.03°C) than the TN group (39.9 ± 0.04°C). ALP ($P = 0.0003$), GGT ($P = 0.0158$) and IL-1β ($P < 0.05$) were all lower in the HOT sheep. Creatinine concentration ($P = 0.0038$) and CK ($P > 0.05$) were higher in the HOT sheep. LPS concentration was greater ($P < 0.05$) in HOT compared with TN. The remaining parameters were not affected ($P > 0.05$) by treatment. Elevated CK, creatinine and TRUM suggest that the HOT sheep were heat stressed. There is some evidence pointing to impaired immune status. However, the data is equivocal, and in some cases confounding (e.g., greater IL-1β expression in TN, but greater LPS in HOT).

Key Words: sheep, heat stress, blood parameters

1286 Stocking rates and parasite load in yearling steers grazed season long in the Northern Great Plains.

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Intestinal parasitism of grazing ruminants can result in poor performance and compromised systems, especially in younger animals. Twelve pastures (12.9 ± 0.8 ha) were stocked at four stocking rates: light 1.83 ± 0.38 AUM · ha^{-1}, moderate 3.26 ± 0.30 AUM· ha^{-1}, heavy 4.98 ± 0.78 AUM · ha^{-1}, and extreme 6.18 ± 0.68 AUM · ha^{-1}. Yearling steers (317 ± 32 kg) were grazed on the pastures from mid-May to mid-September, 2015. Before turnout, the steers were dewormed with an injectable dewormer, as well as implanted with Revalor GTM to maximize live weight gains. The steers were also supplemented with dry distillers grains with solubles at 0.3% of body weight. Steers were weighed monthly during which time fecal grab samples were collected. Results demonstrated that initially the worming treatment before turnout proved effective in the early part of the grazing season as there was no difference ($P > 0.05$) among treatments in egg counts per gram (epg) in June, with corresponding low epg. However, a significant difference ($P < 0.05$) in epg was detected between the light and extreme treatment groups in July, with low levels in the light treatment, and higher levels in the extreme treatment. Egg counts over 35 epg, which has been proved as a performance threshold in grazing yearling cattle, were noted in individual animals on all treatments except the lightly grazed treatment in August and September. This study demonstrates an association between high stocking rates and increases in detectable parasite load, and supports the conclusion that individual yearling cattle that are susceptible to parasitism may be negatively impacted by season long systems that are stocked from moderate to extreme levels in the northern Great Plains.

Key Words: parasitism, northern Great Plains, yearling cattle, season long grazing

PRODUCTION, MANAGEMENT AND THE ENVIRONMENT SYMPOSIUM: IMPACTS OF LIVESTOCK PRODUCTION ON ENVIRONMENTAL REACTIVE NITROGEN

1287 The world's nitrogen cycle and human impacts.

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Perhaps 40% of the people alive today are sustained from increased grain yields attributed to the use of synthetic nitrogen fertilizer. While the Haber-Bosch process of converting atmospheric nitrogen to ammonia (i.e., fertilizer) has transformed agricultural production, it has also caused an unprecedented shift in the global nitrogen balance. Despite many improvements in nitrogen use efficiency in both crop and livestock systems, a large fraction of agricultural nitrogen inputs are lost to the environment. This "fugitive" nitrogen is causing a host of environmental problems at local and global scales. Excess nitrogen has been shown to alter biogeochemical processes and ecosystem function across the globe. Because nitrogen can be easily transported in water or air through natural processes, or by the transport of grain and livestock; the impacts of agriculture nitrogen are often observed far from where the nitrogen was initially used. A good example of this process is the observed increases in the atmospheric deposition of reactive nitrogen across many areas, including many pristine ecosystems. Nitrogen deposition is often linked to ammonia-derived aerosols, compounds that can travel hundreds of kilometers from the source before being redeposited back to the surface. Because livestock account for over 50% of all ammonia emissions in many regions; beef feedlots, dairies, and swine and poultry operations are often linked to this air quality issue. While there is no question that livestock ammonia emissions are large, quantifying the actual impact of reactive nitrogen on the environment is a complex question. One must consider atmospheric transport at both local and regional scales, chemical reactions with pollutants from other industries, and other non-livestock sources and forms of nitrogen. Perhaps nowhere has this issue been more investigated than along the Front Range of Colorado, where a mature cattle feeding industry is located relatively close to the pristine ecosystems in Rocky Mountain National park. This presentation will begin with the role of livestock in the global and U.S. nitrogen cycle, and then narrow the scope to specific issues facing livestock producers in Colorado regarding atmospheric ammonia. Summary comments will suggest how animal scientists and industry leaders might respond to these growing concerns.

Key Words: Colorado producers, atmospheric ammonia, nitrogen

1288 Reactive N emissions from beef cattle feedlots. R. W. Todd*, H. M. Waldrip, D. B. Parker, and N. A. Cole, *USDA Agricultural Research Service, Bushland, TX.*

Large amounts of nitrogen (N) are fed to meet the nutritional needs of beef cattle in feedlots. However, only from 10 to 15% of fed N is retained in animals. Most N is excreted. Chemical and biological processes transform manure N into ammonia (NH_3), nitrous oxide (N_2O) and nitrate (NO_3^-). These reactive forms of N (N_r) are those most readily lost into the environment. Our objectives are to outline the forms and impacts of N_r lost from beef feedlots, present patterns and magnitudes of emissions, and examine ways to mitigate emissions. We will focus on NH_3, the major form of $N_r$emitted from beef feedlots. Fugitive NH_3 is a precursor to particulates in the atmosphere that cause air quality problems or overburden N-sensitive terrestrial ecosystems and initiate species changes and loss of diversity. Reactive N contributes to the eutrophication of surface waters and the creation of hypoxic zones in the Gulf of Mexico. Nitrous oxide is a greenhouse gas with almost 300 times the global warming potential of carbon dioxide (CO_2). Stringent regulations to control runoff have virtually eliminated NO_3^- as a source of N_r from beef feedlots. Direct N_2O emissions from beef cattle production are only about 0.1% of the national greenhouse gas inventory of CO_2–equivalent emissions. However, animal agriculture is the major source of U.S. NH_3 emissions (81%), and beef cattle production contributes about 15% to the total national NH_3 emissions. Research on NH_3 emissions has matured to where we have a good understanding of the pattern and magnitude of emissions. Ammonia volatilization depends on temperature, reflected in the daily and annual patterns of emission, with peak emissions during the warmest time periods. The magnitude of NH_3–N emissions is consistent across the cattle-feeding region from Texas to Nebraska. Reported winter emissions range from 25 to 35% of fed N, while summer emissions range from 50 to 75% of fed N. Research on multiple scales shows that crude protein content of diets is a critical driver of emissions. Diets that meet NRC guidelines for crude protein lose about 50% of fed N as NH_3–N. Diets with byproducts like distillers grains often exceed recommendations, with increases in NH_3 emissions from 25 to 50%. Several technologies offer promises of NH_3 emission mitigation, but most are expensive and hard to apply. Carefully managed cattle diets remain the most effective and practical way to limit the loss of NH_3 from beef feedlots.

Key Words: nitrogen

1289 Reactive nitrogen losses from dairy production systems. A. B. Leytem*[1] and C. A. Rotz[2], *[1]USDA-ARS, Kimberly, ID, [2]USDA-ARS Pasture Systems and Watershed Management Research Unit, University Park, PA.*

Reactive nitrogen (N_r) losses from dairy production vary depending on housing type, manure storage system, and manure land application practices. To illustrate on farm N_r losses, we compared 3 systems: a dry-lot in ID with 213 lactating and 137 young cattle, a free-stall operation in NY with 1,261 lactating and 925 young cattle, and a free-stall and grazing operation in the Netherlands (De Marke) with 78 lactating and 57 young cattle. The De Marke farm was designed to reduce N_r losses through an efficient feeding program, barn flooring to reduce ammonia (NH_3) losses, enclosed manure storage, injection of manure on cropland and the use of cover crops. Farms were modeled using the Integrated Farm System Model (IFSM) to estimate N_r losses and evaluate effects of mitigation strategies on the ID and NY dairies. Total estimated Nr losses ranged from 5,727 to 139,455 kg N yr^{-1} and comprised 34%, 46% and 50% of imported N from the ID, NY, and De Marke dairies, respectively. The N_r lost per animal equivalent (AE) was 121, 98, and 65 kg N AE^{-1} for the ID, NY, and De Marke dairies, respectively. The N_r losses differed between production systems with 80% of N_r lost as NH_3 (63% from housing) on the ID dairy, while the NY dairy lost 49% of N_r as NH_3 (52% land application of manures) and 46% due to leaching from crop fields. On the De Marke dairy the majority of N_r loss was due to leaching from crop fields and pasture comprising 52% of total N_r lost. To mitigate N_r losses at the ID dairy, strategies targeted the housing sector by feeding a balanced ration that reduced overall dietary CP, reducing housing emissions by 10 kg AE^{-1}along with a 1 kg AE^{-1}reduction from manure storage. Immediate incorporation of land applied manure decreased N_r losses by 1.7 kg AE^{-1}. These combined practices led to a 12.5% reduction in total N_r lost. A reduction in dietary CP on the NY dairy coupled with covering the lagoon reduced N_r losses from housing and manure management combined by 5.4 kg AE^{-1}, while immediate incorporation of land applied manure reduced field losses by 7.8 kg AE^{-1}. These practices combined reduced total farm N_r loss by 27%. While Nr losses from dairy production can be large, mitigation strategies are available, however they must be targeted to address issues within each production system individually to ensure system-wide reductions.

Key Words: nitrogen, dairy production, environment

1290 Reactive N emissions from crops and pastures.
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1291 Measurement and mitigation of reactive nitrogen species from swine and poultry production facilities.
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Reactive nitrogen (Nr) species include oxides of nitrogen (nitric oxide, nitrogen dioxide and nitrous oxide [N_2O]), anions (nitrate and nitrite) and amine derivatives (ammonia [NH_3], ammonium salts and urea). Of the different Nr species, air emissions from swine and poultry facilities are dominantly NH_3 followed by N_2O. Excreta emissions are NH_3, ammonium ions, and urea with trace amounts of nitrate and nitrite. Farm systems and practices that handle manure as a wet product without pH modification favor almost exclusive NH_3 production while systems and practices associated with dry manure handling and bedded systems emit more NH_3 and result in greater N_2O production than that produced in wet systems. Results from a turkey grow-out study estimated that just under 1% of consumed nitrogen was emitted as N_2O from housing, compared to just under 11% emitted as NH_3. Despite generally lower N_2O emissions from animal housing compared to crop field emissions, N_2O emissions from housing are greater than often estimated. Lagoon systems emit more N_2O than either slurry or deep pit swine systems. Deep pit swine buildings emit as much as two-thirds less N_2O than deep bedded swine systems and laying hen, broiler chicken and turkey buildings emit over 4 times as much N_2O as swine housing, on an animal unit basis. Critical control points for mitigation center on 1) reducing the amount of nitrogen excreted and therefore excreted nitrogen available for loss to air or water during housing, manure storage or following land application of manures, 2) capturing excreted nitrogen to prevent release of nitrogen-containing compounds to air, water or soil resources or 3) conversion/treatment of nitrogen-containing compounds to non-reactive nitrogen gas.

Key Words: air emissions, poultry, swine

1292 Modeling atmospheric reactive nitrogen.
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Nitrogen is an essential building block of all proteins and thus an essential nutrient for all life. Reactive nitrogen, which is naturally produced via enzymatic reactions, forest fires and lightning, is continually recycled and cascades through air, water, and soil media. Human activity has perturbed this cycle through the combustion of fossil fuels and synthesis of fertilizers. The anthropogenic contribution to this cycle is now larger than natural sources in the United States and globally. Until recently, little progress has been made in modeling of the nitrogen cycle in the environment due to the complexity of and uncertainty in its transport and transformation between soil, water and atmospheric media. The lack of understanding of these multimedia transport processes is due to the typical focus of research on specific media and the difficulty in parameterizing the human dimension of anthropogenically fixed reduced nitrogen and input into the environment, primarily through mineral fertilizer application to crops, the largest source of environmental reactive nitrogen. Here we will focus on modeling of the atmospheric component of the nitrogen cascade, with an emphasis on ammonia, emerging measurement techniques, and the potential for model improvements using emerging measurements, existing networks and modeling. The USEPA's Community Mulitscale Air Quality (CMAQ) model will be evaluated against observational trends in nitrogen deposition and ambient air quality from 2002 to 2012 and the sensitivity of CMAQ to NH_3 emissions will be explored. These findings will be presented with an emphasis on how the sensitivity of the modeling system to animal husbandry emissions and how the representation of these emissions can be improved.

Key Words: nitrogen cycle, emissions, environment

BIG DATA IN ANIMAL SCIENCE: USES FOR MODELS, STATISTICS AND META-APPROACHES

1293 Modeling in animal science: an introduction to quantitative understanding and prediction.
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In animal science, continuous advances in technology, computing, and engineering result in the generation of data at a rapidly increasing rate. Mathematical models enable quantitative analysis and integration of data to study the behavior and complexity of biological systems. This review highlights several aspects of modeling in the context of understanding, predicting and modifying complex processes in farm animal systems, and offers a current perspective for animal scientists without requiring specialized knowledge of mathematics or bioinformatics. A mathematical model is an equation or set of equations which represents the behavior of a system, and can be viewed as an idea, hypothesis or relation expressed in mathematics. In animal science, the system may range from the molecules in cells up to herd or flock level, with any level of the system being composed of subsystems lying at a lower

level, or being a subsystem of higher level systems itself. In empirical models, experimental data are used directly to quantify relationships based at a single level. Alternatively, mechanistic models are process-based and seek to understand causation in the system of interest by describing a system level in terms of components and associated processes at subsystem levels. Furthermore, models may be static, capturing behavior of the system at a particular point in time, or dynamic, describing how quantities in the system change with time. Several key benefits have been attributed to modeling. First, models can provide an integrative, quantitative understanding of mechanisms and associated relationships between responses of a system at various levels. Second, building a model may pinpoint areas where data or knowledge are lacking, and may indicate priorities for further research and development. Third, models provide quantitative assessments of management practices for the animal production sector including policymakers. This aspect becomes particularly important when observations are hardly possible because of time scale (changes emerging after several years or decades only) or technical difficulty of measurements. Two areas are in need of further development. Emerging–omics data on genetic and metabolic regulatory networks at the molecular and cellular level require further modeling methodology efforts to integrate such data with processes at a higher system level. Second, further advances in understanding and prediction at integrated levels will be obtained on combination of models that differ in underlying methodology. Examples include the integration of mechanistic models of animal metabolism with linear programming and life cycle assessment models.

Key Words: modeling; animal science; system

1294 Traditional versus structure-based model development strategies. L. O. Tedeschi[*1], R. R. White[2], C. F. Nicholson[3], B. L. Turner[4], M. A. Fonseca[1], and M. D. Hanigan[2], *[1]Texas A&M University, College Station, [2]Virginia Tech, Blacksburg, [3]The Pennsylvania State University, University Park, [4]Texas A&M University-Kingsville, Kingsville.*

An important challenge in agriculture modeling is deciding how to mathematically represent biological phenomena. The objective of this paper is to compare more traditional model development methods (e.g., empirical models) with structure-based modeling (SBM) such as system dynamics (SD). Substantial overlap exists between traditional and SBM approaches, but there are important differences. The overall steps of the modeling process and scientific rigor are quite similar, but their focus and implementation can differ substantially. The steps of both modeling approaches often comprise the 1) identification of a problem (research objective), 2) formulation of the mathematical (and/or statistical) statements, 3) data collection (experimentation), 4) model evaluation and quantitative analysis relevant to the modeling objectives. SBM often differs from traditional approaches in each of these phases such as defining the problem as the replication of observed dynamic behavioral modes (e.g., s-shaped growth or oscillations) rather than situational point prediction or statistical estimation of parameters (step 1), giving more attention to system structure based on cause-effect relationships in terms of the stock-flow (i.e., level variables and rate variables) and feedback processes that generate observed behavior and visualizing these relationships in causal loop diagrams (CLD) and stock and flow diagrams (SFD) (step 2), and data collection that encompasses a broader range of sources (experimental, secondary, expert opinion, participatory exercises) and may include concepts hypothesized to be important but for which limited data are available (step 3). Model evaluation criteria can also differ due to the intrinsic nature of SBM as greater focuses are given to behavioral mode replication and feedback loop dominance analysis (step 4). In general, traditional modeling approaches focus on defining analytical functions and their statistical consistency with observed biological responses, whereas SBM focus on the mechanistic explanations for system behaviors and the feedback relationships that led to them. For example, a traditional modeling approach could use a saturating function to describe movement of a substrate across a membrane, whereas SBM would focus on feedback processes that represent decreasing affinity of the membrane for that substrate as concentration increases. Although they can differ substantially in their implementation, these 2 mathematical modeling strategies should be viewed as complementary rather than competing tools.

Key Words: modeling, simulation, methodology

1295 Big data analysis techniques. N. St-Pierre*, *Ohio State University, Columbus.*

The term ‘big data’ has recently entered our lexicon. Data scientists and statisticians have loosely defined big data as datasets with billions (10^9) of rows (tupples) of data. Hence, very few datasets in the animal sciences would qualify as true big data. At best, we deal with large datasets in the millions of tupples. Regardless, some of the same issues surrounding big data analyses are shared with large data: 1) near certainty of the presence of outliers, and 2) low signal to noise (irrelevant variables, subtle relationships, data imbalance, near collinearity). In large datasets, outliers are more than unidimensional: higher dimensions must be scrutinized. An example of this involved the characterization of feed composition data. Techniques used to address the low signal to noise issue can be classified into 2 groups: opaque techniques and black box techniques. The most prevalent techniques in the first group are: visualization through smoothing, regression, principal component analysis (PCA), decision trees, clustering methods, and multivariate adaptive splines (MARS). Black box techniques include neural networks, k-nearest neighbor

(KNN), K-mean, support vector machines and genetic algorithm. Each technique will be briefly explained using an example. With PCA, we first find a direction that has maximum variance. A second direction is then found, which has maximum variance of all directions perpendicular to the first. The process is repeated until there are as many directions (vectors) as original variables. Advantages of PCA are the dimension reduction and the ability to handle more predictors than observations. Disadvantages are that they often lack interpretation, and are linear models. Issues when only summary statistics are available (i.e., meta-analysis) will be explained, including the importance of properly weighing observations and accounting for the inherent blocking in the meta-design.

Key Words: big data, principal component analysis, meta-analysis

1296 Evaluation of multilevel mixed effect models.

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Simple mixed effect models have been extensively used in animal science literature. However, in some instances biological relationships require that models account for deviations of individual animals from that of the population. Furthermore, some animals might share similar genetic background because they are closely related (e.g., pig littermates) thus specification of animal within litter relationship (i.e., nested random effects) is necessary to model the hierarchical data structure. In some cases measurements taken on the same individual may not be independent (e.g., weekly BW measurements). This will result in models with heteroskedastic and serial correlated errors, which need to be evaluated and the errors minimized. Recent developments in statistical theory and computational power allow for specification of multilevel mixed effect models, especially nonlinear models. To demonstrate implementation of such models, an example is provided using data collected from an experiment with 40 pigs of 3 sexes originating from 17 litters and their BW measured weekly or every 2 wk up to 1,007 d. A multilevel mixed effects model was used within a growth function because it allows for estimation of all growth profiles simultaneously, and different sources of variation. Furthermore, variance in-homogeneity and within-animal correlation were introduced to the growth function. In the basic model, the variance was assumed to equal to identity matrix, i.e., the within-animal errors are independent, identical and random vectors. The basic model fit suggested that the within-animal variability increased with increasing BW and auto-correlation was also present. The variance-covariance matrix was then relaxed and decomposed into variance structure component and a correlation structure component that allows specification of model variance heterogeneity and serial correlation. Variance of the within-animal errors was modeled using a variance function, which when implemented reduced Bayesian Information Criteria (BIC) values to 8,950 compared to 9,861 for the basic model but did not remove the strong auto-correlation in the residuals. A continuous time autoregressive process of first order was applied to the within-animal errors because it deals with unequally spaced observations. This further reduced BIC to 7,146 due to removal of the serial correlated errors and thus inclusion of a continuous auto regressive process of first order is recommended when modeling frequently sampled growth data.

Key Words: multilevel mixed effect model, variance structure, autocorrelation

RUMINANT NUTRITION

1297 Effect of lactose inclusion in calf starters on rumen fermentation of weaned calves.

A. Saegusa*[1], K. Inouchi[2], M. Ueno[3], Y. Inabu[4], S. Koike[3], T. Sugino[4], and M. Oba[5], *[1]ZEN-RAKU-REN, Fukushima, Japan, [2]ZEN-RAKU-REN, Nishi-shirakawa, Japan, [3]Hokkaido University, Sapporo, Japan, [4]Hiroshima University, Higashi-hiroshima, Japan, [5]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada.*

The objective of this study was to evaluate the effects of lactose inclusion in calf starters on ruminal pH and VFA profile. Sixty Holstein bull calves were raised on an intensified nursing program using milk replacer containing 28% CP and 15% fat, until 56 d of age. Calves were fed texturized calf starters containing lactose at 0% (Control), 5.0% (LAC5), or 10.0% (LAC10; $n = 20$ for each treatment) on a DM basis. All calf starters were formulated for 23.1% CP. All calves were fed treatment calf starters ad libitum from d 7 and their hay (Klein grass) intake was limited to 150 g/d (as fed). Ruminal pH was measured every 2 min using small ruminant rumen pH loggers (Dascor, CA) immediately after weaning (d 55 to 62) for 15 calves (5 calves per treatment), and 3 wk after weaning (d 77 to 80) for the other 45 calves (15 calves per treatment). Daily mean, minimum, maximum ruminal pH, and duration and area under rumen pH 5.8 were not affected by treatment for both periods (d 55 to 62 and d 77 to 80). However, Spearman's correlation coefficient (r_s) was 0.306 ($P < 0.05$) between lactose intake and minimum ruminal pH for d 77 to 80, indicating that actual lactose consumption may affect ruminal pH. In addition, hay intake was not affected by treatment, but it was positively correlated with daily mean ($r_s = 0.338$, $P < 0.05$) and maximum ruminal pH ($r_s = 0.408$, $P < 0.01$), and the variation in hay intake might have masked treatment effects on ruminal pH. Ruminal molar ratio of acetate (mean ± SE) was 40.6 ± 1.26 (Control), 42.8 ± 1.26 (LAC5), and 45.3 ± 1.26% (LAC10), molar ratio of propionate was 40.2 ± 0.98 (Control), 38.1 ± 0.98 (LAC5), 35.3 ± 0.98% (LAC10), and acetate/propionate ratio was 1.01 ± 0.06 (Control), 1.15 ± 0.06 (LAC5), 1.29 ± 0.06% (LAC10) on d 80, and the differences were significant

between Control and LAC10 ($P < 0.05$) for ruminal fluid samples collected on d 80. However, molar ratio of butyrate was not affected by treatment. These results indicate that inclusion of lactose in calf starter affects ruminal VFA profile, but its effects on rumen pH warrants further investigation.

Key Words: calf, lactose, rumen

1298 Methionine:lysine ratio for crossbred suckling calves fed milk replacer and an amino acid complex. J. C. Chagas[1], M. A. Ferreira[1], M. R. Entjes[2], F. S. Machado[3], L. F. Costa e Silva[4], and M. I. Marcondes[*5], *[1]Universidade Federal Rural de Pernambuco, Recife, Brazil, [2]VHL University of Applied Sciences, Leeuwarden, Netherlands, [3]EMBRAPA, Juiz de Fora, Brazil, [4]Universidade Federal de Vicosa, Vicosa, Brazil, [5]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Brazil.*

Knowledge about the amino acid (AA) requirements of dairy cattle is rare, and information regarding limiting AAs for suckling calves does not exist. Due to the difficulties in studying the AA requirements for ruminants, research is necessary to evaluate and determine optimal levels when including these AAs in the diet. Based on studies demonstrating lysine (Lys) and methionine (Met) as limiting AAs for neonates, we hypothesized that it is possible to determine the Met:Lys ratio that maximizes the performance of suckling dairy calves. This study evaluated the effect of increasing dietary Met:Lys ratios (DMLR) on performance and body composition of crossbred suckling calves of two different ages. Thirty-six male calves (Holstein-Gyr) were introduced in the experiment on the eighth day of age and randomly distributed among two slaughter ages (16 animals slaughtered at 30 d of age, and 20 animals slaughtered at 60 d of age) and four DMLR (44, 48, 52, and 56%), which were provided in the form of an AA complex (18.93 g) added to 905 g of milk replacer. The experimental diets were provided without permission of refusals, so the intake of dry matter and nutrients were the same for all animals, regardless of DMLR. Average daily gain (ADG), gain composition and body composition were evaluated separately for the two age groups for the linear and quadratic effects of DMLR. When necessary, the linear-plateau model was adjusted. Calves from 0 to 30 d of age did not show an improved performance due to increased DMLR; it is possible that animals up to 30 d of age had other metabolic priorities over body growth and protein deposition. For calves from 30 to 60 d of age, a linear-plateau response was observed for ADG and crude protein gain (CP); the greatest ADG observed was 590 g/d for a DMLR of 52.56% ($P = 0.001$), and the greatest CP deposition observed was 89 g/d for a DMLR of 52.33% ($P = 0.027$). Total body CP presented a quadratic behavior, with a maximum of 11.72 kg of CP for a DMLR of 53.91% ($P = 0.040$). The increased DMLR did not influence performance of calves from 0 to 30 d, and the optimal DMLR that ensured the best performance of calves from 30 to 60 d of age was situated between 52 and 54%.

Key Words: bovine, body composition, crude protein

1299 Effects of organic or inorganic Co, Cu, Mn, and Zn supplementation to weaned calves during preconditioning on their productive and health responses. K. Lippolis[*1], R. F. Cooke[1], L. G. T. da Silva[2], K. M. Schubach[1], A. P. Brandao[1,2], R. Marques[1], C. K. Larson[3], T. DelCurto[4], and D. W. Bohnert[1], *[1]Oregon State University- EOARC Burns, Burns, [2]UNESP- FMVZ, Botucatu, Brazil, [3]Zinpro Corporation, Eden Prairie, MN, [4]Oregon State University- EOARC Union, Union.*

This experiment compared productive and health parameters of weaned calves receiving or not supplemental Co, Cu, Mn, and Zn from an organic or inorganic source during a 45-d preconditioning program. Ninety Angus × Hereford calves were weaned on d −1 and immediately allocated according to weaning BW and age (BW = 261 ± 2 kg, age = 224 ± 2) to a18-pen drylot with 5 calves per pen (steers, $n = 4$; heifers, $n = 1$). Pens were randomly assigned to receive: 1) supplementation with inorganic sulfate sources of Cu, Co, Mn, and Zn (INR), 2) supplementation with an organic source of Cu, Mn, Co, and Zn (ORG; Availa®4; Zinpro Corporation, Eden Prairie, MN), and 3) no supplementation of Cu, Co, Mn, and Zn (CON). During the preconditioning phase (d 0 to 45), calves received mineral treatments while offered free-choice hay and 2.7 kg/d of corn-soybean meal concentrate. The INR and ORG were included into the concentrate, and formulated to provide the same daily amount of Cu, Co, Mn, and Zn. Calf ADG during preconditioning was calculated based on average initial BW (d −1 and 0) and final BW (d 44 and 45). Liver samples were collected via needle biopsy on d 0, 22, and 45. Calves received vaccination on d 15 and 29. Blood samples were collected on d 15, 29, and 45, and analyzed for plasma concentrations of antibodies against *Mannheimia haemolytica*. No differences were detected ($P \geq 0.15$) among CON, INR, and ORG calves for initial (d 0) liver Co, Cu, Mn, and Zn concentrations. On d 22 and 45, liver Cu and Co concentrations were greater ($P < 0.01$) for INR and ORG calves compared with CON. Moreover, ORG calves had greater ($P = 0.05$) liver Co concentrations on d 45, but similar ($P = 0.35$) liver Co on d 22 and similar ($P \geq 0.63$) liver Cu on d 22 and 45 compared with INR calves. Liver Zn and Mn concentrations were similar ($P \geq 0.14$) among CON, INR, and ORG calves on d 22 and 45. No differences ($P \geq 0.17$) were detected among treatments for feed intake, BW gain, health variables, or antibodies against *M. haemolytica*. Therefore, supplementation with inorganic or organic Co, Cu, Mn, and Zn during a 45-d preconditioning period

did not impact performance and health response of weaned feeder calves.

Key Words: beef cattle, performance, preconditioning, trace minerals

1300 Dynamics of prepartum β-carotene supplementation among cow, colostrum, and calf. C. M. Prom*[1], M. A. Engstrom[2], and J. K. Drackley[1], [1]*University of Illinois, Urbana,* [2]*DSM Nutritional Products, LLC, Parsippany, NJ.*

Little is known about transfer of dietary β-carotene into colostrum, its absorption by the calf, and its effects on vitamins A and E in the cow when dietary vitamin A is adequate. Our objective was to assess the impact of β-carotene supplementation during the close-up dry period on the cow, colostrum, and calf. The study was conducted on a large commercial dairy farm in Indiana during early summer of 2015. Ninety-four multiparous Holstein cows were assigned to either control (CON) or β-carotene (BC) treatments. While locked in headgates each morning, each cow received a topdress of β-carotene (Rovimix, 8 g/d; provided 800 mg β-carotene) or carrier from 21 d before expected calving until calving. Blood samples were collected at 21 d before expected calving (before treatments began), 7 d before calving, immediately following parturition, and 7 d postpartum. Colostrum was collected immediately following parturition. Calf blood samples were obtained within 2 h of birth before receiving the dam's colostrum, at 24 h after birth, and at 7 d and 60 d of age. Blood serum was analyzed for vitamins A and E, cholesterol, and β-carotene. Colostrum was analyzed for β-carotene, vitamins A and E, and colorimetry profile. Data were assessed using the MIXED procedure in SAS. Calf serum β-carotene data were analyzed using the FREQ procedure. Compared with CON cows, BC cows had higher concentrations of β-carotene ($P < 0.01$), vitamin A ($P < 0.01$), and vitamin E ($P < 0.01$), and a greater vitamin E:cholesterol ($P < 0.01$) in serum at all times. Colostrum β-carotene was higher for BC cows ($P < 0.01$). Colostrum from BC cows had increased a* ($P < 0.01$) and b* ($P < 0.01$) colorimeter values, indicating that β-carotene altered colostrum color. Before receiving colostrum, the concentration of β-carotene in calf serum was below the detectable threshold of 0.05 ug/mL. At 24 h of age, the number of calves with detectable β-carotene concentrations increased, with more calves from BC cows (52.1%) having detectable concentrations than calves from CON cows (6.1%, $P < 0.01$). No differences in concentrations of vitamins A or E were observed in calves. In pregnant cows already receiving adequate vitamin A, supplementation of β-carotene increased concentrations of β-carotene, vitamin A, and vitamin E, increased concentration of β-carotene in colostrum, and increased serum β-carotene in calves.

Key Words: β-carotene, transition cows, colostrum

1301 Effect of supplementing increasing levels of RUP on growing performance in calves fed a silage-based diet. C. R. Oney*[1], R. G. Bondurant[1], F. H. Hilscher[1], A. K. Watson[1], G. E. Erickson[1], J. C. MacDonald[2], and T. J. Klopfenstein[1], [1]*University of Nebraska, Lincoln,* [2]*University of Nebraska-Lincoln, Lincoln.*

An 84-d growing study, utilizing 60 steers (initial BW = 290; SD = 18 kg), evaluated the effects of supplementing increasing levels of RUP on growing performance of calves fed a silage-based diet. All steers were individually fed using the Calan gate system. Five levels of supplementation were evaluated with 12 steers per level of supplement. Supplement levels consisted of 0, 3.25, 6.5, 9.75, and 13% RUP (as a % of diet DM). The RUP supplement consisted of 60% SoyPass and 40% Empyreal. The diet consisted of 85% corn silage with the remaining 15% of the diet being accounted for in the supplement (DM basis). Supplement included RUP, urea, minerals, and carrier replaced by RUP. Initial and ending BW were obtained by collecting BW across 3 consecutive days and averaging after cattle had been limit fed a 50% Sweet Bran and 50% alfalfa diet at 2% of BW for 5 d. Cattle were assigned to treatment based on d −1 and 0 BW. Interim BW were collected on d 36 and 37 and shrunk 4% to account for gut fill. There were no differences in DMI ($P = 0.33$) among treatments for period 1 (d 1 to 37). However, ADG ($P < 0.01$) and G:F ($P < 0.01$) both increased linearly as RUP inclusion increased during period 1. Using the NRC model, MP balance for period 1 increased from −200 to +65 g/d as RUP inclusion increased from 0 to 13%. At 9.75% RUP inclusion MP balance was reached at +2 g/d. There were no differences in DMI ($P = 0.16$), ADG ($P = 0.11$) or G:F ($P = 0.32$) for period 2 (d 38 to 84). For the overall growing period (d 1 to 84), as supplemental RUP inclusion increased from 0 to 13%, a linear increase was observed in ending BW ($P < 0.01$). With no difference in DMI ($P = 0.19$) between the five treatments, averaging 7.67 kg/d, and a linear increase in ADG ($P < 0.01$), G:F linearly increased ($P < 0.01$) from 0.148 to 0.174 as RUP inclusion increased. The MP balance increased from −186 to +98 g/d as RUP inclusion increased from 0 to 13%, at 9.75% RUP inclusion MP balance was reached at +26 g/d. Increasing the amount of RUP in silage growing diets increases ending BW, ADG and G:F by meeting MP requirements.

Key Words: corn silage, growing cattle, rumen undegradable protein

1302 The effects of a high- or low-plane of nutrition pre-weaning on growth and starter intake of group-housed calves. J. Haisan[*1], M. Oba[1], D. J. Ambrose[2], and M. Steele[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]Livestock Research Branch, Alberta Agriculture and Forestry, Edmonton, AB, Canada.*

The objective was to determine the effects of plane of nutrition, when fed through an automated calf feeder, on starter intake and growth of group-housed calves. Twenty-six female Holstein calves were fed 8L of colostrum in the first 36 h of life before being offered pasteurized whole milk and randomly assigned to either a HIGH (10L/d; n = 12) or LOW (5L/d; n = 14) plane of nutrition. All calves were allowed 2.5L of milk per meal until d 48 when a 10-d weaning transition began, where milk was reduced by 10% per day, resulting in all calves being weaned at d 58. Calf starter and water were provided ad libitum starting on d 3. Calves were housed in individual pens for the first 21 ± 3 d and fed using the Calf Rail system (Förster-Technik, Germany) before moving to a group pen where they were fed through an automated calf feeder. Individual starter intake was measured via an automated system on a daily basis from d 25 to 70, and body weights (BW) were measured weekly from birth to d 70. Blood samples were taken in the first week of life and with no differences observed in serum protein (5.3 ± 0.32 vs. 5.3 ± 0.32 mg/dL; P = 0.95) or immunoglobin concentration (17.67 ± 1.80 vs. 15.35 ± 1.80 g/L; P = 0.37). Birthweight of calves was not different between the treatment groups (40 ± 1.25 vs. 42 ± 1.25 kg; P = 0.27) however BW at d 70 was greater for HIGH than LOW calves (113.5 ± 2.03 vs. 100.11 ± 2.03 kg; P < 0.01). Pre-weaning average daily gain was greater for HIGH than LOW (0.90 ± 0.03 vs. 0.65 ± 0.03 kg/d; P < 0.01), however no difference was seen post-weaning (1.30 ± 0.06 vs. 1.29 ± 0.06 kg/d; P = 0.96). Before the weaning transition (d 42 to 48) starter intake (g/d) was greater in calves on the LOW than HIGH plane of nutrition (591 ± 89 vs. 1,273 ± 93, P < 0.01, respectively). Starter intake over the 10-d weaning transition tended to be greater for LOW than HIGH calves (1,490 ± 112 vs. 1,181 ± 116; P = 0.07), however post-weaning no difference was seen between treatments (2,723 ± 200 vs. 3,188 ± 200; P = 0.11). Results indicate that feeding more milk pre-weaning may suppress starter intake, however, the effect is not carried post-weaning and does not compromise growth.

Key Words: feeding system, group housing, starter intake

1303 Evaluation of stay strong for new born dairy calves. K. Froehlich[*1] and D. P. Casper[2], *[1]South Dakota State University, Brookings, [2]Dairy Science Department, South Dakota State University, Brookings.*

Stay Strong (SS) is a blend of essential oils designed to help diminish health challenges and stresses experienced by newborn calves. Current feeding inclusion rates are unknown to achieve optimal performance in the first 8 wk of life. Study objectives were to determine feeding inclusion rates of SS when added to milk replacer (MR) to achieve optimal performance, while comparing performance to a yeast cell wall (YCM) gut health technology. One hundred Holstein calves were used for the study blocked by birth date and randomly assigned to 1 of 5 treatments; 24:20 control MR (C), 24:20 MR with an inclusion rate of either 1.25 g (SS-0.5), 2.5 g (SS-1.0) or 3.75 g (SS-1.5) calf/feeding, or 24:20 MR with an inclusion of YCM at a rate of 2 g/calf/feeding. Calves were sourced from a commercial SD dairy farm where they were fed colostrum for the first 2d and then were transported to SDSU. 24:20 MR was fed at a rate of 0.28 kg/calf/d at 2x/d for 14d via bucket, and then increased to a feeding rate of 0.43 kg/calf/d at 2x/d until 35d. Feedings were reduced to 1x/d at 36d to facilitate weaning at 42d. Decoquinate was added to MR at 37.8 g/ton for coccidiosis control. Calves were housed in individual Calf-Tel hutches bedded with straw with ad libitum access to a 20% CP calf starter (CS) and water. SS-0.5 average daily gain (ADG) through 56d was greater (P < 0.05) compared to SS-1.0 and YCM, and tended (P < 0.10) to be greater for C and SS-1.5. ADG averaged 1.44, 1.57, 1.41, 1.40, and 1.39 kg/d for C, SS-0.5, SS-1.0, SS-1.5, and YCM, respectively. Total gain was increased for SS-0.5 vs. SS-1.0 and YCM, with body gains averaging 81.2, 87.89, 78.32, 78.9, and 78.04 kg for C, SS-0.5, SS-1.0, SS-1.5, and YCM, respectively. Body length gain was similar among treatments with an exception of SS-0.5 having a greater gain vs. SS-1.5 (P < 0.02). Hip width was similar among treatments. Wither height gain through 56d was greater for SS-0.5 vs. C, SS-1.0, SS-1.5, and YCM. Hip height gain was also increased for SS-0.5 vs. C, SS-1.0, SS-1.5 and was similar for SS-0.5 and YCM. This data demonstrates that feeding SS at 1.25 g/calf/d to a 24:20 MR will enhance growth rates compared to calves fed a modified accelerated 24:20 MR and a 24:20 MR containing YCW technology.

Key Words: calf, essential oils

1304 Effects of supplementing pasteurized waste milk with vitamins A, D and E on fat-soluble vitamin status, growth, and health of calves. L. Blakely*[1], M. Kweh[1], M. Poindexter[1], R. L. Stuart[2], and C. D. Nelson[3], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*Stuart Products Inc, Bedford, TX,* [3]*University of Florida, Gainesville.*

The objective of this study was to determine the effects of a milk supplement, MILKADE® (Stuart Products, Inc.), on growth, health and fat-soluble vitamin status of calves fed pasteurized whole milk. The MILKADE supplement contained 50,000 international units (IU) vitamin A as retinyl-palmitate, 50,000 IU vitamin D_3, and 500 IU vitamin E as *RRR-α-tocopherol* per milliliter of product. Forty Holstein calves (19 bulls, 21 heifers) were enrolled at birth and assigned to either control (n = 18, no supplement), 0.25 mL MILKADE (0.25ADE, n = 12), or 0.5 mL MILKADE (0.5ADE, n = 10) treatments. Calves were provided 2.85 L of pasteurized waste milk twice per day and the supplement was added individually to the calves' milk at the morning feeding. Feed intake and health scores were recorded daily. Bodyweight and height and serum samples were collected weekly from birth until 3 wk (bulls) or 6 wk (heifers) of age. Responses to treatments were analyzed as repeated measures. Serum retinol concentrations averaged near 400 ng/mL during the trial and were not different (P = 0.45) between treatment groups. In contrast, control calves were vitamin D deficient throughout the trial with average 25-hydroxyvitamin D (25(OH)D concentrations < 10 ng/mL of serum, whereas, 25(OH)D concentrations of 0.25ADE and 0.5ADE calves reached 90 and 150 ng/mL of serum, respectively, after 3 wk (P < 0.001). Similarly, serum α-tocopherol concentrations of control calves remained below 1.5 μg/mL throughout the trial but reached approximately 4.5 μg/mL of serum for both 0.25ADE and 0.5ADE groups after 5 wk (P < 0.05). There was a treatment effect on overall body weight (P = 0.004) such that 0.25ADE and 0.5ADE calves weighed less than control calves (49.3 kg and 46.4 kg vs. 52.1 kg, P = 0.013 and P < 0.001, respectively) at 3 wk of age. However, there was no difference in BW of heifers at week 6 of the trial (P = 0.171). There was no difference in feed intake or fecal and respiratory scores between groups (P > 0.05). In conclusion, calves fed pasteurized whole milk are deficient in vitamins D and E. Daily intakes for vitamins A and E were within ranges determined optimal for calves. Upper limits for supplemental vitamin D have not been established but the high serum 25(OH)D of the supplemented calves indicates vitamin D intakes above 10,000 IU/d are perhaps excessive for neonatal calves.

Key Words: dairy calves, nutrition, vitamins

1305 Effect of phytogenic compounds fed to preweaned calves. B. G. Miller*[1] and C. Scheider[2], [1]*Biomin USA, Warrenton, MO,* [2]*BIOMIN Holding GmbH, Herzogenburg, Austria.*

Maximizing early muscle growth is important in lifetime muscle development. Additionally, growth promoting antibiotics that have been typically used in the past may not be available in the future. Phytogenic (herbal) compounds may represent a potential to replace growth promoting antibiotics. A trial was conducted using Belgian Blue and Simmental bull calves in which mixed phytogenic products included in milk replacer and calf starter. Calves were separated into group based on breed and initial weight. (Control calves weighed 93 kg, Treatment calves weighed 94 kg) Calves were fed for 52 d. Control calves received a diet of calf milk replacer, for the first 3 wk. Cereal grains and a "calf starter feed" were offered from the first week on. Hay was made available throughout the trial and corn silage was offered from Day 21 to 52. Treatment calves received the same diet as control with the exception of Digestarom Milk (phytogenic product) added to the milk replacer at a rate of 500 gm/MT of calf milk replacer. The treatment calves also received Digestarom Calf in the calf starter at a rate of 300 gm/MT. Feed intake for calves was measured throughout the trial period. Calves were weighed on Days 21, 42, and 56. Data was analyzed via independent t test (SPSS). Control calves consumed numerically, but not statistically (P > 0.10) less average intake per day through out the total period, Days 1 to 56, than did treatment calves, 2.41 vs. 2.46 kg, respectively. Calves receiving Digestarom products improved in average daily gain throughout the trial at each weighing, and for the 56 d period demonstrated and increase of 0.10 kg in average daily gain (P < 0.05). Control calves gained 1.23 kg per day, while treatment calves gained at 1.33 kg per day (P < 0.05). Feed conversion improved numerically from 1.97 for control calves to 1.86 for treatment calves (P > 0.10). This work supports previous work with these and similar phytogenic products that have demonstrated a positive effect on the growth rate of neonatal and young ruminants. As such these and similar products represent a potential replacement of alternative growth promoting technologies.

Key Words: phytogenic calves

1306 Feeding steers extruded flaxseed and hay in a total mixed ration or sequentially can have substantial effects on beef fat polyunsaturated fatty acids and biohydrogenation intermediates.
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There has been growing interest in increasing the content of polyunsaturated fatty acid (PUFA; esp. α-linolenic acid, ALA) and their biohydrogenation intermediates (BHI) in beef, particularly *trans* 11–18:1 (VA, vaccenic acid) and *cis* 9, *trans* 11–18:2 (RA, rumenic acid) due to their potential positive health effects. However, high variability in PUFA and BHI have been found in beef between and within trials. The present trial was designed to determine if feeding steers extruded flaxseed (Linpro-R™; O&T Farms Ltd.,SK, Canada) and hay (25% and 75%; DM basis) together as a total mixed ration (TMR), or sequentially (non-TMR) would result in different enrichments of PUFA and BHI in different beef adipose tissues. Forty-eight Continental crossbred steers (325 ± 16 kg SD) were stratified by weight to 6 pens of 8 steers, pens were randomized to either TMR or non-TMR and steers were fed ad libitum for 240 d. At slaughter, subcutaneous fat (SCF) and perineal fat (PRF) samples were collected, freeze dried and directly methylated with 0.5 M sodium methoxide, and analyzed by GC using a 100 m CPSil 88 capillary column. Data were analyzed as a one-way ANOVA using the PROC MIXED procedure of SAS with diet as the main factor and pen as the experimental unit. Treatment means were generated and separated using the LSMEANS and PDIFF options, respectively. Compared to TMR steers, non-TMR steers had greater proportions of PUFA, *trans*-18:1, conjugated linoleic acids, and conjugated linolenic acids in both SC (+9.7%, +9.8%, +43.4%, +63.7%) and PR (+14.1%, +10.5%, +52.9%, +75.6%). In SCF, the percentages of ALA, VA and RA were increased ($P < 0.001$) from 0.91%, 4.92% and 1.91% in TMR steers to 1.10%, 6.82% and 2.69% in non-TMR steers. In PRF, the percentages of ALA,VA and RA were increased ($P < 0.001$) from 0.89%, 7.29% and 0.72% in TMR steers to 1.06%, 10.32% and 1.13% in non-TMR steers. Our results suggest that the method of feeding PUFA sources (e.g., flaxseed) can profoundly affect the enrichment of PUFA and their BHI in beef fat. In addition, the enrichment of these fatty acids also depends on fat depot, with PRF having greater proportions of VA, while SCF being higher in RA, which is likely due to the greater delta-9 desaturation of VA to RA in SCF.

Key Words: beef, flaxseed, feeding management, omega-3, rumenic acid, vaccenic acid

1307 Fatty acid composition of intramuscular lipids from Nellore and Brangus bulls fed diets supplemented with cottonseed.
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Finishing bulls were used in a factorial design with 2 breeds and 2 diets with contrasting fat levels to evaluate changes in marbling and fatty acid profile of intramuscular lipids. Nellore ($n = 20$) and Brangus ($n = 20$) bulls were randomly assigned to a low (LFD) or a high fat diet (HFD): 3.2% vs. 6.4% ether extract. The diets had similar energy and protein levels and were composed by sorghum silage (30% DM), soybean hulls, ground corn, soybean meal, urea and a mineral mixture. HFD additional fat derived from cottonseed (18% DM), in substitution to ground corn (31% vs. 52%, on HFD and LFD, respectively). The experiment lasted 71-d. All carcass were evaluated for marbling (1 to 18 scale) and back fat thickness (BFT). *Longissimus dorsi* (LD) samples were randomly selected from four animals of each treatment for fatty acid analysis by gas-chromatography. Fatty acid composition is expressed as g/100 g of total lipids. All data were analyzed using the GLM procedure of SAS (SAS, 2011) with animal as the experimental unit and genetic group, diets and the interaction between them as class variables. Back fat thickness was similar among treatments (5 mm, on average), but marbling was higher for Brangus. There was significant breed vs. diet interaction ($P < 0.01$), mainly because marbling with LFD was much more intense for Brangus than Nellore (8.0 vs. 3.3), while for HFD it was quite similar (Brangus = 5.8 vs. Nellore = 5.3). Fatty acid composition of intramuscular lipids showed that samples from Brangus bulls had more palmitic (C16; 17.7% vs. 15.3% $P < 0.05$), stearic (C18; 11.9% vs. 8.9% $P < 0.05$), oleic (C181c9; 28.1% and 23.3%), and elaidic (C181t9; 0.15% and 0.12%, $P < 0.05$) acids. They also had 20% and 18% greater saturated (SFA) and monounsaturated (MUFA) fatty acids ($P < 0.05$), respectively. HFD diet increased the amount of stearic acid (C18; 11.5% vs. 9.3% $P < 0.05$) and resulted in more than 20% higher ($P < 0.05$) elaidic acid and C18:2 non conjugated isomers, whereas the content of rumenic acid (C182c9t11, mean 0.19%) was unaffected by genetic group or diet. Differences in fatty acid content among Brangus and Nellore LD are in accordance with higher marbling from the former. Cottonseed fatty acid profile may have been extensively biohydrogenated, as suggested by the higher levels of stearic acid in HFD samples. Marbling differences among breeds had more impact in intramuscular fatty acid profile than supplementation with cottonseed.

Key Words: Meat, Lipid, Zebu

1308 Effects of dietary fat on fertility of dairy cattle: a meta analysis and meta-regression.

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There is increasing evidence of positive effects of feeding fats during transition on fertility and the adaptation to lactation. This study utilized meta-analytic methods to explore the effects of including fats in the transition diet on the risk of pregnancy to service ('proportion pregnant') and calving to pregnancy interval. Meta-analysis was used to integrate smaller studies, and increase the statistical power over that of any single study and explore new hypotheses. We explored the effect of fats and diet composition on fertility using meta-regression methods. There were relatively few highly controlled studies providing detailed descriptions of the diets used that examined interactions between fat nutrition and reproductive outcomes. Only 17 studies containing 26 comparisons were suitable for inclusion in statistical evaluations. Reproductive variables evaluated were risk of pregnancy 'proportion pregnant', primarily to first service, and calving to pregnancy interval. Production variables examined were milk yield, milk composition, and body weight. The sources of heterogeneity in these studies were also explored. A 27% overall increase in pregnancy to service was observed (RR = 1.27; 95% Confidence interval Knapp Hartung 1.09 to 1.45) and results were relatively consistent (I^2 = 19.9%). A strong indication of a reduction in calving to pregnancy interval was also identified, which was consistent across studies (I^2 = 0.0%) supporting a conclusion that overall, the inclusion of fats does improve fertility. Further exploration of the factors contributing to proportion pregnant using bivariate meta-regression identified variables that reflected changes in diet composition or animal response resulting from inclusion of the fat interventions in the experimental diets fed. Increased fermentable neutral detergent fiber and soluble fiber intakes increased the proportion pregnant while increased milk yield of the treatment group decreased this measure. Unexpectedly, the estimated energy costs of urea production also had a positive association with proportion pregnant. The limited number of suitable studies for the analysis highlights the need for more work to improve understanding of the critical nutritional factors affecting fertility. These factors include specific fatty acids in dietary interventions that contribute to increasing fertility of cows in dairy production systems.

Key Words: dietary fat, fertility, conjugated linoleic acid

1309 Altering the ratio of palmitic, stearic and oleic acids in diets with or without whole cottonseed impacts production responses and energy partitioning of dairy cows.

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We evaluated the effects of varying the ratio of dietary palmitic (C16:0), stearic (C18:0), and oleic (*cis*-9 C18:1) acids in diets with or without whole cottonseed on nutrient digestibility and production response of dairy cows. Twenty-four mid-lactation Holstein cows were used in split plot Latin square design. Cows were allocated to a main plot receiving either a basal diet without whole cottonseed (SH, n = 12) or a basal diet with whole cottonseed (CS, n = 12; 8% diet DM). Within each plot a 4 × 4 Latin square arrangement of treatments was used in four consecutive 21-d periods. Fatty acid (FA) treatments were: 1) Control (CON; no supplemental fat); 2) C16:0 supplement (PA; ~80% C16:0); 3) C16:0 and C18:0 supplement (PA+SA; ~40% C16:0 + ~40% C18:0); and 4) C16:0 and *cis*-9 C18:1 supplement (PA+OA; ~45% C16:0 + ~35% *cis*-9 C18:1). The final 5 d of each period were used for sample and data collection. The statistical model included the random effect of cow and the fixed effects of basal diet, FA treatment, period, and their interactions. Compared with SH diets, CS diets increased milk fat yield (1.71 vs. 1.51 kg/d; P = 0.05), yield of preformed milk FA (623 vs. 507 g/d; $P < 0.01$), and BW gain (1.0 vs. 0.71 kg/d; $P = 0.04$), tended to increase yield of de novo milk FA (396 vs. 383 g/d; $P = 0.06$), but reduced NDF digestibility (41.9 vs. 46.4%; $P < 0.01$) and total FA digestibility (74.2 vs. 76.3% $P = 0.05$). Compared with other treatments, PA increased yield of milk fat (1.60, 1.70, 1.64 and 1.64 kg/d; $P < 0.05$) and 3.5% FCM (45.2, 47.8, 46.8 and 46.5 kg/d; $P < 0.01$) for CON, PA, PA+SA and PA+OA, respectively. PA+OA increased BW gain compared with other treatments (0.82, 0.84, 0.70 and 1.05 kg/d; $P < 0.05$) for CON, PA, PA+SA and PA+OA, respectively. PA and PA+OA tended to increase NDF digestibility compared with PA+SA and CON (43.2, 44.9, 43.1 and 44.5%; $P < 0.10$) for CON, PA, PA+SA and PA+OA, respectively. Compared with the other treatments, PA+SA reduced 16-carbon (77.6, 73.0, 66.0 and 79.1%; $P < 0.01$), 18-carbon (79.2, 79.5, 72.0 and 79.7%%; $P < 0.01$), and total FA digestibility (78.6, 77.4, 68.2 and 79.4%; $P < 0.01$) for CON, PA, PA+SA and PA+OA, respectively. In conclusion, diet inclusion of C16:0 increased energy output in milk, while inclusion *cis*-9 C18:1 increased BW gain. The combination of C16:0 and C18:0 reduced NDF and FA digestibilities, which likely explains its reduced performance compared with other treatments.

Key Words: fat supplementation, animal performance, fatty acids

1310 Effect of high-oleic acid whole, heated soybeans or extruded soybean meal on production performance, milk fatty acid composition, and enteric methane emission in dairy cows.
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The objective of this study was to investigate the effect of 3 soybean sources differing in fatty acid profile and processing method on productivity, milk composition, and enteric CH_4 emission in lactating dairy cows. The soybean sources were: extruded conventional soybean meal (SBM; 48% CP and 8.7% ether extract; 22% oleic acid), extruded Plenish® (DuPont Pioneer, Johnston, IA), a high-oleic acid variety SBM (51.4% and 8.4%, respectively; 75% oleic acid), and whole, heated Plenish® soybeans (40.0% and 20.2%, respectively). The study involved 15 Holstein cows (54 ± 8.3 d in milk) in a replicated 3 × 3 Latin square design experiment with 3, 28-d periods. The inclusion rate of the 3 soybean sources in the diet was (all data are on DM basis): 17.1, 17.1, and 7.4%, diets CESBM, PESBM, and WHPSB, respectively, providing 1.4 to 1.5% soybean oil. The rest of the dietary ingredients were: corn silage, 41%; alfalfa haylage, 16%; grass hay/straw mix, 4%; ground corn grain, 10%; cottonseed hulls, 4%; molasses, 4.9%; and a mineral/vitamin premix, 3%. The WHPSB diet also contained 9.7% solvent-extracted SBM. The diets had similar content of CP (17.0 and 17.6%), NDF (31.0 and 32.0%), ether extract (3.8 and 4.0%), and NE_l (1.53 and 1.54 Mcal/kg). Compared with CESBM, the Plenish® diets tended to increase ($P = 0.09$) DMI (27.1, 27.8, and 27.8 kg/d, CESBM, PESBM, and WHPSB, respectively). Milk yield was not affected ($P \geq 0.10$) by treatment (average of 42.2 kg/d; SEM = 1.41). The Plenish® diets increased ($P < 0.01$) milk fat content (3.55, 3.74, and 3.76%, respectively). Feed efficiency was decreased ($P < 0.001$) by the Plenish® diets, compared with CESBM (1.50 and 1.51 vs. 1.57 kg/kg, respectively). Treatments had no effect ($P \geq 0.13$) on enteric CH_4 (average of 463 g/d, SEM = 29.7) or CO_2 (average of 12,113 g/d, SEM = 241.5) emissions and methane emission yield (16.6 to 17.2 g/kg DMI). Diets had a marked effect on milk fatty acid profile. Generally, the Plenish® diets increased ($P \leq 0.01$) mono-unsaturated and *cis*-9 18:1 and decreased ($P \leq 0.01$) poly-unsaturated, total trans-, and conjugated linoleic fatty acids concentrations in milk fat. In this study, compared with conventional extruded SBM, the Plenish® soybean treatments had no effect on milk yield, increased milk fat concentration, decreased feed efficiency, and modified milk fatty acid profile in a manner expected from the greater concentration of oleic acid in Plenish® soybean oil.

Key Words: high-oleic acid soybean, milk fatty acid, methane, dairy cow

1311 Biohydrogenation kinetics of oleic, linoleic and α-linolenic acids in vivo.
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Biohydrogenation (BH) of unsaturated fatty acids (FA) has been extensively studied in vitro; however, in vitro BH rates and extents may not parallel BH pathways in vivo. The objective was to assess rate and extend of oleic (OA), linoleic (LA) and α-linolenic acid (ALA) biohydrogenation in vivo. Each FA was characterized in a separate experiment (EXP.1– oleic, EXP.2– linoleic, and EXP.3– α-linolenic) using 4 ruminally cannulated lactating Holstein cows in each experiment. A single bolus consisting of 200 g of an oilseed (EXP.1 87% OA sunflower, EXP.2 70% LA safflower, and EXP.3 54% ALA flaxseed) and 12 g of heptadecanoic acid (17:0) was mixed with rumen contents. Rumen digesta was collected at −1, −0.25, 0.1, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, and 6 h relative to the bolus. Samples were immediately placed on dry ice, stored at −20°C, freeze-dried, methylated and analyzed by GC-FID. On the day of infusion, cows were fed at a rate of 4.2%/h of expected daily DMI. The geometric mean of the 4 cows was calculated and the disappearance of 17:0, OA, LA, and ALA was fit to a single exponential decay model using the nonlinear procedure of JMP Pro. Overall, the boluses increased total fat in the rumen from 4.1 to 7.4% and enriched 17:0 from 0.4 to 2.5% of FA. The bolus enriched OA from 9.0 to 30.1% of FA in EXP. 1, LA from 12.5 to 35.9% of FA in EXP.2, and ALA from 1.9 to 19.8% of FA in EXP.3. The fractional rate of 17:0 disappearance was 10.9, 8.5, and 6.7%/h in EXP.1, 2, and 3, respectively, and was used as a marker of FA passage. The fractional rate of disappearance of OA was 55%/h, LA was 61.2%/h, and ALA was 93.9%/h in EXP.1, 2, and 3, respectively, and all three unsaturated FA reached pre-bolus concentration within 4 h. Based on kd/(kd+kp), the extent of BH was 83.4% for OA, 87.8% for LA, and 93.3% for ALA in EXP.1, 2, and 3, respectively. Assuming that BH equals disappearance minus passage, the BH rates were 44.0, 52.7, and 87.1%/h for OA, LA, and ALA in EXP.1, 2, and 3, respectively. In conclusion, the extent of oleic, linoleic, and α-linolenic biohydrogenation was near expected values, but the rate of ruminal biohydrogenation was higher than that commonly observed in vitro for these three unsaturated FA.

Key Words: rumen, biohydrogenation

1312 Production response, nutrient digestibility, and energy partitioning of post-peak dairy cows when palmitic acid-enriched supplements are included in diets: a meta-analysis and meta-regression. J. de Souza*, R. J. Tempelman, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

This analysis was performed to evaluate the effects of palmitic acid-enriched supplements (PA; > 80% C16:0) on production response, nutrient digestibility, and energy partitioning of post-peak dairy cows. The database was formed with 1,056 individual observations from 215 dairy cows in 12 studies. Diet mean nutrient content (% DM) was 30% NDF (range 24 to 37%), 17% CP (range 16.7 to 17.8%), 27% starch (range 22 to 32%), and 3.95% fatty acids (FA; range 2.1 to 5.6%). PA was fed on average at 1.8% of diet DM (range from 0.75 to 2.25%) replacing either soyhulls or ground corn in diets. The effects of PA were compared to non-fat supplemented diets used as controls (CON). The meta-analysis was performed to calculate the mean difference in least square means between CON and PA treatments using a model considering the random effects of study and cow. The meta-regression evaluated the effect of C16:0 intake using a random regression model. PA compared with CON did not affect DMI ($P = 0.32$), milk yield ($P = 0.37$), BW ($P = 0.70$), or BCS ($P = 0.75$), but increased milk fat content (3.81 vs. 3.58%; $P < 0.01$), milk fat yield (1.59 vs. 1.49 kg/d; $P < 0.01$), 3.5% FCM (44.8 vs. 43.0 kg/d; $P < 0.01$), and feed efficiency (3.5% FCM/DMI; 1.60 vs. 1.53; $P < 0.01$). PA increased 16-carbon milk FA yield (590 vs. 475 g/d; $P < 0.01$) compared with CON but did not affect de novo ($P = 0.23$) or preformed ($P = 0.76$) milk FA yields. PA increased NDF digestibility (44.3 vs. 41.5%; $P = 0.02$), 18-carbon FA digestibility (80.3 vs. 78.4%; $P = 0.02$) and DM digestibility (68.2 vs. 66.7%; $P = 0.01$), but reduced 16-carbon FA digestibility (68.4 vs. 74.3%; $P < 0.01$), and total FA digestibility (71.5 vs. 75.8%; $P < 0.01$) compared with CON. PA increased net energy intake (47.4 vs. 46.0 Mcal/d; $P = 0.04$), milk energy output (31.1 vs. 29.9 Mcal/d; $P = 0.01$) and partitioned more dietary energy to milk (66.6 vs. 65.0%, $P = 0.03$) compared with CON. Using the random regression model we observed positive linear relationships between C16:0 intake and milk fat yield ($P < 0.01$; $R^2 = 0.57$), 3.5% FCM ($P < 0.01$; $R^2 = 0.53$), and 16-carbon milk FA ($P < 0.01$; $R^2 = 0.87$), as well as NDF digestibility ($P = 0.01$; $R^2 = 0.55$) and energy partitioned toward milk ($P = 0.01$; $R^2 = 0.47$), but a negative linear relationship for total FA digestibility ($P = 0.01$; $R^2 = 0.64$). In conclusion, supplementation of palmitic acid-enriched supplements increased yields of milk fat and 3.5% FCM, feed efficiency, and NDF digestibility with no reduction in DMI or loss of BW or BCS.

Key Words: fat supplementation, meta-analysis, production response

1313 Effect of potassium carbonate and soybean oil supplementation on rumen microbial population linked to lipid metabolism. A. R. Alfonso-Avila*[1], J. Chiquette[2], P. Y. Chouinard[3], E. Charbonneau[1], and R. Gervais[3], *[1]Département des sciences animales, Université Laval, Quebec, QC, Canada, [2]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, QC, Canada, [3]Département des sciences animales, Université Laval, Québec, QC, Canada.*

The rumen microbial ecosystem plays a crucial role in productivity through digestion of feeds and supply of nutrients to the host animal. It was suggested that milk fat synthesis in dairy cows is stimulated by a positive dietary cation-anion difference (DCAD). Despite that rumen bacteria are largely involved in hydrolysis and biohydrogenation of dietary lipids, the impact of DCAD on rumen microbiome is unknown. The objective of this study was to evaluate the effect of increasing DCAD, using K_2CO_3, in diets containing soybean oil (SBO) on rumen microbial population associated with lipid metabolism. Twenty four early lactation Holstein dairy cows (39 ± 22 DIM) were used in a randomized complete block design (6 blocks) based on DIM and number of calving with a 2 × 2 factorial arrangement of treatments. Within each block, cows were fed a basal diet formulated to achieve 40% forage (58% corn silage), 60% concentrate, and 47% non-fibrous carbohydrates, with 0 (DCAD: +95 mEq/kg) or 1.5% K_2CO_3 (DM basis; DCAD: +316 mEq/kg), and 0 or 2% SBO. Effects of K_2CO_3, SBO and the interaction K_2CO_3 × SBO were evaluated. Treatment period lasted 28 d; the last 5 d were used for data and sample collection. Equal volumes (?1.0 L) of rumen fluid and solid digesta were collected from different rumen sites 4-h postfeeding. Extracted DNA was amplified by quantitative real-time PCR. The absolute amount for each microbial group was expressed as logarithm (base 10) of DNA copies/g of fresh matter. A companion abstract showed an interaction between K_2CO_3 and SBO on milk fat yield and *t*10/*t*11 ratio (JDS 98-Suppl. 2:128). Supplementing diets with K_2CO_3 stimulated the growth of *Butyrivibrio hungatei* (5.79 vs. 5.62; $P = 0.03$), a bacteria recognized to produce *t*11 18:1 during biohydrogenation. Conversely, feeding SBO reduced the growth of i) *Butyrivibrio*/*Pseudobutyrivibrio* group (8.60 vs. 8.80; $P = 0.04$), also known to produce *t*11 18:1, ii) fibrolytic *Fibrobacter succinogenes* (9.34 vs. 9.63; $P = 0.04$), iii) *Butyrivibrio proteoclasticus,* a bacteria involved in 18:0 production (6.67 vs. 6.79; $P = 0.06$), and iv) amylolytic *Streptococcus bovis* (6.84 vs. 7.01; $P = 0.06$). Feeding K_2CO_3 had no effect on these four bacteria. Total eubacteria and total protozoa did not differ between treatments ($P > 0.13$). Feeding K_2CO_3 and SBO had distinct effects on rumen bacteria. However, the absence of interaction between treatments on microbial population does not allow to establish a clear link with

previously observed effects on milk fat yield and *t*10/*t*11 ratio.

Key Words: DCAD, rumen bacteria, biohydrogenation

1314 Abomasal infusions of linoleic and linolenic acid in lactating dairy cows differentially alter the fatty acid composition of plasma lipid fractions and immune cells.

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The balance of n-3 and n-6 fatty acids (FA) in immune system tissues can influence the degree of inflammatory responses in dairy cattle. Linoleic acid (C18:2 n-6) and linolenic acid (C18:3 n-3) are the most abundant n-6 and n-3 FA in lactating dairy cow rations, and are associated with pro-inflammatory and anti-inflammatory responses, respectively. Our objective was to evaluate the incorporation of these FA, and their downstream oxidized FA (oxylipids), into plasma and white blood cells (WBC) following supplementation. Six mid-lactation dairy cows were abomasally infused 4x/d for 7-d treatment periods with 7-d washout intervals in a replicated balanced Latin square design with 3 treatments: 1) CON = ethanol carrier, 2) LA = 45 g/d C18:2 n-6, and 3) LNA = 45 g/d C18:3 n-3. Blood was collected on d 7 of the treatment periods and analyzed for WBC and plasma lipid fraction FA and plasma oxylipid composition. Yields of milk and milk components were calculated for d 6 and d 7 of the treatment periods. Statistical analysis was performed using linear mixed models. Dry matter intake was not affected by treatment ($P = 0.68$). LA treatment increased the yield of milk and milk protein compared to CON and LNA ($P \leq 0.05$). LNA treatment increased milk fat concentration compared to CON and LA ($P \leq 0.05$). The concentration of C18:3 n-3 in WBC was increased by LNA (0.86 g/100 g FA; $P \leq 0.05$), compared to LA (0.39 g/100 g FA) and CON (0.34 g/100 g FA), but C18:2 n-6 was unaffected by treatment ($P = 0.15$). LNA increased C18:3 n-3 (3.17 g/100 g FA) and C20:5 n-3 (0.43 g/100 g FA) in the phospholipid fraction of plasma, compared to CON and LA ($P \leq 0.01$), while LA increased C18:2 n-6 (38.7 g/100 g FA), compared to the other treatments ($P < 0.01$). Plasma phospholipid C20:4 n-6 concentration was not altered by treatment ($P = 0.65$). LNA decreased C20:4 n-6-derived 8,9-DiHETrE ($P < 0.01$) and tended to decrease C18:2 n-6-derived 12,13 EpOME in plasma ($P = 0.09$). When C18:3 n-3 and C18:2 n-6 were abomasally infused at the same dose, C18:3 n-3 had a greater influence on the profile of plasma FA and oxylipids and the FA composition of WBC. These changes have the potential to mediate inflammatory responses in cattle at risk of infection.

Key Words: linoleic acid, linolenic acid, abomasal infusion

1315 Effect of increasing doses of abomasally infused linseed oil on animal performance and oxidative stability of milk in Holstein dairy cows.

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To evaluate the effect of increasing doses of post-ruminal supply of linseed oil (LO), as a source of polyunsaturated fatty acids (PUFA), on animal performance and oxidative stability of milk, five Holstein dairy cows (36 ± 2 DIM, 38.7 ± 4.7 kg milk/d; Mean ± SD) were randomly distributed in a 5 × 5 Latin square design (14-d periods; 11 d of adaptation). All cows were fed the same ration and LO was abomasally infused continuously at 0, 75, 150, 300, and 600 g/d using peristaltic pumps. Oxidation measurements were done on fresh non-homogenized milk and on homogenized milk stored at 4°C during 11 d under fluorescent light. Data were analyzed using a mixed model including the random effects of period and cow, and the fixed effects of treatment, time and their interaction in the repeated measures analyses. A peroxidability index (PI) was calculated as: 0.025×Monoenoates + 1×Dienoates + 2×Trienoates + 4×Tetraenoates + 6×Pentaenoates + 8×Hexaenoates, to account for individual oxidation sensitivity of FA. Dry matter intake and yield of energy corrected milk decreased linearly with increasing dose of LO ($P < 0.05$). Milk fat concentration decreased quadratically ($P < 0.05$) reaching a nadir at 300 g of LO/d, whereas the yields of fat and protein decreased linearly ($P < 0.05$). The concentration and yield of lactose were not different among treatments. The concentration of PUFA increased linearly with LO dose ($P < 0.001$). Accordingly, the PI of fresh milk increased linearly with dose from 2.0 mg/g milk in the control, to 10.8 mg/g milk at the highest dose ($P < 0.001$). Conjugated diene hydroperoxides in fresh milk increased linearly with dose ($P < 0.001$), whereas conjugated triene hydroperoxides and redox potential were not affected. Volatile lipid oxidation products such as propanal, hexanal, *trans*-2-hexenal/hex-*cis*-3-enal, and hept-*cis*-4-enal increased linearly with dose ($P < 0.001$), whereas 1-octen-3-one was not affected, and *trans*-2, *cis*-6-nonadienal and *trans*-2, *trans*-4-nonadienal were not detected in fresh milk. During storage, similar increasing trends were observed across treatments for propanal, hexanal, *trans*-2-hexenal/hex-*cis*-3-enal, hept-*cis*-4-enal, and *trans*-2, *cis*-6-nonadienal in homogenized milk (time $P < 0.001$). Treatment by time interactions were detected for 1-octen-3-one and *trans*-2, *trans*-4-nonadienal. In conclusion, increasing doses of abomasally infused LO negatively affected animal performance. Despite small differences among individual oxidation products, overall, a linear increase in milk PUFA led to a quadratic response in total identified volatile compounds

which tended to reach a plateau at 300 g of LO/d.

Key Words: dairy cows, n-3 fatty acids, oxidation

1316 Palmitic acid feeding increases ceramide availability in association with increased milk yield, NEFA availability, and adipose tissue responsiveness to a glucose challenge. J. E. Rico, A. T. Mathews, and J. W. McFadden*, *West Virginia University, Morgantown.*

Reduced insulin action facilitates glucose partitioning for milk synthesis and facilitates lipolysis during early lactation. Insulin sensitivity increases beyond peak milk yield, while circulating NEFA and milk production decline. Palmitic acid (C16:0) promotes insulin resistance in monogastrics through ceramide-dependent mechanisms, and ceramides are elevated in hyperlipidemic insulin resistant early lactation cows. We hypothesized that feeding C16:0 to mid-lactation cows would enhance circulating ceramide, and ceramide would be positively associated with milk yield. Twenty multiparous Holstein cows were enrolled in a study consisting of a 5 d covariate, 49 d treatment, and 14 d post-treatment evaluation. Cows were randomly assigned to a sorghum silage-based diet containing no supplemental fat (control; n = 10; 138 ± 45 DIM) or C16:0 at 4% of ration DM (PALM; 98% C16:0; n = 10; 136 ± 44 DIM). Blood was collected at routine intervals and milk yields were recorded. Intravenous glucose tolerance tests (GTT) were performed at d −1, 21, and 49 relative to start of treatment. Plasma sphingolipids were quantified using liquid chromatography tandem mass spectrometry. Data were analyzed as repeated measures using a mixed model (fixed effects of treatment and time). Pearson correlations were analyzed. The most abundant sphingolipids included C24:0-ceramide, C24:0-monohexosylceramide (GlcCer), and C16:0-lactosylceramide (LacCer). Relative to control, plasma concentrations of total ceramide, GlcCer, and LacCer decreased as lactation progressed (P < 0.01). Total ceramide and C24:0-ceramide were increased by d 8 of treatment in PALM, and remained elevated throughout the 7 wk treatment period (+80% average; P < 0.001). Similarly, C16:1-, C22:0-, C22:1-, C24:1-, and C26:0-ceramide levels were greater in PALM (P < 0.05). Post-treatment, total ceramide concentrations in PALM returned to control levels. PALM increased total GlcCer and C24:0-GlcCer levels in plasma by 32 and 33% at wk 3 and 7, respectively (P < 0.01). Also, PALM increased C16:0-, C22:0-, C22:1-, and C24:1-GlcCer in plasma (P < 0.01), but had no effect on LacCer levels. We observed a decline in GlcCer and LacCer concentrations as lactation progressed (e.g., C24:0-GlcCer; P < 0.01). Plasma C24:0-ceramide was positively correlated with plasma NEFA and milk yield, and inversely correlated with NEFA disappearance following GTT (r = 0.52, 0.44, and −0.57, respectively; P < 0.001), relationships shared by most detected ceramides. We conclude that increasing C16:0 intake to augment ceramide supply delayed the decline in ceramide supply observed with the progression of lactation. Future research should evaluate whether ceramide is intrinsically involved in the homeorhetic adaptation to lactation.

Key Words: ceramide, insulin resistance, lactation

1317 Effect of supplemental enriched palmitic acid in free fatty acid form vs. calcium salts of palm fatty acids on production performance in early postpartum cows. J. E. Nocek*[1], C. Wan[2], and T. M. Londergan[2], *[1]Overture Enterprises, LLC, Auburn, NY, [2]Centriq, Seattle, WA.*

Sixty multiparous cows were randomly assigned at calving to one of three treatment regimens to evaluate fat supplementation on production performance in postpartum dairy cattle. Cows entered the pens at calving and remained through 12 wk. postpartum. There were 4 cows/pen and 5 pens/trt. Pens were identical in layout. Treatments were Control (no supplemental fat), Control diet with supplemental calcium salts of fatty acids (MegaLac, Princeton, NJ,: ML) and Control diet with high palmitic acid (98%) fatty acids (PrimaFat 16, Centriq, Seattle, WA,: PF). Cows were fed a Fresh (1 to 21 d) and High (22 to 84 d) diet. Corn meal was removed from the Control diet to provide equal supplemental fat content in both Fresh and High diets among treatments (Fresh:1.95 and 1.55% of DM and High: 1.78 and 1.46% of DM for ML and PF, respectively). Daily pen intakes and milk weights (3X) were recorded and averaged by week. Milk samples were collected weekly for milk composition. Blood samples were collected for NEFA and BHBA analysis on wk. 1 and 3 postpartum. Pen was the experimental unit. Mean group DMI was similar among treatments. Milk yield was similar for both fat products and higher (P < 0.01) than Control (47.3, 47.8 and 46.4kg for ML. PF and Control respectively). Both FCM and ECM were higher (P < 0.01) for PF compared to Control and ML (54.9, 50.8 and 52.2, and 52.7, 48.8 and 50.2 kg for FCM and ECM respectively). Milk Fat (% and yield) were higher (P < 0.01) for PF compared to Control and ML (4.42, 4.11, and 4.17%, and 2.10, 1.89, and 1.95 kg, respectively). Milk protein yield was higher (P < .01) for PF compared to Control, with ML not being different from either (1.36, 1.27, and 1.31 kg, respectively). MUN was lower (P < 0.01) for PF compared to ML and Control (11.8, 12.6, and 13.1 mg/dL, respectively). There was no effect of trt on BHBA, however, wk 1 NEFA tended to be lower (P = 0.14) for PF compared to ML and Control (0.55, 0.83, and 0.81 mEq/L), whereas wk 3 NEFA were lower (P = 0.04) for PF and Control compared to ML (0.46, 0.42, and 0.85 mEq/L). These results demonstrate that early postpartum cows supplemented with fat produced more milk than non-supplemented cows and supplementing with an enriched C16 fat increased fat percentage and yield compared to Ca-salts of palm fatty acid and increased protein

yield compared to no fat supplementation.

Key Words: palmitic acid, milk fat, dairy cows

1318 Hepatic oxidation is responsive to prepartum energy and peripartum rumen protected choline supplementation. V. Caprarulo[*1,2], T. L. Chandler[1], M. G. Zenobi[3], B. A. Barton[4], C. R. Staples[3], and H. M. White[1], *[1]Department of Dairy Science University of Wisconsin, Madison, [2]Department of Health, Animal Science and Food Safety, University of Milan, Milan, Italy, [3]Dep. of Animal Sciences, University of Florida, Gainesville, [4]Balchem Corporation, New Hampton, NY.*

Controlling prepartum energy intake or supplementing rumen-protected choline (RPC) during the periparturient period, are 2 strategies to preserve hepatic metabolic function. The objective of this study was to examine the regulation of hepatic gluconeogesis and oxidation during the transition to lactation. At −48 d relative to calving (DRTC), multiparous Holstein cows were assigned to either a controlled (1.40 Mcal of NEL/kg DM; CE) or high (1.63 Mcal NEL/kg DM; HE) energy prepartum diet with or without RPC (top-dressed daily from −21 to +21 DRTC). Postpartum diets only differed by addition of RPC. Liver tissue biopsy samples were collected at −14, +7, +14, and +21 DRTC for RNA isolation and cDNA generation (n = 16/treatment). Quantitative PCR was performed and mRNA abundance was normalized to reference genes. Data were analyzed by Proc Mixed (SAS 9.4) with repeated measures in a model that accounted for the main effects of RPC, energy, DRTC, and corresponding 2-way and 3-way interactions, and the random effect of cow (energy × choline). When interactions were significant ($P < 0.05$), energy × choline means were separated by Tukey's and time interactions were separated within time point by slice. Data are presented as least squares means ± SE, arbitrary units (AU). *Pyruvate carboxylase* (*PC*) expression increased ($P < 0.05$) after calving. There was an energy×choline ($P < 0.05$) and choline×DRTC ($P < 0.05$) interaction where RPC increased PC expression at −14 and +7 DRTC. There was no interaction ($P > 0.1$) of prepartum energy and DRTC. Expression of *cytosolic phosphoenolpyruvate carboxykinase* (*PEPCKc*) was greatest ($P < 0.05$) at +14 and lowest at −14 and +7 DRTC (1.62a, 0.75b, and 0.62b ± 0.16 AU, respectively). Expression of *PEPCKc* was decreased ($P < 0.05$) in cows fed HE+RPC compared with other treatments (0.57b, 1.00ab, 1.26a, 1.21a ± 0.09 AU; HE+RPC, HE, CE+RPC, CE). Expression of *glucose-6-phosphatase* was increased ($P < 0.05$) at +14 and +21 DRTC, and decreased (energycholine; $P < 0.05$) in cows fed the CE+RPC (1.36 vs. 2.32, 2.33, 2.24 ± 0.17 AU; CE+RPC, CE, HE+RPC, HE). Expression of *carnitine palmitoyltransferase 1A* was greatest at +21 DRTC ($P < 0.05$) but was unaltered ($P > 0.1$) by energy or choline. The transcription factor *PPARalpha* was increased ($P < 0.05$) in CE+RPC (1.35 vs. 0.86, 0.68, 0.90 ± 0.08 AU; CE+RPC, CE, HE+RPC, HE). Increased *PC* peripartum with RPC, across energy treatments, may support increased oxidative capacity at calving. Decreased*PEPCKc*in HE+RPC may serve to increase oxidation of increased circulating NEFA by maintaining the oxaloacetate pool.

Key Words: gluconeogenesis, TCA cycle, transition cow

1319 Rumen-protected methyl donors during the transition period: hepatic short-chain acyl CoA concentration in response to supplemental methionine or choline. Z. Zhou[*1], C. L. Girard[2], B. Ouattara[2], M. Vailati Riboni[1], D. N. Luchini[3], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [3]Adisseo S.A.S., Alpharetta, GA.*

Hepatic short-chain acyl CoAs are key intermediary metabolites of liver metabolism. Elevated concentration of acetyl CoA was associated with lower dry matter intake (DMI) in lactating dairy cows. Objectives were to measure hepatic acyl-CoA profiles in response to rumen-protected methionine (MET) or rumen-protected choline (CHO) supplemented during the transition period. Forty multiparous Holstein cows were used in a randomized complete block design with 2 × 2 factorial arrangement of MET and CHO level (with or without). Treatments were control (CON), no MET or CHO; CON+MET (SMA); CON+CHO (REA); and CON+MET+CHO (MIX). Cows received the same diet (1.52 Mcal NE_L/kg DM) from −21 d (close-up) to calving. From calving to 30 d, cows were on the same diet (1.71 Mcal NE_L/kg DM) and continued to receive the same treatments through 30 d. MET supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow/d. Liver samples were harvested at −10, 7, 20, and 30 d relative to calving. Free CoA, acetyl-CoA, propionyl-CoA, succinyl-CoA, malonyl-CoA, and methylmalonyl-CoA were determined by HPLC. Data were analyzed using PROC MIXED in SAS. The CORR procedure of SAS was used to evaluate correlations between selected variables. Both pre- and post-partum DMI was greater with MET ($P = 0.01$) but did not change with CHO ($P > 0.05$). MET supplementation led to greater ($P = 0.03$) hepatic total CoA and had a strong tendency ($P = 0.07$) for increasing free CoA compared with other treatments. Positive correlations (168 observations, $P < 0.01$) were obtained for both total and free CoA with DMI ($r = 0.27$ and 0.30, respectively) and NE_L intake ($r = 0.29$ and 0.34, respectively). Hepatic acetyl-CoA concentration has been reported to be negatively correlated with DMI, but no correlation ($P > 0.05$) was detected between acetyl-CoA, DMI, or NE_L. In fact, acetyl-CoA was lower ($P < 0.01$) with CHO and did not change with MET ($P > 0.05$). Although MET cows had lower ($P < 0.01$) propionyl-CoA, succinyl-CoA concentration was greater ($P = 0.02$) and overall positively correlated (168 observations, $P <$

0.01) with DMI ($r = 0.23$) and NE_L ($r = 0.25$). Overall, results indicate that methyl donor supplementation altered hepatic short-chain acyl-CoA concentrations during the peripartal period. The greater DMI in response to MET supplementation might have been associated with higher hepatic succinyl-CoA concentration, potentially leading to greater gluconeogenesis.

Key Words: methionine, choline, CoA

1320 Development and validity of a lipid accessibility index that quantifies reaction exposure of internal fatty acids in animal feeds.

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Excessive lipid in the diet of dairy cattle can shift the pathways of biohydrogenation and the accumulation of conjugated linoleic acid isomers that cause milk fat depression. However, computer models that predict animal performance from unsaturated fatty acid load have been inconsistent in assessing the consequences of dietary lipid. One reason for their failure is the inability to determine the extent that lipid within the natural structure of plant matter will be released and exposed to the ruminal microorganisms. The purpose of this experiment was to develop and verify a lipid accessibility index (LAI) that could predict exposure of plant lipid to the microbial population. Based on the assumption that plant factors that limit microbial exposure would also limit chemical exposure of internal lipid, a LAI was developed by determining the proportion of fatty acids in samples quantified in a 10 min methylation relative to fatty acids quantified in the normal 2 h methylation. The 4 samples tested were alfalfa pellets, corn, cottonseed, and soybeans that were each tested in duplicate at four particle sizes; unground, finely ground through a 0.5-mm sieve in a centrifugal mill, and 2 intermediate sizes obtained by grinding for different lengths of time in a coffee grinder. Data were analyzed as a completely randomized design with a 4 × 4 factorial arrangement of treatments that included the effects of feed source, grind size, and the feed source × grind size interaction. The LAI for the main effect of grind size ($P < 0.05$) averaged 21.6, 35.2, 53.5, and 97.2% (SEM = 1.79%) going from unground to the most finely ground. For the main effect of feed source ($P < 0.05$), the LAI averaged 30.7, 45.4, 47.5, and 83.9% (SEM = 1.79%) for soybeans, corn, cottonseed, and alfalfa pellets, respectively. Relationships between grind size and LAI were linear for alfalfa, corn, and cottonseed with R^2 of 0.828, 0.937, and 0.957, respectively. A second order polynomial ($R^2 = 0.961$) best described the relationship between grind size and LAI for soybeans (0, 6.7, 17.1, and 99.1% LAI for whole to finely ground). The LAI proposed in this study was successful in reflecting differences in chemical reaction exposure of internal fatty acids across several feed sources and particle sizes suggesting it might also serve to quantify feed lipid exposure to microbial reaction in the rumen.

Key Words: lipid accessibility, feedstuffs, particle size

1321 Comparison of flax oil with varying lipid supplements in dairy ration: A meta-analysis.

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Feeding flax oil, a source of trienoic fatty acids (TRI-FA), to dairy cows contributes to improve fertility, reduce methane emissions and increase milk fat content of n-3 FA. However, studies on the effect of flax TRI-FA on milk production and composition have yielded contradictory results. The objective of this meta-analysis was to evaluate the effects of flax TRI-FA on lactation performance when compared with different sources of dietary lipids in which dienoic (DI), monoenoic (MONO), or saturated (SAT) FA were predominant. Three databases including 30, 20, and 15 studies, published between 1998 and 2015, were used for the comparisons of flax TRI-FA vs. DI-FA, vs. MONO-FA, and vs. SAT-FA supplements, respectively. For each database, dairy cow performance was adjusted with a linear mixed model where lipid source and supplemental lipid concentration were the independent variables, and study effect was included as a random variable. Concentrations of supplemental lipids, determined by ether extraction, varied from 0.7 to 6.0% (DM basis) for flax TRI-FA (3 databases combined), 0.5 to 6.6% for DI-FA, 0.9 to 5.9% for MONO-FA, and 1.0 to 4.1% for SAT-FA supplements. The interactions between lipid sources and their dietary concentrations were never significant and were removed from the models. Feeding flax TRI-FA tended to increase DMI (0.38 kg/d; $P = 0.07$) compared with SAT-FA, but no difference was observed with DI-FA or MONO-FA supplements. Actual, fat corrected, and energy corrected milk yields were not different between flax TRI-FA and the lipid categories evaluated. Feed efficiency of cows receiving flax TRI-FA was lower (−0.03 kg milk/kg DMI) compared with SAT-FA ($P = 0.03$), whereas no difference was observed with DI-FA and MONO-FA supplements. Milk fat and protein concentrations and yields were not different between flax TRI-FA and the other three lipid categories. Feeding flax TRI-FA increased lactose concentrations compared with DI-FA and SAT-FA supplements by 0.02 ($P = 0.03$) and 0.03 ($P = 0.03$) percentage unit, respectively. Despite minor effects on lactose, there was no difference between flax TRI-FA and other dietary unsaturated lipids on animal performance. Nevertheless, as a result of an increase in DMI, efficiency of milk production was reduced by feeding flax TRI-FA compared with SAT-FA supplements.

Key Words: dietary lipids, linseed, milk composition

1322 Milk bioactive fatty acids decrease in cows grazing pearl millet versus a cool-season pasture.

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Use of warm-season annuals, such as pearl millet (PM), has increased on northeast organic dairy farms because of their ability to grow in the mid-summer heat when cool-season perennial pastures experience less growth. The objective of this study was compare animal performance and milk bioactive fatty acids (FA) in milk of cattle grazed on PM versus cool-season pasture (CSP). Eight multiparous (parity: 2.9 ± 0.6 lactations) mid-lactation (114 ± 20 d in milk) Holstein cows were used in a repeated-measures design with three 4-wk periods. Cattle were grazed on CSP or PM in the following sequence: PM, CSP, and PM. Dry matter intake (DMI) was estimated using a calibrated rising plate meter. Individual milk weights and samples, representing a 24h period, were obtained during the last 2 wk (sampling days: 16 and 23) of each period. Milk samples were analyzed for components (fat, protein, organic solids) by mid-infrared spectrometry. Milk and forage FA proportions were determined using gas-liquid chromatography. Data were analyzed using a repeated measures ANOVA in the PROC MIXED procedure of SAS (vs. 9.4). CSP forages provided a higher content of n-3 FA when compared to PM (12.07 vs. 6.51 mg/g DM; $P < 0.05$), and higher content of polyunsaturated FA (17.17 vs. 8.33 mg/g DM; $P < 0.01$). Forage type had no effect ($P \geq 0.05$) on estimated DMI (17.2 and 17.4 kg/day for PM and CSP, respectively), milk production (13.8 and 13.1 kg/d for PM and CSP, respectively), fat yield (0.44 and 0.43 kg/d for PM and CSP, respectively), or protein yield (0.41 and 0.40 kg/d, for PM and CSP, respectively). Milk saturated FA were lower when cows grazed CSP compared to PM (59.5 vs. 63.0 g/100 g FA, respectively; $P < 0.001$). The content of CLA was higher during CSP treatment (2.11 g/100 g FA) than PM treatment (1.67 g/100 g FA; $P < 0.01$). Similarly, milk from cows grazing CSP had a twofold higher proportion of total n-3 FA when compared to PM (1.06 vs. 0.59 g/100 g FA; $P < 0.001$) and higher proportion of total n-6 FA in milk fat (1.29 and 1.04 g/100 g for CSP and PM, respectively; $P < 0.01$). Total branched-chain FA in milk fat were higher when cows grazed PM than CSP (3.12 vs. 2.86, respectively; $P = 0.01$). In conclusion, there was no difference in animal performance of cows grazing a CSP or PM, however, the contents of various bioactive FA were higher in milk fat of cows grazing a CSP compared to PM.

Key Words: milk production, n-3 fatty acids, branched-chain fatty acids

1323 Effect of early lactation feeding strategy on production, metabolic and endocrine responses of primiparous dairy cows.

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Primiparous Holstein cows ($n = 18$; 528 ± 40 kg BW, 3.2 ± 0.2 BCS) calved in fall were used in a randomized block design to study the effect of feeding strategy on production, metabolic, and endocrine responses in early lactation. At calving, cows were assigned within block to 1 of 2 feeding strategies during the first 65 d postpartum (DPP). Feeding strategies were either (G0) total mixed ration (TMR) ad libitum (17 kgDM/d offered; 70% forage, 30% concentrate) or (G1) grazing of alfalfa (*Medicago sativa*; 6-h am grazing in 3-d strips; pasture allowance = 20 kgDM/d) + TMR (70% of ad libitum TMR; 12 kgDM/d offered). Both groups consumed 2.2 kgDM/d of a commercial ration at each milking. Cows were milked twice a day, milk yield was recorded daily and samples were collected weekly for milk composition. Cow BW and BCS were recorded every 2 wk from −40 to +65 DPP. Blood samples were collected for metabolite and hormone analyses at −7 ± 2 and +42 ± 3 DPP. Data were analyzed as repeated measures with a mixed model that included: feeding strategy, DPP, and its interaction as fixed effects, block as random effect and calving date as a covariate. Milk yield (26.7 vs. 25.1 ± 0.58 kg/d), total solids (3.38 vs. 3.1 ± 0.09 kg/d) and NEL output (20.9 vs. 19.2 Mcal NEL/d) tended ($P < 0.07$) to be greater for G0 than G1 cows, being differences more marked from +30 to +60 DPP. Cow BW and BCS did not differ ($P > 0.30$) between feeding strategies. Concentrations of plasma NEFA decreased ($P < 0.01$) at +42 DPP when compared to −7 DPP and at +42 DPP tended ($P = 0.10$) to be greater for G0 than G1 cows (0.34 vs. 0.25 ± 0.03 mmol/L. Plasma BHB concentration at +42 DPP was greater ($P = 0.02$) for G0 than G1 cows (0.46 vs. 0.27 ± 0.05 mmol/L) as it decreased from −7 to +42 DPP only in the latter group. In contrast, plasma insulin was reduced ($P = 0.05$) in G0 than G1 cows at +42 DPP (11.7 vs. 7.2 ± 1.3 uU/mL) as it increased from −7 to +42 DPP only in the latter group. Concentrations of cortisol, leptin and adiponectin were not different ($P > 0.20$) at −7 than +42 DPP and neither differed between feeding strategies at +42 DPP. Metabolic and endocrine profile would indicate a greater lipolysis in early lactation in G0 than G1 cows which would be probably associated to their greater milk production.

Key Words: TMR, dairy cows and grazing

1324 Ratios of milk fatty acids accurately estimates plasma non-esterified fatty acid concentrations as an indicator of animal energy balance.

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Negative energy balance and elevated plasma NEFA in dairy cows can negatively affect animal health and milk production. Also, in short term feeding trials, failing to correct for negative energy balance can lead to overestimating the energy content of a given diet or the true feed efficiency for a given cow. The objective of this study was to evaluate the precision and accuracy of individual milk fatty acid proportions (IMFAP, g/100 g milk total fatty acids) or milk fatty acids ratios (MFAR) to predict plasma NEFA concentrations. Four models were developed using a dataset from three studies (n = 204 observations, individual animal). The developed models were: model 1 (IMFAP including the terms: C14:0, C15:0, C17:0, and C18:1), model 2 (MFAR C18:1 to C15:0), model 3 (MFAR C17:0 to C15:0) and model 4 (MFAR C18:1 to C14:0). Predicted model output for plasma NEFA was compared to 90 treatment means from an independent data set from 21 papers published in the literature. All models were developed based on an individual animal-level dataset, and validated with average values from groups of animals (literature dataset). Quality of the original prediction models was evaluated using the r^2 between the observed and predicted values, mean bias (MB), concordance correlation coefficient (CCC) and root mean square error of prediction (RMSEP). Results indicated that plasma NEFA predicted by model 2 (NEFA = 71.13 (± 68.04) + 8.87 (± 0.67) * C18:1/C15:0, r^2 = 0.55) and model 3 (NEFA = −47.50 (± 36.3) + 625.30 (± 40.63) * C17:0/C15:0, r^2 = 0.54) yielded more precise and accurate predictions (model 2: r^2 = 0.89, MB = −27.39 μEq/L, CCC = 0.92, RMSEP = 51.86 μEq/L, and model 3: r^2 = 0.89, MB = −77.79 μEq/L, CCC = 0.86, RMSEP = 102.32 μEq/L,) than the NEFA predicted by model 1 (r^2 = 0.74, MB = −186.08 μEq/L, CCC = 0.54, RMSEP = 233.17 μEq/L), and model 4 (r^2 = 0.81, MB = −69.75 μEq/L, CCC = 0.41, RMSEP = 110.65 μEq/L). Milk C18:1 to C15:0 and C17:0 to C15:0 ratios can be used as an indicator of herd energy balance and therefore the status of herd health.

Key Words: energy balance, fatty acids, transition cow

1325 Effect of linseed oil supplementation on milk fatty acid profile of dairy cows fed diets based on red clover silage or corn silage.

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The objective of this study was to examine the effect of linseed oil (LO) supplementation on milk fatty acid (FA) composition of dairy cows fed diets based on red clover (RCS) or corn silage (CS). Twelve lactating, multiparous Holstein cows (days in milk = 91 ± 25; milk yield = 45.2 ± 4.7 kg) were used in a replicated 4 × 4 Latin square design (35-d periods; 14-d adaptation) with a 2 × 2 factorial arrangement of treatments. Cows were fed (ad libitum; 5% orts on an as-fed basis) a TMR (60:40, forage:concentrate ratio) not supplemented or supplemented with 4% LO (DM basis) and with the forage portion of the TMR consisting of either RCS or CS. Milk FA profile was determined on samples collected over 6 consecutive days. Main effects of forage source, LO supplementation and their interaction were determined using the MIXED Procedure of SAS and significance was declared at $P \leq 0.05$. The *t*10/*t*11 18:1 ratio was unaffected by adding LO to the RCS-based diet, which is consistent with no change in milk fat yield reported in our previous study (JDS, 98:7993). In contrast, the *t*10/*t*11 18:1 ratio increased (2.04 vs. 0.77) and milk fat yield decreased (JDS, 98:7993) when LO was added to the CS-based diet. Milk fat concentration of *c*9*c*12*c*15–18:3 increased in cows fed LO-supplemented diets compared to cows fed non-supplemented diets (0.88 vs. 0.57) and in cows fed RCS compared to cows fed the CS-based diet (1.04 vs. 0.41). An increase in*c*9*t*11*c*15–18:3 concentration was observed when LO was supplemented to the RCS-based diet (0.12 vs. 0.04), but no effect was observed with LO supplementation to the CS-based diet (interaction, $P < 0.01$). Diets supplementation with LO increased the concentrations of *t*11–18:1, *c*9t11–18:2 and *t*11*c*15–18:2, but these increases were more pronounced when LO was added to the RCS-based diet than to the CS-based diet (interaction, $P < 0.01$). Regardless of the forage source, supplementation with LO decreased milk FA from de novo synthesis (< 16 carbon) and from rumen microbial origin (odd- and branched-chain FA) by 21% and 24%, respectively. It is concluded that the effect of LO supplementation (4% DM) on milk FA and more specifically on those originating from ruminal biohydrogenation of *c*9*c*12*c*15–18:3 is modulated by dietary forage source (CS vs. RCS).

Key Words: linseed oil, forages, milk fatty acid

1326 Characterization of rumen bacterial and protozoal fatty acid compositions from lactating Jersey cows offered alternative forage crops. L. M. Cersosimo[*1], R. Tacoma[1], S. Greenwood[1], K. Juntwait[2], A. F. Brito[2], and J. Kraft[1], *[1]University of Vermont, Burlington, [2]University of New Hampshire, Durham.*

Alternative forage crops (AFC) include cool and warm season grasses and legumes that could be used to overcome periods of limited pasture production. Rumen bacteria and protozoa cell membranes consist of varying proportions of fatty acids (FA) that contribute to milk FA. The objective of this study was to compare the rumen bacterial and protozoal membrane FA compositions from lactating Jersey cows fed pasture strip-tilled with AFC vs. a traditional grass-legume pasture mix. In spring (SPR) and summer (SUM), two separate, 21-d experiments were conducted using 16 lactating Jersey cows (SPR, 85 ± 46 DIM; SUM, 143 ± 58 DIM). Cows were divided into control (CON, $n = 8$) and treatment (TRT, $n = 8$) groups, matched by parity, DIM, and milk production, and offered (DM basis) 40% pasture as AFC or traditional and 60% TMR. On a DM basis, SPR TRT pasture consisted of AFC (barley, hairy vetch, triticale, rye, and wheat) representing 2.4% of total diet DM, while the SUM TRT pasture consisted of AFC (buckwheat, chickling vetch, and oats), representing 10% of total diet DM. Individual whole ruminal digesta samples (500 mL) were collected via esophageal intubation on d 20 and 21 of each experiment. Bacterial and protozoal fractions were isolated by differential centrifugation. Microbial FA were analyzed by GLC. Student's *t* tests (JMP Pro 12) were used to determine if least-squares means differed between groups. Total protozoal and bacterial branched-chain FA, PUFA, as well as *trans* 18:1 isomers and 18:0, the products of rumen bacterial biohydrogenation, did not differ by group in either experiment. In the SPR, bacterial *cis*-11 18:1 (CON, 0.57 g/100 g FA; TRT, 0.50 g/100 g FA), *cis*-13 18:1 (CON, 0.44 g/100 g FA; TRT, 0.37 g/100 g FA), and *cis*-15 18:1 (CON, 0.76 g/100 g FA; TRT = 0.68 g/100 g FA) were less abundant in the TRT than CON group ($P < 0.05$). Protozoal levels of CLA from SPR TRT (1.13 g/100 g FA) cows were higher than SPR CON (0.85 g/100 g FA). In the SUM, bacterial 17:0 was lower in cows grazing TRT pasture (0.67 g/100 g FA) than CON pasture (0.71 g/100 g FA; $P < 0.01$). In the SUM, no differences in the protozoal FA compositions were observed. In conclusion, few differences were identified in the microbial FA compositions in cows consuming pasture with or without AFC.

Key Words: branched-chain, microbial, pasture

1327 Effect of frequency of supplementation with Megalac-R on non-esterified fatty acids and blood urea nitrogen concentration in lactating beef cows. M. E. Garcia-Ascolani[*1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], D. D. Henry[1], F. M. Ciriaco[1], P. L. P. Fontes[1], G. C. Lamb[1], N. M. Long[2], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]Clemson University, Clemson, SC.*

An experiment was conducted to determine the effects of supplementing a ruminally-protected lipid (Megalac-R, Church & Dwight, Princeton, NJ) under 3 different frequencies, on the metabolic blood profile of suckled beef cows. Eighteen early lactating beef cows (first 90 d of lactation) were used in a completely randomized design. For 2 wk (d 0 to 14), all cows were individually supplemented an isocaloric, isonitrogenous amount of corn gluten feed (CGF) pellets (4.54 kg/wk, as is), at 3 frequencies (treatments): 3, 5, or 7 d/wk. For the duration of the study, cows and calves were grazing on a ryegrass pasture. From d 11 to 13, blood samples were collected before supplementation, and at 8 and 16 h later. Beginning on d 14, supplementation with Megalac-R was added to the CGF pellets at a rate of 1.59 kg/wk (as is). Supplementation frequency was maintained for the same 6 cows in each treatment for 3 wk. For the last 3 d of the study (d 32 to 34), blood samples were taken pre and post supplementation, similar to d 11 to 13. Blood samples were analyzed for concentrations of serum NEFA and blood urea nitrogen (BUN). Data were analyzed as a completely randomized design with double repeated measures, using cow as the experimental unit. The model included the fixed effects of treatment, day, hour (day), treatment × day, treatment × hour (day) interactions, and the random effect of cow. No effects of treatment ($P = 0.42$) or treatment × hour (day) ($P = 0.86$) were observed on serum NEFA concentrations. An effect of hour (day) ($P = 0.001$), and a treatment × day interaction ($P < 0.001$) were observed for NEFA concentrations; however, within each sampling day, no difference among treatments was observed ($P > 0.10$). No effects of treatment ($P = 0.74$), treatment × day ($P = 0.16$), or treatment × hour (day) ($P = 0.39$) were observed on BUN concentrations. There was an effect of day and hour (day) ($P < 0.001$), however, within each day, no difference among treatments was observed ($P > 0.10$). In conclusion, supplementing a mixture of CGF and Megalac-R either 3, 5, or 7 d/wk provided similar results with respect to concentrations of serum NEFA and BUN of lactating beef cows, thus implying that the frequency of supplementation could be reduced without compromising their health or metabolism.

Key Words: frequency of supplementation, lactating beef cows, Megalac-R

1328 Supplementation of palm oil to lactating dairy cows fed a high fat diet during summer.

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Dairy cows subjected to heat stress can benefit from fat supplementation. We evaluated the response of lactating cows to the supplementation of a basal diet containing fat from whole cottonseed and roasted soybeans [3.2% of DM as ether extract (EE) from oilseeds] with 2 palm oil sources (1.1% of DM as EE from supplements). Thirty cows were fed a standard diet for 14 d and were assigned to a treatment for 63 d, in a covariate adjusted randomized block design with repeated measures over time. Treatments were: Control (CTL), fractionated palm oil (F, 73.5% of fatty acids as C16:0 and 14.7% as C18:1), and calcium salt of palm oil (S, 41.5% of fatty acids as C16:0 and 38.4% as C18:1). Pre-planned contrasts were: CTL vs. (F + S) and F vs. S. The EE concentration of the diet was 7.3% of DM in CTL and 8.4% in F and S. The temperature humidity index was above 68 for 17.1 h/d during the experiment. Palm oil reduced rectal temperature ($P < 0.02$) and respiratory frequency ($P = 0.05$), but had no effect on sudoresis ($P = 0.97$) and jugular blood acid-base balance ($P > 0.31$). Rectal temperature at 2 PM was 38.9°C for S and 39.1°C for F ($P = 0.02$). Palm oil increased milk yield (31.0 vs. 30.1 kg/d, $P = 0.02$) and reduced DMI (19.2 vs. 19.9 kg/d, $P = 0.01$), increasing feed efficiency (1.65 vs. 1.54, $P = 0.01$), and S tended do reduce DMI ($P = 0.07$) and increase feed efficiency ($P = 0.01$) more than F. Secretions of milk fat and lactose were increased by 47 g/d ($P = 0.04$) and 37 g/d ($P = 0.08$) with palm oil, respectively. Plasma glucose concentration was similar among treatments ($P = 0.63$), as well as total tract apparent digestibility of EE ($P = 0.97$) and NDF ($P = 0.43$), the intake of TDN ($P = 0.17$), and BW ($P = 0.87$). The acetate to propionate ratio in ruminal fluid was 2.39 for F and 1.98 for S ($P = 0.05$), suggesting that palm oil sources differed in ruminal inertness. Ingestion time/DMI was 17.3 min for S and 14.9 min for F ($P = 0.01$). Lactating cows fed a diet rich in fat from oilseeds had increased feed efficiency and reduced signs of heat stress when fat from palm oil was supplemented.

Key Words: fat supplementation, heat stress, palm oil

Table 1328.

					P-value		
Item	CTL	F	S	SEM	Treat	CTL *vs.* F + S	F *vs.* S
Breaths/min	63.8	60.0	58.1	1.98	0.13	0.05	0.49
Rectal temperature, °C	39.15	39.07	38.91	0.050	<0.01	<0.01	0.02
DMI, kg/d	19.9	19.4	19.0	0.14	0.01	0.01	0.07
TDN[1], kg/d	15.3	15.1	13.8	0.65	0.17	0.22	0.16
Milk, kg/d	30.1	30.9	31.1	0.28	0.07	0.02	0.57
Fat, kg/d	0.922	0.962	0.975	0.0131	0.02	0.04	0.46
Lactose, kg/d	1.401	1.421	1.454	0.0172	0.08	0.08	0.18
Milk/DMI	1.54	1.62	1.68	0.012	0.01	0.01	0.01
BW, kg	616	617	618	3,1	0.87	0.64	0.81
Glucose, mg/dl	56.6	55.5	55.6	0.93	0.63	0.33	0.94
DNDF, % of intake	57.1	53.7	52.5	2.55	0.43	0.22	0.73
DEE, % of intake	71.0	70.7	70.4	1.87	0.97	0.85	0.90
Acetate/Propionate	1.89	2.39	1.98	0.150	0.06	0.12	0.05

[1] TDN = (Digestible OM intake – Digestible EE intake) + (Digestible EE intake x 2.25)

1329 Effects of dietary fat source on performance of lactating dairy cows fed a pre-mixed concentrate.

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Inclusion of a pre-blended concentrate (OneTrak; Cargill Corn Milling, Blair, NE) in the total mixed ration for dairy cows can benefit the producer by simplifying the daily mixing of dietary ingredients and providing a more uniform mix of dietary ingredients. Cow responses to fat supplementation can be affected by other dietary ingredients, but few studies have evaluated responses to dietary fat in diets reliant on non-forage fiber. OneTrak is a blend of feed ingredients from the wet corn milling industry supplemented with additional protein, minerals, and vitamins for high producing dairy cows. Our

objective was to evaluate productivity responses to dietary fat source when the ration contained 44.1% OneTrak, 35.8% corn silage, 10.8% corn grain, 7.8% alfalfa hay, and 1.5% soyhulls or fat source (DM basis). Seventy-two Holstein cows between 94 and 220 DIM (166 ± 25 DIM, parity 1.7 ± 0.9) were blocked by parity, stratified by DIM, and randomly assigned to pens (n = 6) within strata. Pens were randomly assigned to treatment sequence in a 3 × 3 Latin square design with 21-d periods ending with 4 d of data collection. Treatments consisted of a prilled saturated fat (SAT; Energy Booster 100, Milk Specialties Co., Dundee, IL), calcium salts of long-chain fatty acids (UNS; Megalac, Church and Dwight Co. Inc., Princeton, NJ), or no added dietary fat (CON), with fat sources included to provide 1.2% added fat (DM basis). Milk yield and composition, DMI, BW change, and BCS change were analyzed with mixed models using pen as the experimental unit. Contrasts were used to assess impact of added fat and the source of fat; significance was declared at $P < 0.05$. Milk yield tended to increase with added fat ($P = 0.06$; 33.5, 34.2, and 34.3 ± 1.3 kg/d for CON, SAT, and UNS, respectively). Protein content decreased with fat supplementation, to a greater degree for UNS (3.43, 3.37, and 3.31 ± 0.05% for CON, SAT, and UNS, respectively), but protein yield did not differ. Fat content, fat yield, and energy-corrected milk yield were not affected by treatment. Conversion of feed to milk tended to increase for UNS compared with SAT (1.41 vs. 1.38 ± 0.05; $P = 0.06$). No effects were observed for BW or BCS. Responses to dietary fat in diets containing OneTrak were similar to previous findings with more traditional diets.

Key Words: dietary fat, pre-mixed concentrate, non-forage fiber

1330 Effects of feeding different forms of polyunsaturated fatty acids on performance, plasma metabolites and milk fatty acid composition of dairy cows.

1331 Milk production responses to palmitic acid supplementation when fed as fatty acids or triglycerides. J. de Souza* and A. L. Lock, *Michigan State University, East Lansing.*

We evaluated the effects of feeding a palmitic acid-enriched supplement (PA; 85% C16:0) either as fatty acids (FA) or triglycerides (TG) on production responses of mid-lactation dairy cows. Fifteen Holstein cows (137 ± 49 DIM) were randomly assigned to treatment sequence in a 3 × 3 Latin square design. Treatments were a control diet (CON; no added PA), or 1.5% of FA added either as a FA supplement (PA-FA), or a TG supplement (PA-TG). PA replaced soyhulls and diets were balanced for glycerol content. Diets contained (% DM) 21% forage NDF, 17% CP, and 26% starch. Periods were 21 d in length with the final 5 d used for sample and data collection. The statistical model included the random effect of cow and the fixed effect of treatment, period and interaction between treatment and period. Two preplanned contrasts were used to evaluate: 1) the overall effect of PA treatments [CON vs. PA; 1/2 (PA-FA + PA-TG)]; and 2) the effect of PA as a FA or triglyceride supplement (PA-FA vs. PA-TG). PA treatments increased milk fat content (3.60 vs. 3.41%; $P < 0.01$), milk fat yield (1.69 vs. 1.60 kg/d; $P < 0.01$), yield of 16-carbon milk FA (570 vs. 471 g/d; $P < 0.01$), 3.5% FCM (47.6 vs. 46.5 kg/d; $P = 0.01$), and feed efficiency (3.5% FCM/DMI; 1.69 vs. 1.58; $P < 0.01$). PA did not affect DMI compared with CON (28.5 vs. 29.2 kg/d; $P = 0.13$), milk yield (47.0 vs. 47.4 kg/d; $P = 0.67$), milk protein yield (1.42 vs. 1.45 kg/d; $P = 0.15$), milk lactose yield (2.29 vs. 2.31 kg/d; $P = 0.46$), yield of de novo milk FA (360 vs. 370 g/d; $P = 0.23$), yield of preformed milk FA (642 vs. 630 g/d; $P = 0.56$), BW (720 vs. 723 kg; $P = 0.80$), or BCS (3.14 vs. 3.23; $P = 0.17$). PA-FA increased DMI compared to PA-TG (29.1 vs. 27.8 kg/d; $P = 0.05$), yield of 16-carbon milk FA (596 vs. 545 g/d; $P < 0.01$), and tended to increase milk yield (47.6 vs. 46.4 kg/d; $P = 0.06$), milk fat yield (1.71 vs. 1.66 kg/d; $P = 0.10$), and 3.5% FCM (48.1 vs. 47.2 kg/d; $P = 0.09$). In conclusion, the production response of dairy cows to PA tended to be greater for a FA than a TG supplement. Overall, PA increased milk fat yield, 3.5% FCM and feed efficiency in mid-lactation dairy cows.

Key Words: dairy cows performance, degree of esterification, palmitic acid

1332 Comparison of a palmitic acid-enriched triglyceride supplement and a calcium salts of palm fatty acids supplement on milk production responses of dairy cows. J. de Souza*and A. L. Lock, *Michigan State University, East Lansing.*

We evaluated the effects of feeding a palmitic acid-enriched triglyceride supplement (85% C16:0) and a calcium salts of palm fatty acids (45% C16:0 and 38% *cis*-9 C18:1) supplement on production responses of mid-lactation dairy cows. Fifteen Holstein cows (139 ± 39 DIM) were randomly assigned to treatment sequence in a 3 × 3 Latin square design. Treatments were a control diet (CON; no fat supplement), or 1.5% of fatty acids (FA) added either as a palmitic acid-enriched triglyceride supplement (PA-TG), or calcium salts of palm FA supplement (Ca-FA). The supplements replaced soyhulls and diets were balanced for glycerol and calcium content. Diets contained (% DM) 21% forage NDF, 17% CP, and 26% starch. Periods were 21 d in length with the final 5 d used for sample and data collection. The statistical model included the random effect of cow and the fixed effect of treatment, period and interaction between treatment and period. Ca-FA tended to decrease DMI compared with CON and PA-TG (29.5, 29.6 and 28.7 kg/d; $P = 0.10$; for CON, PA-TG and Ca-FA, respectively). PA-TG tended to increase milk yield compared

with CON, but did not differ from Ca-FA (48.3, 49.5 and 48.9 kg/d; $P = 0.10$; for CON, PA-TG and Ca-FA, respectively). Compared with CON and Ca-FA, PA-TG increased milk fat concentration (3.40, 3.57 and 3.50%; $P < 0.01$) and milk fat yield (1.64, 1.77 and 1.72 kg/d; $P < 0.01$; for CON, PA-TG and Ca-FA, respectively). Compared with CON, both PA-TG and Ca-FA increased 3.5% FCM (47.1, 49.7 and 48.9 kg/d; $P < 0.01$) and feed efficiency (3.5% FCM/DMI) (1.60, 1.68 and 1.71 for CON; $P < 0.01$ for CON, PA-TG and Ca-FA, respectively). Ca-FA tended to increase BW change compared with PA-TG and CON (0.61, 0.62 and 0.78 kg/d; $P = 0.08$) and BCS change (0.05, 0.06 and 0.12; $P = 0.10$; for CON, PA-TG and Ca-FA, respectively). Ca-FA decreased yield of de novo milk FA compared with CON and PA-TG (401, 393, and 371 g/d; $P = 0.01$), but increased yield of preformed milk FA (618, 640, and 700 g/d; $P = 0.01$), whereas PA-TG increased yield of 16-carbon milk FA compared with other treatments (500, 576, and 540 g/d; $P = 0.01$; for CON, PA-TG and Ca-FA, respectively). In conclusion, feeding a palmitic acid-enriched triglyceride supplement increased milk energy output due to increased yields of milk and milk fat, whereas feeding a calcium salts of palm FA supplement increased BW gain.

Key Words: calcium salts of fatty acids, dairy cow performance, palmitic acid

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1333 Changes in milk odd and branched-chain fatty acids during induction and recovery from biohydrogenation-induced milk fat depression.

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We have observed that the concentration of odd and branched-chain fatty acids (OBCFA) in milk fat markedly changes during biohydrogenation (BH) induced milk fat depression (MFD). The objective was to characterize the time course of changes in milk OBCFA during induction and recovery of BH-induced MFD. Nine Holstein cows were randomly assigned to a treatment sequence in a repeated design that allowed analysis of recovery from a MFD diet. A 36.9% NDF and 1.1% PUFA diet was fed during the control and recovery periods, and a 29.5% NDF and 3.7% PUFA diet was fed during the induction period. Treatment periods were 21 d long and milk was sampled every other day. Data were analyzed using the MIXED procedure of SAS with repeated measures, time was the repeated variable, and cow by treatment was the subject. Preplanned contrasts were control versus induction and control versus recovery at each time point. The production data has been previously published (Rico and Harvatine, 2013 JDS 96:6621). Briefly, milk fat percentage and yield decreased progressively during induction and were lower than control by d 3 and 5, respectively. Milk fat concentration and yield increased progressively when cows were fed the recovery diet and were not different from control on d 19 and 15, respectively. During induction of MFD milk fat content of *iso*-14:0, *iso*-15:0, *anteiso*-15:0, 15:0, *iso*-16:0,*anteiso*-17:0, 17:0, and total OBCFA decreased rapidly (3.8 to 3.0% of total FA; $P < 0.01$ for all) and generally the concentration of these fatty acids was lower than control by d 3 ($P < 0.05$ for all). Contrarily, during recovery milk fat content of *iso*-14:0, *iso*-15:0, *anteiso*-15:0, 15:0, *iso*-16:0,*anteiso*-17:0, 17:0, and total OBCFA increased rapidly and the concentration of these fatty acids was not different from control on d 3 ($P > 0.1$ for all). In conclusion, the changes in milk OBCFA during induction and recovery of MFD occur rapidly, suggesting that these milk fatty acids could be used as markers of altered rumen biohydrogenation during milk fat depression.

Key Words: fatty acids, milk, rumen

1334 Dynamics of enrichment of omega-3 fatty acids in plasma lipid fractions following a bolus dose in dairy cows.

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Transfer of dietary omega-3 fatty acids (n-3 FA) to milk is low. Understanding the trafficking of n-3 FA in plasma lipid fractions may allow improvements in this transfer. The objective of this experiment was to investigate the fate of n-3 FA in plasma lipids after an abomasal bolus infusion of n-3 FA. Ten ruminally cannulated, multiparous Holstein cows were used in a crossover design with 7 d periods. Treatments were abomasal infusion of 120 g (infused over 1 h) of a free FA mixture enriched in α-linolenic acid (EALA; 80 g of ALA) or in very long chain n-3 (EVLC; 45.5 g of Eicosapentaenoic acid [EPA] + 33 g of Docosahexaenoic acid [DHA]). Blood samples were collected at −6, 0, 6, 12, 30, 54, and 102 h relative to the bolus infusion. Data was analyzed as repeated measures and the model included random effects of cow nested in sequence, sequence and period and fixed effect of treatment, time and treatment by time (SAS). Plasma concentration of total n-3 FA peaked 6 h post infusion in both treatments and was higher in EVLC than in EALA ($P < 0.001$). At peak, plasma EPA and DHA were enriched 8.3 and 60 fold, respectively, in EVLC and plasma ALA was enriched by 1.3-fold in EALA. After peak, plasma ALA in EALA and EPA in EVLC gradually decreased over time, while plasma DHA in EVLC remained 40-fold enriched over baseline at 102 h. Treatments had no effect on plasma cholesterol esters (CE), phospholipids (PL) and NEFA concentration. In the plasma PL fraction, ALA in EALA and EPA in EVLC (mg/dL) peaked at 1.8 and 11 fold enrichment, respectively, 6 h post infusion and then gradually decreased over time while accumulating in CE, where they reached 1.2 and 2.8-fold enrichments at 102 h. Plasma DHA peaked at 6 h in CE and decreased rapidly back to pre bolus values, however it peaked later (30 h) and remained high in PL (0.03 to 1.28 mg/dL from −6 to 102 h). In conclusion, n-3

FA differ in their enrichment and depletion in specific plasma lipid fractions and their transfer to milk might be limited due to trafficking of very long chain n-3 FA into plasma lipid pools unavailable to the mammary gland.

Key Words: omega-3, fatty acids, plasma lipids

1335 Intravenous nicotinic acid suppresses adipose tissue lipolysis in Holstein dairy cows.

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The mobilization of adipose tissue is linked with insulin resistance in dairy cattle. Feeding rumen-protected nicotinic acid (NA) or abomasal infusion of free NA can suppress lipolysis; however, the efficacy of intravenous NA to lower circulating NEFA is uncertain. Therefore, our objective was to evaluate the effects of intravenous NA infusion on lipolysis and insulin tolerance. Nine non-pregnant, non-lactating Holstein cows (617 ± 51 kg BW) were utilized in a 3 × 3 balanced Latin square crossover design. Treatments consisted of ad libitum feeding, fasting, or fasting with intravenous NA infusion (5 mg of NA/h per kg BW in saline) for 32 h. Equal volumes of saline were infused in cows not administered NA. Post-treatment, all cows were provided ad libitum access to feed and monitored for 8 h. Two 14-d washouts were included. When provided access, cows were fed a mixed ration of grass hay and ground corn to meet or exceed requirements. Fasted cows were provided vitamins and minerals. Jugular catheters were inserted 16 h before use. An insulin tolerance test (0.1 IU/kg BW; ITT) was performed at h 32, relative to initiation of treatment. Blood was collected routinely. Serum was analyzed using colorimetry. Data were analyzed using a mixed model with repeated measures with fixed effects of treatment and time. Relative to feeding, fasting increased lipolysis by h 2 (114 vs. 65 μM; $P < 0.01$), a response that progressively increased to h 32 (749 vs. 76 μM; $P < 0.01$). NA caused a consistent elevation in NEFA compared to fed cows, beginning at h 10 (77 vs. 51 μM; $P < 0.05$). NA reduced fasting NEFA area under the curve (0 to 32 h) by 55% ($P < 0.01$). Characteristic of NA, serum NEFA surged to 2,936 μM following removal ($P < 0.01$), a response accompanied by a treatment-specific increase in serum triacylglycerol and glucose ($P < 0.01$). In contrast, serum glucose and triacylglycerol were not modified with treatment. Relative to feeding, fasting without NA elevated serum cholesterol by h 16 ($P < 0.01$), a response delayed for fasted cows infused NA (h 24; $P < 0.05$). Fasting without NA reduced insulin-stimulated glucose uptake 38% by min 30 of ITT ($P < 0.01$), relative to feeding; however, NA did not improve glucose uptake. We conclude that the intravenous infusion of NA can inhibit lipolysis in dairy cattle; however, complete suppression of NEFA mobilization is not sustained with prolonged infusion.

Key Words: dairy cow, lipolysis, nicotinic acid

1336 Ruminal metabolism of fatty acids from fish oil or algae in steers fed a finishing diet.

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Supplementing cattle with sources of unsaturated fatty acids in the diet could improve the fat profile of the meat, but unsaturated fats suffer biohydrogenation by rumen bacteria. The objective of this study was to evaluate heterotrophically grown microalgae as a source of omega-3 fatty acids in steers fed a high grain finishing diet. Eight steers were used in a replicated 4 × 4 Latin square (LS) design experiment with each period lasting 21 d. The diet was based on cracked corn (75%), corn silage (7.5%) and fescue hay (7.5%) offered at 1.75 × NEm. The treatments were control, tallow (60 g/d), fish oil (60 g/d) and intact algae (100 g/d). All treatments were dosed through a ruminal fistula mixed with 450 g of diet. Total urine and feces were collected d 15 to 21. Reticulum and omasal samples were obtained for each hour from 0700 to 1800 during d 16 to 18. Omasal contents were collected using a vacuum sampling pump and reticulum samples by placing a collection bottle in the reticulum. Rumen fluid was collected at 2 h intervals from 0700 to 1700 on d 19 for pH and VFA analysis. Blood plasma was collected on d 21 of sample collection for fatty acid profile. The experiment was analyzed as a LS design with a 2 × 2 factorial using mixed models in SAS. There was no difference among treatments for DMI, urine or fecal excretion, N balance, total VFA concentrations, omasal or reticular flow, and apparent digestibility. Reticulum samples indicated greater amounts of DM exiting the rumen and were not used for measures of rumen digestibility. Control animals had lower ruminal pH when compared to other treatments ($P = 0.0012$). Animals consuming algae had higher fecal crude fat digestibility ($P = 0.02$) when compared with fish oil. Algae and fish oil had highest percent of total long chain fatty acid digestibility in feces when compared to tallow ($P = 0.0830$). Fish oil, algae and tallow had lower blood plasma C18:0 than control ($P = 0.01$). Algae increased flow of C18:1 isomers compared with fish oil ($P = 0.04$) and increased DHA in plasma ($P = 0.02$) but this was not evident from omasal fatty acid flow. These data indicate that algae feeding may have potential to alter the fatty acid profile of finishing steers.

Key Words: algae, fat, omasum, polyunsaturated fatty acid, DHA

1337 Increases in milk fat yield are maintained with prolonged palmitic acid supplementation in mid-lactation dairy cows.

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Supplementing palmitic acid (C16:0) increases yields of milk and milk fat in mid-lactation dairy cows. Because previous research has characterized the effects of short-term C16:0

Table 1338.

Table 1. Feedlot performance of Nellore bullocks fed different sources of ruminally protected fats

Item	Treatment			SEM	*P*-Value	Contrast	
	CON	NUT	BRP			C1	C2
Initial BW, kg	315	315	315	1.52			
Final BW, kg	476	508	524	7.06	<0.01	<0.01	0.13
DMI, kg/d	7,27	8,15	8,08	0.24	0.03	<0.01	0.83
ADG, kg/d	1,137	1,366	1,475	0.05	<0.01	<0.01	0.11
G:F, kg gain/kg DM	0,156	0,168	0,183	0.003	<0.01	<0.01	<0.01
HCW, kg	268	284	297	4.16	<0.01	<0.01	0.03
Dressing Percentage, %	56.4	55.9	56.8	0.31	0.18	0.91	0.07
Carcass gain, kg	105	121	134	4.05	<0.01	<0.01	0.02
ADG Carcass, kg/d	0,740	0,853	0,946	0.03	<0.01	<0.01	0.03

CON= Control; NUT= Nutrigordura®, ruminally protected soil bean oil; BRP= Blend of ruminally protected vegetable oils.
Considered statistically significant differences at the 10% significance by f test.
DMI = dry matter intake; ADG= average daily gain; G:F = gain-to-feed ratio; FC = feed conversion; HCW= hot carcass weight; Dressing Percentage = ((HWC/BW)*100); Carcass gain = (HWC – Initial Carcass Weight (which was obtained by regression of carcass weight of six animals slaughtered at the beginning of the experiment).
C1= CON vs NUT+BRP; C2= NUT vs BRP.

feeding (~14 to 28 d) on production parameters, our objective was to determine whether prolonged C16:0 supplementation can maintain milk fat yield and FA incorporation into milk fat. Twenty multiparous Holstein cows were enrolled in a study consisting of a 5 d covariate, 49 d treatment, and 14 d post-treatment evaluation. Cows received a sorghum silage-based diet and were randomly assigned to treatments consisting of no added fat (control; soyhull pellets; n = 10; 138 ± 45 DIM) or C16:0 at 4% of ration DM (98% C16:0; PALM; n = 10; 136 ± 44 DIM). Milk yields were recorded and samples were composited at wk 0, 3, and 7 relative to the start of the treatment period, and 2 wk post-treatment. Data were analyzed as repeated measures using a mixed model with the fixed effects of treatment and time. Effects of PALM are presented as changes relative to control. We observed that PALM increased yields of milk and milk fat by wk 3 and 7 (P < 0.05), without changing milk fat concentration (P = 0.33). PALM increases in milk fat yield were preserved post-treatment (P < 0.05). PALM increased milk C16:0 yield by 52 and 46% by wk 3 and 7, respectively (P < 0.01). Similar observations were observed for yields of milk *cis*-9 C16:1. Although yields of de novo synthesized and preformed FA in milk remained unchanged, milk saturated FA yield increased in PALM by wk 3 and 7 (P < 0.01). Post-treatment, the yields of C16:0 (P = 0.19) and *cis*-9 C16:1 (P = 0.49) in PALM were comparable to control. Post-treatment, the sustained increase in milk fat yield with PALM was due to increased yields of de novo and preformed FA in milk (P < 0.01). Comparable to changes in milk FA yields, PALM increased milk C16:0 concentrations by 26 and 21% by wk 3 and 7, respectively (P < 0.01). Concentrations of milk de novo synthesized and unsaturated FA were lower in PALM-fed cows (P < 0.01). We did not observe any differences in the concentrations of milk FA post-treatment. We conclude that feeding mid-lactation dairy cows C16:0 for 7 wk maintained milk fat synthesis for the duration of supplementation because of sustained C16:0 and *cis*-9 C16:1 incorporation.

Key Words: fatty acid, milk fat, palmitic acid

1338 Feedlot performance of Nellore bullocks fed with two different types of ruminally protected fat.

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The objective of the study was to evaluate two different sources of ruminally protected fat on feedlot performance of Nellore bullocks. It was used 53 intact Nellore males with 315 ± 5,9 kg of initial body weight (IBW) and 20 mo old. Six animals were random selected and harvested at the first day of study for carcass gain calculation while 47 animals were allocated in individual pens for feedlot performance evaluation. Trial design was randomized blocks (based on IBW) divided in 3 treatments: Control– no addition of fat (CON, n = 16), Nutrigordura®- ruminally protected soybean oil (NUT, n = 16) and a blend of ruminally protected vegetable oils containing both saturated and unsaturated sources (BRP, n = 15). Animals were fed for 140 d with a 88% concentrate diet (14.2% of CP and 2.74 of Mcal/kg of DM, for NUT and BRP; 14.4% of CP and 2.63 Mcal/kg of DM for CON) composed of grounded corn, citrus pulp, peanut meal, trace minerals supplement and sugarcane bagasse. Diets of NUT and BRP treatments were isoproteic and isoenergetic with the same inclusion of protected fat (3.36% of DM). Animals were fed twice daily with total mixed ration management. Animals were considered as

experimental unit and variables were analyzed using ANOVA ($P \leq 0.10$; PROC MIXED of SAS), and means were compared by contrasts (C1 = CON vs. NUT+BRP; and C2 = NUT vs. BRP). No difference was observed for Dressing Percentage ($P = 0.18$; Table 1). However, differences ($P < 0.01$) were observed for final BW, DMI, and ADG, for animals fed NUT or BRP, compared to CON (C1). Additionally, it was observed differences in both contrasts (C1: $P < 0.01$, C2: $P < 0.10$) for feed efficiency (G:F), Hot Carcass Weight (HCW), Carcass Gain and ADG of carcass, whereas animals fed BRP presented better feedlot performance than CON and NUT (C2). Bullocks fed BRP presented carcasses 13 kg heavier ($P = 0.03$) than NUT. In conclusion, ruminally protected fat increases feedlot performance of Nellore bullocks and BRP provides better benefits (ADG, G:F, HCW and Carcass Gain) than a ruminally protected fat derived from soybean oil.

Key Words: nutrition, protected fat, saturated fatty acid

1339 Studies on different energy density of close-up diets on energy metabolism and lactation performance in montbeliarde-sired crossbred holstein cows.

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The objective of the experiment were to evaluate the effects of prepartum dietary energy density on dry matter intake (DMI), lactation performance, energy metabolism in montbeliarde-sired crossbred holstein cows. Eighteen dry cows (Half primiparous and half multiparous) were blocked and assigned randomly to three groups fed a low concentrate diet (Concentrate is 0.3% of body weight), middle concentrate diet (Concentrate is 0.6% of body weight), high concentrate diet (Concentrate is 0.9% of body weight) from 21 d before expected day of calving, and corn stover was free to access choice. After parturition, all cows were fed the same lactation diet to 28 d in milk. The DMI, net energy intake (NEI) and energy balance (EB) of prepartum were significantly decreased by the reduced amount of concentrate added. The 0.9% group consumed 43.52% more DMI, compared with 0.3% group in the last 1 wk before calving. The different amount of concentrate added had no effect on DMI and NEI, EB, milk yield in first 4 wk of lactation. Overall, energy metabolism and lactation performance of postpartum were not affected by energy density of the three treatments during the close-up period, and the 0.3% group is more economical compared with other groups.

Key Words: transition cow, dietary energy density, energy metabolism

1340 Prepartum body condition score and plane of nutrition affect the hepatic transcriptome during the transition period in grazing dairy cows.

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A transcriptomic approach was used to evaluate potential interactions between prepartum degree of body condition (BCS) and feeding management in the weeks before calving on hepatic metabolism during the transition period. Thirty-two mid-lactation grazing dairy cows of mixed age and breed were randomly allocated to one of four treatment groups in a 2 × 2 factorial arrangement: two prepartum BCS categories [4.0 (thin, BCS4) and 5.0 (optimal, BCS5); based on a 10-point scale], and two levels of energy intake during the 3 wk preceding calving (75 and 125% of estimated requirements). Liver samples were obtained at −7, 7, and 28 d relative to parturition and subsequent RNA was hybridized to the Agilent 44K Bovine (V2) Microarray chip. Data were adjusted for dye and array effect and a MIXED model with repeated measures was then fitted to the normalized $\log_2$–tranformed adjusted ratios using Proc MIXED. Differentially expressed genes (DEG) with fold change ≤ -1.5 and ≥ 1.5, and P-value ≤ 0.01 were considered for downstream analysis. The Dynamic Impact Approach was used for pathway analysis, and Ingenuity Pathway Analysis was used for gene network analysis. The greater number of differentially expressed genes in BCS4 cows in response to prepartum feed allowance underscored that these animals were more responsive to prepartum nutrition management than optimally-conditioned cows. Independent of prepartum BCS, however, pathway analysis revealed that prepartal feeding level had a marked impact on carbohydrate, amino acid, lipid, and glycan metabolism. Altered carbohydrate and amino acid metabolism indicated a greater and more prolonged negative energy balance post-calving in BCS5 cows overfed prepartum. This was surmised by the opposite effect of pre-calving feeding in BCS4 compared with BCS5 cows on pathways related to amino acid, vitamin, and co-factor metabolism. The prepartum feed restriction ameliorated the metabolic adaptation to the new lactation in BCS5 cows, while detrimentally affecting BCS4 cows, which seemed to better adapt when overfed. Alterations in the glycosaminoglycan synthesis pathway supported this idea, indicating better hepatic health status in feed-restricted BCS5 and overfed BCS4 cows. The IPA network analysis indicated liver damage in feed-restricted thin cows, likely due to metabolic overload. Overall, the data indicate that overfeeding in late-pregnancy should be limited to underconditioned cows, while cows with optimal degree of body condition should be maintained on an

Table 1339.

Table 1.Effect of close-up dietary amount of concentrate on DMI, NEI, Milk yield and EB intake

Item	Dietary treatments			SEM	*P*-value
	0.3%	0.6%	0.9%		Diet
DMI，kg/d					
Prepartum					
-3 ~ -1 W	7.04[a]	8.58[b]	9.94[c]	0.196	<0.001
-1 W	6.87[a]	8.37[b]	9.86[c]	0.255	<0.001
Postpartum					
1 W	10.48	10.5	11.00	0.381	0.57
2 ~ 4 W	16.77	18.15	18.97	0.922	0.27
NEI，MJ/d					
Prepartum					
-3 ~ -1W	48.69[a]	60.72[b]	71.23[c]	1.711	< 0.001
-1 W	47.59[a]	59.33[b]	70.67[c]	2.243	< 0.001
Postpartum					
1 W	78.01	78.19	81.75	2.921	0.60
2 ~ 4 W	119.76	129.58	135.43	6.583	0.27
Milk yield，kg/d					
1W	18.41	17.00	18.74	0.825	0.67
2 ~ 4 W	30.36	28.84	31.13	2.161	0.75
4% FCM yield，kg/d					
1W	20.42	19.27	20.27	2.077	0.91
2 ~ 4 W	30.29	29.02	31.49	2.769	0.82
EB，MJ/day					
Prepartum					
-3 ~ -1 W	-9.50[a]	2.04[b]	15.48[c]	1.228	< 0.001
-1 W	-11.88[a]	0.65[b]	14.91[c]	1.697	< 0.001
Postpartum					
1 W	-24.77	-21.23	-20.33	7.072	0.89
2 ~4W	-19.31	-18.38	-16.56	5.886	0.57

0.3%, 0.6%, 0.9% - concentrate is 0.3% ,0.6% and 0.9% of body weight, respectively.

a, b, c - different superscript letters with the same row represent a significant difference between treatments (P<0.05).

energy-restricted diet.

Key Words: BCS, prepartum nutrition, liver transcriptome

1341 Application of *Pediococcus pentosaceus* and chitinase to high moisture alfalfa hay at baling: effects on nutrient digestion and on growth performance of beef cattle.

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The objective of this study was to assess the effect of applying a *Pediococcus pentosaceus* and chitinase mixture (PED+CH) at baling on nutrient digestion and on growth performance of beef cattle. Pure alfalfa was harvested and sun-cured to either 23 to 30% (HMH) or 10 to 13% (NMH) moisture. The HMH (Treatment) was baled with application of PED (6.5×10^{11} cfu/tonne)+CH (1.5 g/tonne) and NMH was baled without additives (Control). A crossover experiment (Exp 1) used eight cannulated heifers that were divided into two groups and fed diets containing 77% of control or treated alfalfa hay and 33% concentrate (DM basis). Each period consisted of a 10-d adaption, 2-d for measuring rumen fermentation products and 7-d for measuring total tract digestibility using chromium oxide (Cr_2O_3) as an indigestible marker. In Exp 2, fifty Angus×Hereford crossed-bred steers (270 ± 1.12 kg) were stratified by BW and allocated randomly to two groups in 10 pens, and fed diets containing 57% (DM basis) of treated or control alfalfa hay for 112 d and DMI, ADG and feed efficiency (FE) were measured. Data were analyzed as a completely randomized design using PROC MIXED procedure of SAS with cattle (Exp 1) or pen (Exp 2) as the statistical unit. Differences among means were identified using LSMEANS with the PDIFF in SAS. Cattle fed both diets had similar ($P > 0.05$) DM, NDF and ADF digestibility. However, HMH alfalfa treated with PED+CH had lower ($P < 0.05$) CP digestibility as compared with NMH alfalfa hay. Both groups of cattle had similar rumen pH, VFA and ammonia concentrations and cellulolytic enzyme activity. The two groups of cattle also had similar ($P > 0.05$) DMI, ADG and FE over the 112-d backgrounding period. The similar rumen fermentation characteristics, nutrient total tract digestibility and growth performance between the 2 groups of cattle indicate that alfalfa HMH preserved with PED+CH exhibited similar ruminal and total tract digestibility and feed value to NMH alfalfa. The PED+CH additive has the potential to conserve high-moisture alfalfa hay so that its nutritive and feeding value is similar to that of sun-dried alfalfa hay.

Key Words: high moisture alfalfa hay, inoculant, digestibility beef cattle, growth performance

1342 The impact of *Saccharomyces cerevisiae* and *Lactobacillus acidophilus* on colon histomorphology and gene expression in rumen and ileum tissues of young dairy calves.

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Direct fed microbials (DFM) are increasingly used as a replacement for antibiotics growth promoters to maintain animal health, enhance performance and reduce environmental contamination. However, little information exists on the impact of DFM on the morphology of the gastro intestinal tract of calves and innate immune response during early life. The aim of this study was to evaluate the impact of *Lactobacillus acidophilus* and *Saccharomyces cerevisiae* on colon histomorphology and innate immune gene expression of rumen and ileum tissues of calves.

Forty eight Holstein calves (2 to 7 d-old) were grouped according to body weight and circulating IgG and randomly separated into 4 treatments: Control (CTRL)- fed milk replacer and starter diet introduced after the second week; CTRL supplemented with *Saccharomyces cerevisiae boulardii CNCM I-1079* (7.5×10^9 cfu/L milk replacer + 3×10^9 cfu/kg feed) (SCB); CTRL supplemented with *Lactobacillus acidophilus BT1386* (2.5×10^8 cfu/L milk replacer + 1×10^9cfu/kg feed) (LA); and CTRL supplemented with tetracycline (528 mg/L) and neomycin (357 mg/L) before weaning and chlortetracyclin (55 mg/kg) after weaning (ATB). Four calves per treatment were euthanized on Days 33 (d33; pre-weaning) and d96 (post-weaning) for RNA isolation and colon histomorphological studies. The expression levels of Muc1, Muc20, Claudin 3, TLR4, TLR6, TLR9 and TLR10 genes were analyzed by qPCR. Morphometric measurements of stained (hematoxylin & eosin and periodic acid Schiff) colon sections were used for the determination of crypt depth (NDPview 2 software) and goblet cell (imageJ software). The effects of treatments were analyzed following a complete randomized block design with repeated measures and Tukey adjustments for multiple comparisons. The levels of expression of genes were low in the ileum. In the rumen, Muc1 gene increased $P = 0.014$ whereas the expression of TLR 6 ($P = 0.07$) and TLR10 ($P = 0.081$) genes tended to increase with SCB when compared to CTRL. Crypt depth for both SCB and ATB decreased significantly ($P < 0.01$) on d33 and d96 as compared to LA and CTRL. Similarly, neutral mucins were increased ($P < 0.05$) with SCB (d33 and d96) and ATB (d33) as compared to LA and CTRL. Muc1 gene was up-regulated in the rumen but not in the ileum on d33 and d96. Data shows that feeding SCB altered the colon morphology and increased neutral mucin; an indication of early

maturation in the SCB treated group. Our results suggest that SCB could improve colon development in young dairy calves.

Key Words: Histomorphology, *Saccharomyces cerevisia, calf, Muc1 gene,* development

1343 Aflatoxin M1 levels reduction in milk after *Saccharomyces cerevisiae* or mannanoligosaccharides addition to aflatoxin B1 contaminated diet of dairy cows.

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The purpose of this study was to evaluate the ability of *Saccharomyces cerevisiae* (SC47) and a mananoligosaccharide (MOS) to bind aflatoxin B1 (AFB_1) in the diet of dairy cows fed with 200 ppb an AFB_1–contaminated diet daily and, consequently, to reduce the aflatoxin M_1 levels in milk. Toxigenic fungi that grow on crops can produce highly carcinogenic metabolites called aflatoxins (B_1, B_2, G_1, G_2). Aflatoxin M_1 is a hydroxylated AFB_1 metabolite secreted (0.3 to 6.2%) in milk of mammary glands of lactating animals. Thirty six early to mid-lactation dairy cows averaging 90 d were used in a 4 × 4 Latin square design with 3 replicates. Cows were blocked by parity, body weight and milk production. Ad libitum access to feed and water was provided. Within each replicate, cows were randomly assigned to 6 dietary treatments for 2 consecutive 7-d periods. Dietary treatments included: T1 Basic Diet (BD); T2 BD + AFB_1 [200 μg of AFB_1/kg of diet dry matter (DM)]; T3- BD + 10 g MOS/cow/day; T4- BD +AFB_1 [200 μg of AFB_1/kg of diet dry matter (DM)] + 10 g MOS/cow/day; T5- BD + 10 g SC47/cow/day and T6- BD + AFB_1 + 10 g SC47/cow/day. Milk samples were collected from first to fourth day, seventh and 10th to 14th day of the experimental period. The cows of treatments T2, T4 and T6 were feed with the AFB_1 contaminated diet until the 10th day of experiment. The AFM_1 analysis was performed using immunoaffinity clean-up and detection by HPLC with fluorescence detector. Adding SC47 or MOS to basal or AFB_1–contaminated diets at 10 g/day/animal had no effect on lactation performance. The maximum levels of AFM_1 averaged at 11th day were 2,04 +0,18 μg/L, 0,7+0,12 μg/L and 0,14+0.03 μg/L, respectively for cows fed BD + AFB_1 (T2), BD + AFB_1 + MOS (T4) and BD + AF + SC47. Transfer rates of AFB_1 from feed to milk (AFM_1) averaged 1.02, 0.35, 1.42, and 0.07% for cows fed BD + AFB_1 (T2), BD + AFB_1 + MOS (T4) and BD +AFB_1 + SC47, respectively. Results indicated that strain SC47 and MOS at 10 g/animal/day were effective in reducing milk AFM_1 concentrations in cows consuming a total mixed ration containing 200 μg of AFB_1/kg of DM.

Key Words: Yeast, mycotoxin, milk quality

1344 Effects of a plant extract-based feed additive on feed intake, milk production and composition, rumen fermentation, digestibility, and nitrogen utilization in lactating dairy cows.

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The objective of this study was to investigate the effect of a plant extract-based feed additive (PE, Laboratoires Phodé, France) on performance, rumen fermentation, nutrient digestibility, and nitrogen utilization in lactating dairy cows fed diets with 2 concentrations of CP. The study involved 21 Holstein cows (123 ± 58.4 d in milk) in a replicated 3 × 3 Latin square design experiment with 3, 28-d periods. Treatments were control (15.8% CP), a low CP diet (LCP, 14.0% CP), and LCP supplemented with 35 g/d PE (LCPPE). PE was mixed with one-third of the ration and top-dressed. The low CP diets decreased ($P < 0.01$) DMI compared with the control and there was no effect of PE on DMI (28.4, 27.4, and 26.9 kg/d for control, LCP, and LCPPE, respectively). Milk yield was similar (36.6 kg/d; SEM = 1.66, $P = 0.27$) among treatments. Treatment had no effect ($P = 0.14$) on feed efficiency (1.31, 1.33, and 1.36 kg/kg, respectively). Milk yield adjusted to 4% fat (FCM) was not affected by treatment; however, FCM feed efficiency as proportion of RUP intake (4% FCM ÷ RUP intake) was increased ($P = 0.05$) by LCPPE compared with the control and LCP (22.8, 20.7, and 20.2 g/g, respectively). Concentrations of milk fat, protein, and lactose and milk fat and protein yields were not affected ($P \geq 0.35$) by treatment. Milk N efficiency was higher ($P < 0.01$) for the low-protein diets compared with the control. Ruminal pH, lactate, ammonia, and VFA concentrations, except valerate, which was lowered ($P < 0.01$) by LCP, were also not affected ($P \geq 0.36$) by treatment. The low-protein diets had slightly higher ($P \leq 0.02$) total tract apparent digestibility of DM and organic matter, but lower CP digestibility than the control. PE did not affect ($P \geq 0.22$) nutrient digestibilities. The low-CP diets decreased ($P < 0.01$) urinary and fecal nitrogen excretions; nitrogen losses were not affected by PE. Excretion of purine derivatives in urine was not affected ($P = 0.17$) by treatment. Ruminal in situ degradability of dietary DM, CP, NDF, and ADF was also similar ($P \geq 0.31$) among treatments. In this study, dietary supplementation of PE had no effect on feed intake, production variables, feed efficiency, or nutrient digestibility, but increased FCM efficiency as proportion of RUP intake in lactating dairy cows.

Key Words: plant extract, dietary protein, milk production, feed efficiency, dairy cow

1345 Monensin and levels of narasin on rumen metabolism in lambs during adaptation to high-concentrate diets. D. M. Polizel*[1], S. S. Marques[2], M. F. Westphalen[3], M. H. Santos[1], M. V. C. Ferraz Junior[1], M. V. Biehl[3], R. G. Silva[1], I. Susin[3], and A. V. Pires[1,3], *[1]FMVZ/University of Sao Paulo, Pirassununga, Brazil, [2]Ponta Grossa State University, Ponta Grossa, Brazil, [3]ESALQ/University of Sao Paulo, Piracicaba, Brazil.*

The objective in this trial was to determine the effects of monensin and levels of narasin on short chain fatty acids (SCFA) profile and ruminal pH during adaptation of lambs fed high-concentrate diets. Fifteen White Dorper × Santa Inês and 15 Dorper × Santa Inês lambs, cannulated in the rumen, were assigned to a randomized complete block design, defined by breed and initial BW. Experimental diets were control (without ionophore), monensin (25 mg/kg DM) and 3 doses of narasin (5, 10, or 15 mg/kg DM), corresponding to the experimental diets C, M, N5, N10, and N15, respectively. The experimental period lasted 29 d. Rumen fluid was collected on Days 1, 7, 14, and 21, every 3 h, starting prior feeding, 3, 6, 9, and 12 after feeding. In every sampling time 20 mL of rumen fluid per animal were collected and these samples were stored in the same vial (1 vial per animal per day). Data were analyzed using the MIXED procedure (SAS Inst. Inc.). There were 2 contrasts previously defined (I: control vs. ionophores; II: monensin *vs*narasin). Orthogonal polynomials for the effects of levels of narasin (control, N5, N10, and N15) responses were determined by linear and quadratic effects. The effects were considered significant when $P < 0.10$, and tendency when $P < 0.15$. Experimental diets did not affect molar proportion of acetate (54.54 ± 1.05 mM/100mM), propionate (32.23 ± 2.00 mM/100mM), butyrate (9.07 ± 0.89 mM/100mM), isovalerate (1.61 ± 0.25 mM/100mM) and valerate (1.42 ± 0.12 mM/100mM). There was a tendency for quadratic effect of levels of narasin on isobutirate (C: 0.64; M: 0.72; N5: 0.85; N10: 0.70; N15: 0.70 mM/100mM; $P = 0.11$). Acetate:propionate ratio (2.04 ± 0.14) and ruminal pH (5.94 ± 0.07) were not affected by experimental diets. Animals fed the diet containing monensin tended to had lower total SCFA than animals fed narasin (C: 113.21; M: 102.24; N5: 110.22; N10: 111.32; N15: 109.25 mM/l; $P = 0.11$). There was no interaction between experimental diets and days for all variables. Monensin and narasin had a tendency to alter SCFA profile without affecting ruminal pH in lambs fed high concentrate diets during dietary adaptation.

Key Words: ionophores,lambs, rumen pH.

1346 Effect of narasin on rumen metabolism and dry matter intake in wethers fed high-forage diets. D. M. Polizel[1], M. F. Westphalen*[2], A. A. Miszura[1], M. H. Santos[1], R. G. Silva[1], A. V. Bertoloni[1], G. B. Oliveira[1], M. V. Biehl[2], M. V. C. Ferraz Junior[1], A. V. Pires[2], and I. Susin[2], *[1]FMVZ/University of Sao Paulo, Pirassununga, Brazil, [2]ESALQ/University of Sao Paulo, Piracicaba, Brazil.*

The objectives in this trial were to determine the effects of increasing levels of narasin on short chain fatty acid profile, pH and rumen protozoa concentration in whethers fed high-forage diets. Five White Dorper × Santa Inês wethers (BW 68.7 ± 2.1 kg), cannulated in the rumen, were used in 5 × 5 Latin Square design. Animals were fed daily and diet was composed of coastcross hay (91.0% DM; 67.2% NDF; 32.1% ADF; 6.8 CP; 5.5% ash). Narasin was offered twice a day and levels were 0 (control), 8, 16, 24 or 32 mg/kg DM, corresponding to 0, 80, 160, 240, and 320 mg of Zimprova 100®. The delivery vehicle of narasin was 20 g of ground corn containing the set dosage of narasin in 1 kg of DM. Every experimental period lasted 20 d and rumen fluid was collected in the last day, every 3 h, starting prior feeding, 3, 6, 9, and 12 h after feeding. Dry matter intake (DMI) was measured on d 20. Short-chain fatty acids (SCFA) and pH were analyzed as repeated measures over time. Protozoa concentration was analyzed at 3 h after feeding. Data were analyzed using MIXED procedure (SAS Inst. Inc.) and the LSMEANS option was used to generate individual means. Orthogonal polynomials for diet responses were determined by linear and quadratic effect. The effects were considered significant when $P < 0.10$. Increasing levels of narasin did not affect DMI (1.00 ± 0.12 kg/d; $P = 0.45$). There was an increased linear response for total SCFA (77.24, 81.30, 90.04, 83.65, 89.60 mM/L, $P = 0.02$). Acetate (78.40 ± 0.64 mM/100Mm, $P = 0.93$), propionate (15.03 ± 0.41 mM/100mM, $P = 0.79$), isobutyrate (0.62 ± 0.11 mM/100mM, $P = 0.97$), butyrate (4.34 ± 0.24 mM/100mM, $P = 0.62$), isovalerate (0.97 ± 0.19 mM/100mM, $P = 0.95$), valerate (0.64 ± 0.07 mM/100mM, $P = 0.30$) acetate-propionate ratio (5.28 ± 0.28, $P = 0.76$), pH (6.64 ± 0.13, $P = 0.46$) and rumen protozoa concentration ($2.44 \pm 0.22 \times 10^5$/ml, $P = 0.69$) were unaffected by the experimental diets. Increasing doses of narasin resulted in higher concentration of total SCFA.

Key Words: SCFA, ionophore, protozoa

1347 Monensin and levels of narasin on rumen metabolism in lambs fed high-concentrate diets.

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The objective in this trial was to determine the effects of monensin and narasin on rumen metabolism of lambs fed high-concentrate diets. Thirty Dorper × Santa Inês lambs, cannulated in the rumen, were assigned to a randomized complete block design, defined initial BW. Animals were fed daily and diets were composed of 90% concentrate and 10% hay. Diets were control, monensin (25 mg/kg DM) and doses of narasin (5, 10, or 15 mg/kg DM), corresponding to the experimental diets C, M, N5, N10, and N15, respectively. The experiment lasted 29 d. The first 24 d were used to adapt the lambs with experimental diets and the remaining 5 d were used for data collection. In the last day, rumen fluid was collected every 3 h, starting prior feeding, 3, 6, 9, and 12 h after feeding. Short chain fatty acids (SCFA) profile and pH were determined. Data were analyzed using the MIXED procedure (SAS). There were 2 contrasts previously defined (I: control vs. ionophores; II: monensin *vs*narasin). The effects of levels of narasin (control, N5, N10, and N15) were evaluated using linear and quadratic orthogonal contrasts. The effects were considered significant when $P < 0.10$. Animals fed diets containing ionophores had higher molar proportion of propionate than animals fed the control diet (C: 26.6; M: 33.3; N5: 31.0; N10: 33.7; N15: 30.2 mM/100mM; $P = 0.07$). There was an increased isobutyrate for animals fed narasin then animals fed monensin (C: 0.8; M: 0.7; N5: 0.8; N10: 0.8; N15: 0.8 mM/100 mM; $P = 0.06$). Diets containing monensin had lower butyrate than narasin ($P = 0.08$), however, the control diet had higher butyrate than the diets containing ionophore (C: 13.5; M: 9.4; N5: 11.5; N10: 11.1; N15: 11.4 mM/100 mM; $P = 0.02$). Experimental diets did not affect acetate (50.0 ± 2.4; $P = 0.41$), isovalerate (1.5 ± 0.2; $P = 0.70$) and valerate (1.3 ± 0.1; $P = 0.42$). Animals fed diets containing ionophore had lower acetate:propionate ratio than animals fed the control diet (C: 2.2; M: 1.7; N5: 1.9; N10: 1.6; N15: 2.0; $P = 0.06$). There was a decreased linear response of narasin levels on total SCFA (C: 133.4; M: 124.3; N5: 135.6; N10: 122.4; N15: 115.7; $P = 0.02$). Treatments did not affect ruminal pH (5.9 ± 0.1; $P = 0.90$). Monensin and narasin altered SCFA profile without effecting ruminal pH in lambs fed high-concentrate diets.

Key Words: acetate-propionate ratio, pH, propionate.

1348 Daily supplementation with an active dry yeast improved feed efficiency in lactating dairy cows.

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Research has demonstrated that supplementation with an active dry yeast (ADY) can have a positive effect on dairy cow performance. The aim of the current experiment was to test a new ADY which had been selected because it improved rumen fermentation in vitro and to measure its effects in vivo. The trial was split into a 3 wk pre-period followed by a 12 wk test period, which was further split into 3 wk periods. Forty-four cows (16 primiparous, 28 multiparous cows) with average DIM = 123 (ranging from 55 to 165) were allocated to 22 blocks on the basis of calving date, parity, weight, milk production and composition in the pre-period. Within block, cows were randomly assigned to either control (CTL) or treatment (LY). In the test period, CTL received 100 g of wheat pollards daily and the LY received 97 g wheat pollards + 3 g live yeast, delivering 60 billion cfu/cow/day, top-dressed on a partial TMR consisting of (on a DM basis) corn silage (65%), grass silage (29%) and protein supplement (6%). Concentrate requirement was delivered via an automated dispenser 3 times daily. Throughout the trial, individual milk yield, weight, and DMI (measured via Calan gates) was measured daily, averaged weekly. Milk composition was measured 4× a week, and BCS every 3 wk. Statistical analysis was performed by ANOVA using the pre-period as a covariate to assess LY effect on feed intake, milk production, milk composition and energy balance. Significance was declared at $P < 0.05$ and trends discussed at $0.05 < P < 0.1$. Results showed that over the total test period, LY tended to increase FPCM (32.25 vs. 31.53 kg/day, $P = 0.09$) and significantly increased feed efficiency kg FPCM yield/kg DMI (1.47 vs. 1.43, $P = 0.032$). Interestingly, in the last 3 wk, the effects on FPCM were higher, and the effects of LY reached significance (31.4 vs. 30.0, $P = 0.025$), driven by a significant increase in butterfat yield (1259 vs. 1193 g/day, $P = 0.009$). There were no significant effects of treatment on any of the other parameters measured. To conclude, daily supplementation of live yeast resulted in a significant increase in feed efficiency. There appeared to be a lag effect on performance and it was hypothesized this was due to time needed for the rumen microflora to adapt. Further trials will test this hypothesis.

Key Words: feed efficiency, lactation, yeast

1349 Effect of saponite (EcoMix) on toxin binding capacity, ruminal fermentation, diet digestibility and growth of steers fed high concentrate diets.

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Three experiments were conducted to determine the effect of increasing concentrations of the clay mineral, saponite (EcoMix, United Minerals Group), on toxin binding, ruminal fermentation, diet digestibility and growth of feedlot cattle. In experiment one, 150 mg of EcoMix was incubated in 10 mL of rumen fluid with 3 incremental concentrations of aflatoxin B_1 (AFB_1) or ergotamine tartate (ET) to determine binding capacity. In experiment two, 6 steers (initial BW = 596 ± 22.2 kg) were randomly allotted to 3 treatments in a replicated 3 × 3 Latin square design (21-d periods) to determine the effects of increasing amounts of EcoMix (0, 1, or 2%) on ruminal pH, VFA, and nutrient digestibility. EcoMix was top-dressed on an 80% concentrate diet at a rate of 0, 113, or 226 g/steer/d to achieve the 0, 1, and 2% treatments, respectively. In experiment three, 72 Angus × Simmental steers were blocked by BW (395 ± 9.9 kg) and allotted to the same 3 treatments (4 pens/treatment, 6 steers/pen) to determine the effects of EcoMix on performance. Steers were slaughtered at a target BW of 606 kg. EcoMix was able to effectively bind AFB_1 and ET at concentrations well above the normal physiological range (52 and 520 μg/mL), but % adsorption was decreased to 35.5 and 91.1% at 5200 μg/mL ($P < 0.0001$) for AFB_1 and ET, respectively. EcoMix linearly decreased ruminal lactate and propionate, and VFA production efficiency ($P \leq 0.04$), linearly increased formate and acetate:propionate ($P \leq 0.03$), and tended ($P = 0.07$) to linearly increase butyrate. EcoMix tended to linearly increase organic matter and crude protein apparent digestibility ($P = 0.06$). Ruminal pH, urine pH, and other digestibility measures did not differ among treatments ($P \geq 0.15$). During the first month there was a quadratic response of EcoMix on ADG ($P = 0.009$) and gain:feed ($P = 0.0003$), increasing from 0 to 1% EcoMix, and then decreasing from 1 to 2% EcoMix. However, during the second month, EcoMix decreased ADG and gain:feed linearly ($P \leq 0.03$) and overall ADG, DMI, or gain:feed were not impacted ($P \geq 0.46$). EcoMix linearly decreased marbling score ($P = 0.05$). Hepatic enzyme activity did not differ among treatments on d 0 or at slaughter ($P \geq 0.15$). In conclusion, EcoMix effectively binds ruminal toxins, decreases ruminal lactate, and improves performance during adaptation to a high concentrate feedlot diet.

Key Words: clay mineral, saponite, feedlot performance

1350 Use of *Aspergillus oryzae* extract containing α-amylase activity in finishing diets for Nellore cattle.

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The objective was to evaluate effects of supplementing *Aspergillus oryzae* extract containing α-amylase activity (Amaize®) in high concentrate diets fed finishing diets for Nellore cattle. The experiment was conducted at the Experimental Confinement Unit of Agência Paulista de Tecnologia dos Agronegócios-Colina/SP/Brasil. Fifty-four Nellore bulls (average age 24 mo.) with initial body weight 353 ± 13 kg were used in the study. Six animals were slaughtered initially (for subsequent calculation of carcass gain) and 48 individually-penned animals were used to evaluate performance. The experimental design was a randomized complete block with two treatments: 1) Control– no enzyme, and 2) Enzyme −5 g/Amaize® (Alltech Inc) per head daily. The experiment lasted 96 d, (24 d adaptation and three periods of 24 d each). The diet consisted

Table 1350.

Table 1. Means and mean standard error of Nellore performance variables in treatment with absence (control) and presence of *Aspergillus oryzae* extract containing α-amylase activity (Amaize®) with high concentrate in finishing diets for Nellore cattle

Variables	Tratament		SEM	*P-Value*
	Control	Enzyme		
DMI, kg/d	8.32	9.07	0.44	0.11
ADG, kg/d	1.187	1.330	0,055	0.08
G:F, kg ganho/kg MS	0.142	0.146	0.002	0.44
HCW, kg	267	276	4.74	0.09
Dressing Percentage, %	57.2	57.4	0.40	0.65
Carcass gain, kg	81.5	90.0	4.76	0.09
ADG Carcass, kg/d	0.87	0.96	0.05	0.09

Differences considered statistically significant at the 10% significance by t test.
ADG= average daily gain; DMI = dry matter intake; G:F = gain:feed; FC = feed conversion; HCW= hot carcass weight; Dressing Percentage = ((HWC/BW)*100); Carcass gain = (HWC – Initial estimated carcass weight (which was obtained by regression of carcass weight of six animals slaughtered at the beginning of the experiment).

of sugarcane bagasse (12.47% DM), ground corn (4 mm-hammer mill) (62.59% DM), citrus pulp (16.96% DM) and protein blend (52% soybean meal, 12% Optigen® (sustained release N), 36% mineral salt. Forage:concentrate was 12:88 and contained MS: 14.1% CP, 23.5% NDF and 2.62 Mcal/kg. The data were analyzed using the MIXED procedure with a fixed effect of treatment and weight block as a random effect, the differences between the means were compared by *t* test at 10% probability. No differences were observed for DMI, G:F and dressing percentage between animals receiving enzymes compared to controls (Table 1). However, there was an effect of Amaize on ADG ($P = 0.08$), which represented ~140 g over ADG when compared to controls. HCW, carcass gain and carcass ADG were numerically superior in cattle fed Amaize in carcass weight, and slaughter with an additional average weight of ~9 kg, which represents 3.37% more when compared to control weight values. Therefore the supplementation of *Aspergillus oryzae* extract containing α-amylase activity (Amaize®) with high concentrate finishing diets improves the performance of Nellore cattle.

Key Words: additives, enzymes, performance

1351 Inclusion of pelleted calcium hydroxide-treated corn stover in lactating Holstein cow diets: Effects on milk production and milk composition.

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Chemical treatment of corn stover with 6.6% $Ca(OH)_2$ (TCS) increases the availability of cellulose and hemicellulose, improving the feeding value of this abundant crop residue. The low bulk density limits transportation and the broader use of TCS. Manufacturing techniques were used to densify and fortify TCS to improve its nutritional value potentially making TCS an alternative to traditional forage sources. The objectives of this study were to evaluate the effects of feeding TCS as part of a pelleted feed supplement blended to have a nutrient profile that resembles corn gluten feed, a common byproduct feed used in US dairy and beef operations. Eight mid-lactation multiparous Holstein cows were used in a replicated 4 × 4 Latin square consisting of four 21-d periods to evaluate the effects of feeding pelleted TCS (PTCS) on milk production and composition. Diets were: 1) control (CON) containing corn silage and alfalfa haylage as the primary forages, or 2) the partial replacement of these forages with 21 (21PTCS) or 3) 40% (40PTCS) of the diet DM with PTCS, or 4) a combination of all ingredients used to manufacture PTCS that were not pelleted and fed at 40% (40NPTCS) of the diet DM. Milk production and 4% energy corrected milk did not differ ($P > 0.05$) among treatments. Compared to the CON, DMI was reduced ($P < 0.05$) with the inclusion of TCS regardless of physical form in the 40 PTCS and 40 NPTCS diets but was not different in the 21 PTCS diet (24.2, 23.0, 21.7, 21.3, and ± 0.97 kg/d, CON, 21PTCS, 40PTCS, and 40NPTCS, respectively). Milk fat percentage was reduced ($P < 0.05$) with the inclusion of TCS in the 21PTCS and 40PTCS diets and tended ($P = 0.09$) to be reduced in the 40NPTCS diet. However, milk fat yield was only reduced when cows were fed the 40PTCS diet. Percent milk protein and percent milk lactose were not affected by the inclusion of TCS in the diet ($P > 0.05$). Data indicate that partial replacement of corn silage and alfalfa haylage with a pelleted feed supplement containing TCS has no impact on 4% energy corrected milk yield although inclusion of PTCS at 40% of the diet DM reduces milkfat yield. These results suggest pelleted feed supplements containing TCS may serve as a valuable replacement for a portion of typical forages fed to lactating dairy cows.

Key Words: pelleted corn stover, milk fat, alternative forage

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1352 Influence of adding slow release urea and zeolite in growth performance and carcass traits of feedlot lambs.

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Twenty-four Pelibuey × Katahdin (45.4 ± 1.1 kg) crossbred male lambs were used in a 42-d feeding trial (6 pens per treatment in a randomized complete block design), to evaluate the influence of slow release urea and zeolite on growth performance and carcass characteristics. Lambs were fed a dry-rolled corn-based finishing diet (1.42 Mcal/kg of NEg; 14.6% of PC). Treatments consisted: 1) Control (C), 2) Slow release urea (SRU) (0.8%), 3) Zeolite (Z) (3%) and 4) combination of SRU and Z; DM intake averaged 1.282 ± 0.042 kg/d and was not affected ($P = 0.40$) by treatments. Compared with control lambs, SRU supplementation increased gain efficiency (13.14%, $P < 0.04$), average daily gain (17.8%, $P < 0.03$) and final body weight (3.60%, $P < 0.04$). Combination of slow release urea and zeolite supplementation affected ($P = 0.032$) hot carcass weight, longissimus muscle area (LM) and carcass dressing percentage (2.3%, $P = 0.04$), kidney-pelvic fat was not affected. Addition of slow release urea and zeolite combination improved growth performance and carcass traits of feedlot lambs.

Key Words: lambs, slow-release urea and zeolite

1353 Effect of different doses of a *Bacillus*-based probiotic on the in vitro digestibility of concentrates and forages. C. A. Oliveira[1], D. O. Sousa[1], J. F. Penso[1], P. F. Menegucci[2], and L. F. P. Silva[*1], [1]*University of Sao Paulo, Pirassununga, Brazil,* [2]*Chr. Hansen, Valinhos, Brazil.*

The objective was to evaluate the effect of different doses of probiotic containing $1.6x10^9$ CFU/g of *Bacillus licheniformis* and $1.6x10^9$ UFC/g of *Bacillus subtilis* (BioPlus® PS, Chr. Hansen) on in vitro digestibility of concentrates and forages. The feedstuffs analyzed included 2 types of concentrates: corn and sorghum, and 2 types of forages: sugarcane silage and *Megathirsus maximus* cv. Mombaça (mombaça-grass). The probiotic was added to the ruminal fluid simulating doses of 0, 1, 2, and 3 g head^{-1} d^{-1}. The doses of probiotic added to the rumen fluid was calculated supposing a volume of 37 L of rumen fluid per animal. Dry matter, NDF, and starch in vitro digestibility of feedstuffs were determined in 0.5 g of sample, in triplicate, after incubation for 6 and 12 h (concentrates); or for 24 and 48 h (forages), using the Daisy Incubator (ANKOM®Technology Corp., Fairpoint, NY, USA). The residues after fermentation were analyzed for NDF in the case of forages, and for starch in the case of concentrates. The experiment was repeated three times. Statistical model included the fixed effect of probiotic, feedstuff, and interaction between both factors, with the experiment repetitions as the random effect. Addition of probiotic improved 24-h NDF digestibility of both roughages (P = 0, 05), without a Dose × Feedstuff interaction (P = 0.36). There was a cubic effect of dose of probiotic on 24-h NDF digestibility, with the dose of 1 g head^{-1} d^{-1} promoting higher NDFD than the control (20.2 vs. 16.3%, P = 0.01). When analyzed after 48 h of incubation, there was a significant Dose × Feedstuff interaction (P < 0.01). Addition of 1 g head^{-1} d^{-1} of probiotic increased (P < 0.01) 48-h digestibility of mombaça-grass, but not of sugarcane silage (P = 0.73). Considering the effects on starch digestibility of concentrates, there was no effect of probiotic after 6 h of incubation (P > 0.05). However, after 12 h of incubation, there was a positive linear effect of addition of probiotic on starch digestibility of both concentrates (P < 0.01), with no Dose × Feedstuff interaction (P = 0.50). The addition of 3 g head^{-1} d^{-1} of probiotic increased by 10.9% starch digestibility after 12 h of incubation. In conclusion, addition of increasing doses of a bacillus based probiotic promoted a cubical increase in NDF digestibility of roughages, and a linear increased in starch digestibility of concentrates.

Key Words: fiber digestibility, starch digestibility, probiotic

1354 Net choline absorption of abomasally infused choline and rumen-protected choline in the lactating dairy cow. M. J. de Veth[*1], V. M. Artegoitia[2], S. R. Campagna[2], H. Lapierre[3], F. M. Harte[4], and C. L. Girard[3], [1]*BioNarus LLC, Cary, NC,* [2]*University of Tennessee, Knoxville,* [3]*Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada,* [4]*The Pennsylvania State University, University Park.*

Choline metabolites have a critical role in many biological processes and choline supplementation to the peripaturient dairy cow improves hepatic lipid metabolism. However, variability in responses to choline supplementation has highlighted a lack of understanding of choline absorption and metabolism in the lactating dairy cow. Our objective was to estimate net choline absorption by measuring net portal fluxes of choline and choline metabolites in cows receiving either dietary supplements of rumen-protected choline (RPC) or abomasal infusion of choline (AIC). Five lactating Holstein cows (237 ± 17 DIM) were used in a 5 × 5 Latin Square design, with 5-d treatment periods and a 2-d interval between periods. Treatments were 1) control (0 g/d choline), 2) 12.5 g/d choline fed as RPC, 3) 25 g/d choline fed as RPC, 4) 12.5 g/d choline provided as AIC, 5) 25 g/d choline provided as AIC. Choline chloride (CC) was the choline form for both sources; RPC (Reashure, Balchem Corporation) and AIC (CC70, Balchem Corporation) contained 21.6% and 52.3% choline ion, respectively. Cows were fed every 2 h to minimize post-prandial variation. On the last day of each period 9 blood samples were collected simultaneously from an artery and portal vein at 30-min intervals and analyzed for betaine, free choline (Cho), lysophosphatidylcholine, phosphocholine and sphingomyelin, using liquid chromatography-tandem mass spectrometry. The net portal flux of Cho (control- 1.7 mmol/h) increased linearly (P < 0.001) with AIC (4.0 and 7.1 mmol/h for 12.5 and 25 g/d AIC, respectively) indicating that the net absorption of Cho was 54% (95% confidence interval of 30 to 79%). No relationship was found between dose of RPC and net portal flux of Cho (P = 0.52). Net portal fluxes of the choline metabolites were not altered by choline treatment. However, the plasma arterial concentrations of betaine and phosphocholine increased (P < 0.001) in response to AIC: 30.6, 102.7 and 151.2 μ*M* and 3.47, 4.21 and 4.96 μ*M* for control, 12.5 and 25 g/d. In addition, plasma arterial concentration of phosphocholine increased (P < 0.01) with RPC, averaging 3.47, 3.81 and 4.08 μ*M* for control, 12.5 and 25 g/d, respectively). The results of this study suggests that AIC taken up by the gastrointestinal wall reached the portal circulation only as Cho and the incomplete recovery may indicate that a portion of AIC is metabolized by the portal-drained viscera of the lactating dairy cow.

Key Words: bioavailability, choline, cow

1355 Effects of Trigestamace on performance of lactating dairy cows. M. M. Masiero*[1], A. L. Kenny[1], R. L. Barnett[1], R. Morrison[2], and M. S. Kerley[1], [1]*University of Missouri, Columbia,* [2]*R&D LifeSciences, Menomonie, WI.*

Objective of this experiment was to determine if Trigestamace (mannan-oligosaccharide, β glucans and enzyme preparation), fed for 60 d to lactating dairy cows, altered milk production, efficiency and composition in early lactation (study initiated 14 to 45 d in milk). Sixty lactating Holstein cows were stratified by previous milk production and parity (2.2 ± 0.03 lactation number) and assigned randomly to control (CON) or CON with Trigestamace included (TRT) diets. Both diets (CON, 48.1% DM, 14.4% CP; TRT 48.1% DM, 15.0% CP) contained (DM basis) 32.5% alfalfa hay, 21.2% corn silage, 13.8% ground corn, 3.8% soybean hulls, 2.6% brewers grain, 26% protein and mineral. Treatment was added at a rate of 0.032% in the diet (as fed basis) providing about 17.7 g/d of Trigestamace based on feed intake. Cows were fed using Calan gates and individual intake measured. Milk yield was recorded twice daily and milk sampled once weekly and analyzed for protein (%), fat (%), lactose (%), somatic cell count (cells/mL) and milk urea nitrogen (%). Data were analyzed as a randomized complete design. Milk yield did not differ (P = 0.50; SEM = 0.22; CON 44.5, TRT 44.2 kg/d) between diets. Dry matter intake was greater (P = 0.01; SEM = 0.11) for cows fed CON (24.6 kg/d) compared to TRT (24.2 kg/d). Milk efficiency was greater (P = 0.02; SEM = 0.007) for cows fed TRT diet (1.86 kg milk/kg DMI) compared to CON (1.83 kg milk/kg DMI). Energy corrected milk (P = 0.97; SEM = 1.44; CON 43.52, TRT 43.44 kg/d) and 3.5% fat corrected milk (P = 0.93; SEM = 1.53; CON 45.1, TRT 44.9 kg/d) did not differ between diets. Milk fat (P = 0.92; SEM = 0.09; CON 3.80%, TRT 3.78%), milk protein (P = 0.42; SEM = 0.03; CON 2.79, TRT 2.82%), lactose (P = 0.59; SEM = 0.02; CON 4.89, TRT 4.91%), milk urea nitrogen (P = 0.96; SEM = 0.32; CON 13.3, TRT 13.4%) and somatic cell count (P = 0.89; SEM = 26.8; CON 79,779, TRT 71,837 cells/mL) did not differ between diets. In conclusion, adding Trigestamace to an early lactation dairy cattle diet reduced DMI without changing milk yield, resulting in a greater milk efficiency.

Key Words: milk performance, mannan-oligosaccharide, β glucans

1356 Effect of imprinted polymer based ergot-alkaloid adsorbent on in vitro ruminal fermentation. M. B. Kudupoje*, *Alltech-University of Kentucky Nutrition Research Alliance, Lexington.*

Previously, we have described the development and characterization of a synthetic polymer designed as an ergot-alkaloid adsorbent. Here, effects of ergotamine imprinted (MIP) and non-imprinted (NIP) methacrylate based polymer adsorbents on in vitro ruminal fermentation were evaluated in an experiment with a completely randomized design. Each adsorbent was evaluated at four different inclusion levels (0.3, 3, 30, 300 mg/0.5 g DM) and compared with a control which contained no adsorbent. Ruminal fluid for inoculum was pooled from 4 steers grazing endophyte-free fescue. Triplicate vessels were inoculated for each treatment in the 2 × 4 + 1 treatment structure. In each vessel, strained ruminal fluid (20 mL) was diluted with buffer (80 mL) under anaerobic conditions and incubated for 30 h at 39°C with 500mg (DM) alfalfa hay substrate. Gas pressure was monitored using an ANKOM RF gas production system at 1 min intervals. Fluid samples were collected following termination of fermentation at 30 h for ammonia-N, VFA and pH measurement. The cumulative gas production and production rate were determined using a Fitzhugh model [$y = (1 \pm e^{-rt})^n$] fit using nonlinear least squares methods. Statistical analysis was conducted using the GLM procedure of SAS, with model terms for polymer type, inclusion amount, and their interaction and orthogonal polynomial contrasts were used to evaluate effects of polymer inclusion level. There were no interactions ($P > 0.10$) between polymer type and inclusion level and no differences ($P > 0.10$) between polymer types. Although there was a quadratic effect ($P < 0.05$) on gas production rate with increasing polymer inclusion level, total gas production (plateau) was unaffected ($P > 0.10$) by inclusion level. Polymers did not affect ($P > 0.10$) total or individual VFAs or ammonia-N concentrations at any inclusion level. The pH declined linearly ($P < 0.01$) with increasing amount of polymer. However, given the logarithmic increase in polymer dose level, the influence on pH was minor (< 0.07 pH units) for all except the 300 mg inclusion level, which depressed pH an average of 0.24 units relative to control. Supplementation of methacrylate based polymer at inclusion rates from 0.3 to 300 mg/500 mg DM did not affect VFA profiles, total VFA concentrations, ammonia-N, or total gas production in rumen fluid containing alfalfa hay substrate. High inclusion levels of both imprinted and non-imprinted polymers lowered pH. However, the inclusion level at which this effect was observed far exceeds levels that would be used in practical supplementation strategies.

Key Words: Ergot alkaloid imprinted polymer rumen fermentation

1357 Effects of *Ascophyllum nodosum* meal and monensin on performance and iodine metabolism in lactating dairy cows. S. F. Reis[*1], A. F. Brito[1], C. P. Ghedini[1], D. C. Moura[2], and A. S. Oliveira[3], *[1]University of New Hampshire, Durham, [2]Universidade Federal de Mato Grosso, Cuiabá, Brazil, [3]Instituto de Ciências Agrárias e Ambientais, Universidade Federal de Mato Grosso– Campus Sinop, Sinop, Brazil.*

Ascoplyllum nodosum meal (ANOD) is a mineral-rich supplement with antimicrobial and antioxidant properties. The objective of the current study was to evaluate the impact of incremental amounts of ANOD on performance and iodine metabolism in lactating dairy cows. It was also of particular interest to compare the effects of ANOD against the ionophore monensin (MON) on animal performance. Five ruminally-cannulated lactating Jerseys cows were randomly assigned to 1 of 5 dietary treatments: 0 g (negative control), 57 g, 113 g, or 170 g of ANOD or 300 mg of MON (positive control) in a 5 × 5 Latin square design. Each experimental period lasted 28 d with 21 d for diet adaptation and 7 d for data and sample collection. Treatments were administered daily placed directly in the rumen. Cows were fed a TMR consisted (DM basis) of 40.5% mixed-mostly grass haylage, 25.5% corn silage, 21% corn meal, 3.5% roasted soybean, 7.5% soybean meal, and 2.0% minerals-vitamins premix. The TMR averaged (DM basis) 15.8% CP, 37.3% aNDFom, and 24.8% ADF. Milk samples were collected and analyzed for components using mid-infrared reflectance spectroscopy. Spot urinary and fecal grab samples were collected with internal markers used to estimate urinary volume (creatinine) and fecal output of DM (indigestible ADF). Blood was collected approximately 4 h after the morning feeding. Milk, feces, urine, and serum were analyzed for iodine using inductively coupled plasma mass spectrometry. The degrees of freedom for treatment were partitioned into 4 single-degree-of-freedom non-orthogonal contrasts: linear, quadratic, ANOD diets vs. MON diet, and 170 g ANOD diet vs. control diet. Results are shown in Table 1. Dry matter intake and serum concentrations of T_3 and T_4were not affected by treatments. Milk yield, concentrations and yields of milk fat and protein, and MUN responded quadratically in cows fed increasing amounts of ANOD. Iodine output in milk, urine, and feces, and serum iodine concentration increased linearly with feeding incremental amounts of ANOD. Concentrations of milk fat, protein, MUN, and yield of milk fat were greater when feeding MON vs. ANOD, and the difference was particularly larger when comparing MON vs. 170 g ANOD. Overall, ANOD supplementation linearly increased the concentration of iodine in serum, and the output of iodine in milk, feces, and urine. Feeding MON improved concentration and yields of milk components, but increased MUN when compared with ANOD.

Key Words: *Ascophyllum nodosum*, dairy cows, iodine

1358 Lactation performance and nutrient digestibility by dairy cows supplemented with calcium montmorillonite clay during an aflatoxin feeding challenge. A. D. Thomas[*1], C. Maki[2], E. M. Jimenez[3], S. E. Elmore[2], L. Kinman[3], A. Romoser[2], R. B. Harvey[2,4], T. Phillips[2], and H. A. Ramirez Ramirez[1], *[1]Iowa State University, Ames, [2]Texas A&M University, College Station, [3]Tarleton State University, Stephenville, TX, [4]United States Department of Agriculture, College Station, TX.*

Fifteen primiparous crossbred dairy cows (114 ± 14 DIM and 662 ± 52 kg BW) were used in replicated 5 × 5 Latin squares to evaluate the effects of feeding calcium montmorillonite clay (NovaSil Plus, NSP) on milk production and nutrient digestibility in rations contaminated with aflatoxin (AF). The

Table 1357.

Table 1. Effects of *Ascophillum nodosum* meal (ANOD) or monensin (MON) on performance and iodine metabolism in dairy cows

	ANOD (g/d)						Contrasts (*P*-values)			
Item	0	57	113	170	MON	SEM	Linear	Quad.	ANOD vs. MON	170 g ANOD vs. MOM
DMI, kg/d	20.1	19.8	19.7	19.8	19.2	0.60	0.48	0.61	0.10	0.17
Milk yield, kg/d	20.9	20.2	20.0	20.8	20.2	0.58	0.76	<0.01	0.65	0.10
Milk fat, %	4.70	4.70	4.80	4.60	5.00	0.06	0.85	0.001	<0.001	<0.001
Milk fat, kg/d	0.96	0.94	0.95	0.95	1.00	0.02	0.89	0.04	<0.01	0.02
Milk protein, %	3.59	3.62	3.62	3.55	3.64	0.11	0.07	<0.01	0.01	<0.001
Milk protein, kg/d	0.74	0.73	0.71	0.73	0.72	0.02	0.33	0.05	0.50	0.22
MUN, mg/dL	10.3	9.8	10.4	10.6	11.2	0.66	0.06	0.04	<0.001	0.01
Milk iodine, mg/d	7.3	14.4	19.5	24.6	6.1	1.7	<0.001	0.54	<0.001	<0.001
Urinary iodine, mg/d	4.3	13.0	15.3	22.3	6.3	1.9	<0.001	0.66	<0.001	<0.001
Fecal iodine, mg/d	20.5	48.1	60.6	86.6	20.1	8.0	<0.001	0.91	<0.001	<0.001
Serum iodine, ng/mL	106	208	303	362	109	20.1	<0.001	0.09	<0.001	<0.001
Serum T_3, ng/mL	1.08	1.03	1.01	0.97	1.02	0.71	0.27	0.97	0.79	0.57
Serum T_4, ng/mL	40.6	40.5	43.4	39.1	43.0	3.3	0.88	0.41	0.49	0.27

experiment consisted of five 14 d periods in which d 1 through 7 of each period were considered for data collection and d 8 through 14 were considered a wash-out phase. In each period, cows were randomly assigned to 1 of 5 dietary treatments: 1) control (CON), consisting of a basal total mix ration (TMR); 2) high dose NSP diet (NSP-1%), consisting of TMR plus 230 g of NSP; 3) aflatoxin diet (AFD), consisting of the TMR plus AF challenge; 4) low dose NSP with AF (NSP-0.5%+AFD), composed of TMR plus 115 g of NSP and AF challenge; 5) high dose NSP with AF (NSP-1%+AFD), consisting of TMR plus 230 g of NSP and AF challenge. Feed intake was recorded daily, TMR, milk and fecal samples were collected on d 6 and 7 of each period. Indigestible acid detergent fiber was used as an internal marker. Data were analyzed using the MIXED procedure of SAS where square, period within square and treatment were fixed effects and cow within square was random. Feed intake ($P = 0.34$) and fecal output ($P = 0.74$) were similar across treatments and averaged 19.7 ± 0.56 kg/d and 7.2 ± 0.56 kg/d, respectively. Digestibility of dry matter ($P = 0.75$), acid detergent fiber ($P = 0.74$), neutral detergent fiber ($P = 0.51$), and organic matter ($P = 0.75$) was similar across treatments averaging 64.0 ± 2.0%, 40.0 ± 3.2%, 41.6 ± 2.9%, and 68.0 ± 1.6%. Addition of NSP reduced milk AFM_1 from 1.10 ± 0.06 µg/L with the AF diet to 0.58 and 0.32 ± 0.06 µg/L with the NSP-0.5%+AF and NSP-1%+AF diets, respectively with no effect on milk yield. These results demonstrate that inclusion of calcium montmorillonite clay is an effective way to reduce aflatoxin excretion in milk with no deleterious effects digestibility of nutrients by dairy cows.

Key Words: food safety, mycotoxins

1359 Impact of a ferulic acid esterase producing lactobacilli on nutrient digestion of barley silage.

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Ferulic acid esterase (FAE) producing *Lactobacillus buchneri* inoculants have been shown to improve aerobic stability and ruminal fiber digestion. This study aimed to assess the effects of a FAE-producing inoculant applied at ensiling on rumen metabolism and nutrient total tract digestibility of whole crop barley silage. Approximately 100 tonnes of whole crop barley was cut at mid-dough and ensiled without (Control) or with a FAE producing-*L buchneri* mixed inoculant (Inoculated) in bunker silo. A crossover experiment was conducted using 8 cannulated heifers fed diets containing 73% (DM basis) of either control or inoculated silage that was ensiled for 104 d. Each period consisted of a 10-d adaption, 2-d sampling of rumen fluid and 7-d for measurement of digestibility using chromium oxide (Cr_2O_3) as an indigestible marker. Inoculated silage contained greater ($P < 0.01$) concentrations of acetic acid, propionic acid, NDF, and ADF concentration, but less ($P < 0.001$) water soluble carbohydrate than control silage after 104-d ensiling. Heifers fed diets containing inoculated silage had lower ($P < 0.05$) DMI than those fed the control diet, likely due to greater concentrations of acetic and propionic acid. Cattle consuming both diets had similar ($P > 0.05$) DM, NDF, ADF and CP digestibility, suggesting that the inoculant had no effects on total tract digestibility of these nutrients. Both groups of cattle had similar ($P > 0.05$) ruminal pH, protozoal numbers and fibrolytic enzyme activity. Ruminal concentration of total VFA tended ($P = 0.078$) to be lower whereas NH_3 tended ($P = 0.071$) to be greater in heifers fed inoculated as compared to control silage. Ruminal molar proportion of propionate was greater ($P < 0.001$) but molar proportion of butyrate was lower ($P < 0.001$), resulting in a lower ($P < 0.05$) acetate: propionate ratio in heifers fed inoculated as compared to control silage. These results indicate that FAE-producing inoculant applied at ensiling altered fermentation from a homolactic to heterolactic pattern during ensiling, had no effect on nutrient total tract digestibility but did have a positive impact on the acetate:propionate ratio.

Key Words: ferulic esterase-producing lactic acid bacteria, barley silage, total tract digestibility, rumen metabolism

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1360 Excretion of fumonisin B1 by dairy cows supplemented with calcium montmorillonite clay during a mycotoxin challenge.

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Six multiparous Holstein cows (662 ± 52 kg BW) in early lactation were used in a 2 × 2 crossover design to evaluate the effects of feeding calcium montmorillonite clay (Nova-Sil Plus, NSP) on excretion of fumonisin B1 (FB1) during a 3-d challenge consuming this mycotoxin. It was predicted that cows would consume 26 kg of dry matter, therefore NSP was fed at a dose equivalent to 0.5% of predicted dry matter intake equivalent to130 g/d. The FB1 challenge was performed by feeding 80 mg FB1/d via top dressed supplement. The experiment consisted of two 7-d periods in which d 1 through 3 of each period were considered for data collection and d 4 through 7 were considered a wash-out phase. In each period, cows were randomly assigned to 1 of 2 dietary treatments: 1) challenge diet (FBCH), consisting of a basal total mix ration (TMR) plus FB1 challenge; and 2) treatment diet with FB1 (NSP-0.5%+FBCH), consisting of basal TMR plus NSP supplement and FB1 challenge. Feed intake and

milk production were recorded daily, milk and urine samples were collected in the morning and evening from d 1 through 3 of each period. Data were analyzed using the MIXED procedure of SAS where period, treatment and period×treatment were fixed effects and cow within sequence was random. Milk yield was similar across treatments (P = 0.44) and averaged 40.5 ± 3.2 kg/d with no differences in milk composition for any treatment; presence of FB1 was not detected in milk samples. Concentration of FB1 in urine was not affected by treatment (P = 0.68) and averaged 0.51 and 0.47 ± 0.09 for FBCH and NSP-0.5%+FBCH, creatinine adjusted excretion was similar for both treatments (P = 0.86) averaging 0.89 ± 0.17 ng FB1/mg creatinine. These results demonstrate that dietary FB1 is not transferred to mammary secretions and that bovine urine is a suitable biomarker of fumonisin B1 exposure; further research is warranted to fully elucidate the effects of including calcium montmorillonite clay to reduce FB1 absorption by dairy cows.

Key Words: food safety, mycotoxins, milk quality

1361 Effect of rumen-protected *Capsicum* oleoresin on productivity and responses to a glucose tolerance test in lactating dairy cows.

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The objective of this experiment was to investigate the effects of rumen-protected *Capsicum* oleoresin (RPC) on productivity and responses to a glucose tolerance test in dairy cows. Nine multiparous Holstein cows (100 ± 9.1 d in milk; 665 ± 83.3 kg BW) were used in a replicated 3 × 3 Latin square design experiment balanced for residual effects with 3, 28-d periods. Treatments were 0 (control), 100, and 200 mg RPC/cow/d. RPC was mixed with a small portion of the total mixed ration and top-dressed. DMI (29.5 kg/d; SEM = 0.74) was not affected (P = 0.72) by RPC. Milk yield tended to increase (P = 0.06; SEM = 1.27) for RPC compared with the control: 42.8, 44.7, and 43.9 kg/d for the control, 100, and 200 mg RPC/cow/d, respectively. Feed efficiency was linearly increased (P < 0.01; SEM = 0.056) by RPC supplementation: 1.48, 1.52, and 1.57 kg/kg, respectively. Concentrations of fat, true protein, and lactose in milk were not affected ($P \geq 0.69$) by RPC. On the day of the glucose challenge, glucose was intravenously administered at 0.25 g/kg BW and blood samples were collected at 0, 5, 10, 15, 20, 30, 40, 50, 65, 80, and 110 min following administration. Serum glucose concentration peaked 5 min post-glucose administration. RPC did not affect serum glucose concentration during the glucose tolerance test. Insulin concentration at 5, 10, and 40 min and the area under the insulin concentration curve were lower ($P \leq 0.04$) for both RPC application rates compared with the control. Peak concentration of insulin tended to be decreased (P = 0.07) by RPC. Concentration of NEFA in serum was linearly increased (P = 0.03) by RPC at and after 65 min following glucose administration. Concentration of β-hydroxybutyrate in serum was not affected (P = 0.17) by RPC during the glucose tolerance test. In summary, milk yield and feed efficiency were increased by RPC in this experiment. RPC increased serum NEFA and decreased insulin concentration during the glucose tolerance test whereas glucose concentration was not affected by treatment. Data suggest that dietary supplementation of RPC increased insulin sensitivity and likely redirected glucose for lactose synthesis and milk production and also slightly enhanced fat mobilization in lactating dairy cows.

Key Words: capsicum, insulin sensitivity, milk production

1362 Supplementation of β-mannanase (CTCZYME) to lactating dairy cattle diets improves feed conversion efficiency and somatic cell count.

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Improving feed conversion efficiency (FCE) and health status of animals has economic and environmental benefit in dairy operations. Fibrolytic enzymes such as mannanases may improve nutrient digestion and utilization by releasing compounds contained within non-structural carbohydrates such as mannan and xylan, and may also help immune status. A trial was conducted to investigate the effects of β-mannanase supplementation on nutrient digestibility, FCE, and enteric methane emissions in lactating dairy cows. Twelve post peak-lactation multiparous Holstein cows producing 45.5 ± 6.6 kg/d milk at 116 ± 19.0 DIM were randomly allocated to one of 3 treatments in a 3 × 3 Latin square design with 3 18-d periods. Cows were fed the same basal diet with treatment 1 used as control and treatments 2 and 3 contained β-mannanase supplementation at 0.1% (low supplement [LS]), or 0.2% (high supplement [HS]) of DM. Effects of β-mannanase supplementation on nutrient intake and utilization, milk production efficiency, BW change, and methane emissions were determined using the MIXED procedure of SAS (version 9.4). Supplementation of β-mannanase enzyme did not affect DMI, milk yield, and milk composition. Somatic cell counts in milk was lower (P = 0.023) for cows fed the LS diet compared to cows fed control and HS diets. Methane yield (per unit of DMI) and intensity (per unit of milk yield or milk protein yield) were not affected by β-mannanase supplementation. Cows fed LS diet had lower DM, OM, and CP digestibility compared to cows fed control and HS diets. Starch, NDF, and ADF digestibility were not affected. Cows fed LS significantly improved (P < 0.05) FCE, BW gain, and efficiency of converting dietary N to milk protein compared to cows fed the control diet. β-mannanase supplementation had no effect on N excreted in

feces and urine. Dietary supplementation of β-mannanase can improve FCE, BW gain, and udder health of mid-lactating dairy cows without affecting methane emissions and manure N excretions. The role of β-mannanase supplementation may be more critical for early lactating cows, which are generally under significant metabolic and immune challenges and more likely to be in negative energy balance.

Key Words: dairy, feed efficiency, b-mannanase

1363 Effects of essential oils and exogenous enzyme in feedlot finishing cattle diets high in flint corn ground at different particle sizes.

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The objective of this study was to evaluate the interaction between 2 feed additives– MON (Sodium Monensin, Tortuga®) vs. CRINA-RUM (the combination of essential oils- Crina® Ruminants, DSM® and α-amylase- Ronozyme® RumiStar™) and 2 different groundflint corn particle sizes- ground corn (GC = 1.82 mm average particle size) vs. coarsely ground corn (CGC = 2.53 mm average particle size) on performance of finishing Nellore bulls. Two hundred fifty-six Nellore bulls (initial BW = 360 kg ± 38) were fed during 99 d with diets containing 82.5% ground corn (1.82 or 2.53 mm), 8.5% sugarcane bagasse, 5% soybean meal, 3% minerals-vitamins supplement and 1% urea. Animals were blocked based on initial BW and randomly allocated in 48 pens. Treatments were: GC + MON (1.82 mm ground corn and sodium monensin- 26 mg/kg DM), GC + CRINA-RUM (1.82 mm ground corn and the combination of essential oils- 90 mg/kg DM + α-amylase- 560 mg/kg DM), CGC + MON (2.53 mm ground corn and sodium monensin- 26 mg/kg DM) and CGC + CRINA-RUM (2.53 mm ground corn and the combination of essential oils- 90 mg/kg DM + α-amylase- 560 mg/kg DM). The data were analyzed using PROC MIXED of SAS in a 2 × 2 factorial arrangement (2 ground corn particle sizes and 2 feed additives). Pen was considered the experimental unit. No effect of treatment ($P > 0.05$) was observed for final BW. Animals fed CGC (2.53-mm) showed a tendency to greater average daily gain (ADG; $P = 0.08$) than animals fed GC (1.82 mm) – 1.60 and 1.50 kg, respectively. Effect of additive was also observed for DMI. Sodium Monensin (MON) decreased ($P = 0.013$) DMI compared to the combination of essential oils and α-amylase (CRINA-RUM) – 8.70 and 9.34 kg, respectively. No effects of treatment ($P > 0.05$) were observed on feed efficiency (G:F) and dressing percentage. There was an interaction effect ($P = 0.02$) between ground corn particle size and feed additives for hot carcass weight (HCW). Animals fed CGC diets and CRINA-RUM presented 11.5 kg greater HCW ($P < 0.05$) compared to animals fed CGC and MON- 295.2 and 283.7 kg, respectively. On the other hand, no effects ($P > 0.05$) of additives were observed for HWC on GC diets. The CRINA-RUM combination for finishing cattle fed flint CGC diets increases HCW and can be an effective substitute for sodium monensin.

Key Words: beef, carcass, starch

1364 The potential of a buffer (calcified marine algae) or plant extract (*Capsicum*) in combination with or to replace an ionophore (monensin) in lamb feedlot diets.

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Ionophore antibiotic supplementation is standard practice in almost all feedlots in South Africa and many other countries due to its positive effects on feed efficiency and feed intake. Public concern over the emergence of antibiotic resistant bacteria and the consumers' demand for safe, high quality nutritious food has stimulated the search for natural alternatives to ionophores in ruminant diets. The objective of this study was to evaluate the effect of a buffer (calcified marine algae [AB]) and/or plant extract (*Capsicum* [Caps]) in combination with or replacing an ionophore (monensin [Mon]) on the performance of lambs in a commercial feedlot. Two thousand three hundred and twenty-seven lambs were randomly allocated to 6 different treatments with 6 pens per treatment with pen being the experimental unit. Treatments were: 1) Mon; 2) AB; 3) Caps; 4) AB + Mon; 5) Caps + Mon and 6) AB + Caps. Mean starting live weight of lambs was 30.9 kg. The lambs were individually weighed on Day 0, 10, 21, 35, 50 and at slaughter. All lambs were slaughtered at a pre-determined end live weight of ± 48 kg. Average daily gain, dry matter intake, feed conversion ratio, cold carcass mass, rumen fluid pH and rumen score were among the parameters determined. The corn (23% to 37%), alfalfa hay (20% to 10%) based diets (starter, grower and finisher) were the same for all treatments with adjustments to the specific treatments. Days on feed were different between some treatments ($P < 0.05$). Difference in rumen pH (Day 30 minus Day 13) as well as rumen pH on day 1 and 3 were different between some treatments ($P < 0.05$). Other performance parameters such as average daily gain and feed conversion ratio did not differ between treatments ($P > 0.05$). Results suggest that monensin can be successfully replaced in lamb feedlot rations with natural alternatives (AB and/or Caps) with little impact on production performance. Further research, however, is needed on determining the dietary dependant responses and adaptation of rumen microbial populations. Furthermore, the cost: benefit

ratio should be determined under the prevailing conditions in different countries.

Key Words: ionophore, calcified marine algae, *Capsicum*

1365 Health, milk yield and milk quality records evaluated in 787 dairy herds before and during OmniGen-AF® supplementation to dry and lactating cows. J. D. Chapman[1], S. S. Bascom[1], L. O. Ely[2], G. A. Holub[1], J. P. Jarrett*[1], J. S. Lanier[1], D. Kirk[1], D. E. Nuzback[1], A. D. Rowson[1], and T. J. Wistuba[1], *[1]Phibro Animal Health Corporation, Quincy, IL, [2]University of Georgia, Athens.*

Health, milk yield and milk quality records representing 473,711 cows from 787 dairy herds from the U.S. and Canada were collected to evaluate herd effects of feeding *OmniGen-AF*® (Phibro Animal Health Corp., Quincy, IL) to the entire herd. *OmniGen-AF* (OG) was fed at 56 g/hd/d to all dry and lactating cows for a minimum of 90 d (Post-OG). Health and production metrics were compared to the previous 90 d period (Pre-OG). Herds were enrolled in all months of the year (Jan-Mar, $n = 239$; Apr-June, $n = 224$; Jul-Sep, $n = 176$; Oct-Dec, $n = 149$) and herd size ranged from 31 to 9,046 cows. Health and production records were collected from DC305, DRMS and PCDART systems and the data were analyzed using paired *t* test (SAS, Statistical Analysis System) comparing the Pre-OG to Post-OG health events and production. The data were analyzed for all herds ($n = 787$) by herd size ($\leq$ 100 hd, $n = 188$; 101 to 500 hd, $n = 340$; 501 to 1,000 hd, $n = 120$; $\geq$ 1,001 hd, $n = 141$). Monthly cases of mastitis, late term abortions, dead cows, and number of hospital cows/d, expressed as a % of total herd cows, differed ($P < 0.001$) between the Pre- and Post-OG 90 d periods (−24.6%, −28.6%, −23% and −17.4%, respectively). Health event responses to feeding OG were observed to vary by herd size and Pre-OG SCC; however significant reductions in cases/mo. of mastitis, abortions, deaths and metritis were common in all herds regardless of size and SCC during the Pre-OG period. Herds were also stratified by Pre-OG SCC cells/ml (< 200,000, $n = 309$; 200,001 to 300,000, $n = 237$; 300,001 to 400,000, $n = 146$; $\geq$ 400,001, $n = 95$).The average Pre-OG SCC across all herds was 275,753 cells/ml with 73% of herds reporting a reduction in SCC during the Post-OG period. Changes in SCC were proportional to the Pre-OG SCC level. Significant reductions ($P < 0.001$) in SCC were observed in herds with Pre-OG SCC of 200,001 to 300,000 (−23,087), 300,001 to 400,000 (−57,850) and > 400,001 (−128,465) cells/ml. Milk production was reported by 532 herds with an average milk yield change from Pre-OG to Post-OG of +0.35 kg/hd/d ($P <$ 0.001). Maintaining good health is a key component to cow productivity and these data suggest that feeding *OmniGen-AF* along with sound nutrition and management practices for dry and lactating cows can influence health, milk yield and milk quality in commercial dairies.

Key Words: Health, SCC, *OmniGen-AF*

1366 Comparison of the effects of laidlomycin propionate plus chlortetracycline vs. monensin plus tylosin and multiple β-agonist feeding strategies on feedlot performance and carcass characteristics. A. J. Thompson*[1], Z. K. F. Smith[1], M. Corbin[2], L. B. Harper[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Zoetis, Florham Park, NJ.*

One hundred ninety-two steers (initial BW = 354 ± 23.5 kg) were used in randomized complete block design to examine the effect of various ionophore and ractopamine hydrochloride (RH) supplementation strategies on performance and carcass characteristics. Twelve pens of 4steers were assigned to each of the following treatments: unsupplemented control (CON), laidlomycin propionate plus chlortetracycline (CTC) with or without RH (LP and LPRH, respectively), and monensin sodium plus tylosin with RH (MON). Steers were fed for a total of 151 d, of which RH supplemented treatments received the β-agonist for the final 32 d. Laidlomycin propionate and CTC were removed during this period for the LPRH treatment, as no combination clearance exists for the commercially applied β-agonist (Actogain; Zoetis LLC, Florham Park, NJ). When included in the diet, LP, CTC, monensin, tylosin, and RH were supplemented at 10.7 g/ton, 343 mg/(head · d), 32.0 g/ton, 10.7 g/ton, and 255 mg/(head · d) (DM basis), respectively. Upon harvest, carcass data was collected by trained personnel. Before RH supplementation (d 0 to 118), both LP and LPRH treatments had greater ADG ($P < 0.02$) and G:F ($P < 0.01$) than CON, while MON was intermediate. During the RH supplementation period (d 119 to 150), LP maintained greater DMI ($P < 0.01$) than both RH treatments; however, over the same period, MON treated cattle had improved G:F ($P < 0.02$) compared to LP supplemented cattle and CON. Feeding LP without RH increased final BW ($P = 0.02$) over CON, and all ionophore supplemented treatments had improved ADG ($P < 0.05$) and G:F ($P < 0.05$) over the entire 151 d feeding period. Hot carcass weight was significantly greater ($P =$ 0.04) in cattle fed LP with no β-agonist than CON, where LP cattle yielded an average of 12 kg more HCW, while both RH supplemented treatments were intermediate. Monensin plus tylosin with RH yielded significantly greater LM area ($P =$ 0.03) than unsupplemented controls; however LP and LPRH treatments were unaffected. All other carcass characteristics were not significantly different. The results of this study indicate that LP supplementation without the use of a β-agonist may yield similar live performance and carcass responses associated with the administration of RH. These results also suggest that performance and carcass characteristics for cattle fed LP plus CTC are similar to those of cattle fed monensin

plus tylosin throughout the feeding period.

Key Words: β-agonist, ionophore, laidlomycin propionate

1367 Effect of different inclusion rates of Fermenten on performance, carcass characteristics, and total tract digestibility of growing Angus crossbred steers. M. E. Garcia-Ascolani*[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], D. D. Henry[1], F. M. Ciriaco[1], G. M. Silva[2], P. L. P. Fontes[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]UF/IFAS, Range Cattle Research and Education Center, Ona, FL.*

The objective of this study was to assess the effects of including increasing inclusion rates of the feed additive Fermenten (FER; Church & Dwight Co., Inc., Princeton, NJ) on performance, carcass characteristics, and total tract digestibility of growing steers. Eighty-one Angus crossbred steers (189 ± 22 kg) were used in a generalized randomized block design. Initial BW was used as the blocking factor. Steers were randomly assigned to one of 3 treatments: 0, 2, and 4% FER in the diet DM of a backgrounding diet comprised of peanut hulls, corn gluten feed, soybean hulls and soybean meal. Diets were formulated to contain equal amounts of RDP and energy (6.5% RDP, 70.6% TDN, DM basis). From d 0 to 56, steers were housed in 9 pens (9 steers/pen), with ad libitum access to diets. Individual intake was recorded using a GrowSafe feed intake monitoring system. From d 57 to d 112, steers were moved to a paddock with ad libitum access to a basal diet common to all animals, without FER, to assess potential residual effects of FER feeding. Every 14 d, unshrunk BW was recorded, and blood samples were collected to measure glucose, blood urea nitrogen (BUN) and NEFA in serum. Every 28 d carcass ultrasound was performed to assess fat thickness (FT) and longissimus dorsi area (LDA). Apparent total tract digestibility of nutrients was measured in a subsample of 27 steers (9/treatment) using indigestible NDF as a marker. Data were analyzed as a generalized randomized block design, using steer as the experimental unit. The model included the random effect of steer, and fixed effect of treatment, block and pen. Steers fed 4% FER had decreased ($P < 0.05$) DMI, BW (d 56), ADG (d 0 to 56), and G:F compared with 0 and 2% FER. No differences were observed ($P \geq 0.05$) in blood parameters, LDA, FT, DMI as a percentage of BW, final BW at d 112, and ADG from d 56 to 112. The inclusion of 4% FER increased the digestibility of DM, OM, NDF, and ADF compared with 2, and 0% FER ($P \leq 0.05$). Inclusion of Fermenten above 2% of the diet DM may reduce DMI, thus decreasing the performance and feed efficiency of growing Angus crossbred steers.

Key Words: fermenten, beef cattle, performance

1368 A meta-analysis of lasalocid effects on rumen measures, beef and dairy performance, and carcass traits in cattle. H. M. Golder*[1], T. Cowper[2], and I. J. Lean[1], *[1]Scibus, Camden, Australia, [2]Zoetis Australia, Sydney, Australia.*

The objective of this study was to evaluate the effects of feeding lasalocid on rumen measures, beef and dairy performance, and carcass traits in cattle, using meta-analytic methods. Meta-regression was used to investigate sources of heterogeneity. Rumen measures were assessed using 10 studies (20 comparisons). Lasalocid increased total VFA and ammonia concentrations by 6.46 and 1.44 m*M*, respectively. Lasalocid increased propionate and decreased acetate and butyrate molar percentage (M%) by 4.62, 3.18, and 0.83%, respectively. Valerate M% and pH were not affected. Meta-regression found butyrate M% increased linearly with duration of lasalocid feeding (DUR; $P = 0.017$). When > 200 mg/d was fed, propionate and valerate M% were higher and acetate M% was lower ($P = 0.042$, 0.017, and 0.005, respectively). Beef performance was assessed using 31 studies (67 comparisons). Lasalocid increased ADG by 40 g/d, improved feed-to-gain (F:G) by 410 g/kg, and improved feed efficiency (FE; combined measure of G:F and the inverse of F:G). Lasalocid did not affect DMI, but heterogeneity in DMI was influenced by DUR ($P = 0.004$) and linear effect of entry BW ($P = 0.011$). Heterogeneity of ADG was influenced by the linear effect of entry BW ($P = 0.028$) but not DUR. Combining entry BW $\leq$ 275 vs. > 275 kg and DUR showed cattle entering at > 275 kg fed $\leq$ 100 d had the highest ADG. The FE ($P = 0.025$) and F:G ($P = 0.015$) improved linearly with dose, and entry BW > 275 kg improved F:G ($P = 0.038$). Fourteen studies (25 comparisons) were used to assess carcass traits. Lasalocid increased HCW by 4.73 kg, but not dressing percentage, mean fat cover, or marbling score. Heterogeneity of carcass traits was low and not affected by DUR or dose. Seven studies (11 comparisons) were used to assess dairy performance but the study power was relatively low. Lasalocid decreased DMI in TMR-fed cows by 0.89 kg/d, but had no effect on milk yield, milk components, or component yields. Dose linearly decreased DMI ($P = 0.049$). The DUR did not affect heterogeneity of dairy measures. This work showed lasalocid improved ADG, HCW, FE, and F:G for beef production. These findings may reflect improved energy efficiency from increased propionate and decreased acetate and butyrate M%. Large dairy studies are required for further evaluation of effects of lasalocid on dairy performance.

Key Words: feedlot, ionophore, meta-regression

1369 Close-up diet DCAD, urine pH, and total plasma calcium at calving on a commercial Jersey herd. A. Valldecabres*, D. Rolle, V. J. Ramírez, S. Rodríguez, and N. Silva-del-Rio, *Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare.*

The objectives of this study were to 1) evaluate the daily variability of close-up dietary cation-anion difference (DCAD) and the DCAD feedbunk distribution, 2) evaluate the daily variability of urine pH, 3) determine if acidification levels were maintained as parturition approached, 4) investigate if DCAD and urine pH were associated, and 5) evaluate if peri-partum urine pH and pospartum calcium levels were related on a commercial 3,500 Jersey herd. Before enrollment all cows had to be fed close-up diet > 10 d. Over a 40 d period feedbunk samples were collected daily for wet chemistry. Mixing uniformity was evaluated weekly by sampling 5 feedbunk locations. Midstream urine of 70 multiparous cows was collected via manual stimulation from enrollment to calving. Urinary pH was measured cow-side with a handheld meter (Horiba, Montpellier, FR). Coccygeal blood samples were collected after calving for total plasma calcium analysis (47 cows). Changes on urinary pH −10 to 0 d relative to calving (RC) was conducted with MIXED procedure of SAS with repeated measurements. The association between DCAD and urine pH was evaluated using CORR procedure of SAS. DCAD ranged from −136 to 151 mEq/kg of DM with a coefficient of variation (CV) of 216% and DCAD distribution throughout the feedbunk was highly variable (CV = 36 to 182%). The within-day variation on urine pH ranged from 3 to 19% of CV. There was a tendency for an effect of day of the week ($P = 0.07$) on urine pH, greatest on Monday (6.2) and lowest on Saturday (5.9). Urine pH was lower from −10 to −6 d RC (from 5.6 to 6.1) compared to −5 to 0 d RC (from 6.0 to 6.2; $P = 0.08$). There was a tendency for a weak association between the dietarian DCAD fed 24 h prior and the urine pH ($r = 0.31$; $P = 0.09$). Although urine pH was not associated with postpartum total plasma calcium from −10 to −4 d RC, it was from −3 to 0 d RC ($P = 0.02$); mostly because cows with acidic urine (pH < 5.8) had lower calcium levels. Our results indicate that in the study herd there was a wide within and across day variation in DCAD as well as urinary pH, and suggest that urine pH might not be a good indicator of postpartum plasma calcium levels.

Key Words: DCAD, urine pH, total plasma calcium

1370 Effects of bismuth subsalicylate and calcium-ammonium nitrate on in vitro fermentation of bahiagrass hay with supplemental molasses. D. D. Henry*[1], F. M. Ciriaco[1], R. C. Araujo[2], M. E. Garcia-Ascolani[1], P. L. P. Fontes[1], N. Oosthuizen[1], C. D. Sanford[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil.*

A randomized complete block design was used to determine the effects of increasing amounts of bismuth subsalicylate (BSS) and calcium-ammonium nitrate (CAN) on in vitro fermentation of bahiagrass hay (*Paspalum notatum*). Serum bottles (125-mL) containing 100 mL of a 4:1 buffer:ruminal fluid inoculum and 0.7 g of an 80:20 bahiagrass hay:molasses substrate (DM basis) were incubated for 48 h. Three d (block) of incubation were performed. Treatments were arranged as a 4 × 3 factorial with 4 concentrations of BSS (0.00, 0.33, 0.66, and 1.00% of diet DM) and 3 concentrations of CAN (0.0, 1.2, and 2.4% of diet DM). Treatments were made isonitrogenous with urea. Two ruminally cannulated crossbred steers (348 ± 29 kg BW) fed bahiagrass hay ad libitum and 2.27 kg/d (as is) of a 50:50 molasses:crude glycerol mixture, were used as ruminal fluid donors. In vitro OM digestibility (IVOMD) was determined in a separate set of tubes. Data were analyzed using PROC MIXED of SAS with fixed effects of BSS, CAN, BSS × CAN, and random effect of day. Gas production and IVOMD were linearly decreased ($P \leq 0.001$) as CAN and BSS increased. Ammonia-N was linearly decreased ($P = 0.001$) as CAN increased. Methane production (mmol/g substrate fermented) was linearly reduced ($P < 0.001$) as CAN and BSS increased. Both CAN ($P = 0.032$) and BSS ($P < 0.001$) reduced H_2S production, with 0.33% BSS reducing production by 61% compared with 0.00%. There was no effect ($P > 0.05$) of CAN on concentrations or molar proportions of any VFA analyzed. As BSS increased, concentration of acetate ($P = 0.002$), propionate ($P = 0.007$), and total VFA ($P = 0.003$) decreased linearly. When comparing treatment means, no difference ($P = 0.119$) in total VFA was observed between 0.33% and 0.00% BSS. The acetate:propionate (A:P; $P = 0.005$) and molar proportions of acetate ($P = 0.041$), and propionate ($P = 0.005$) were quadratically affected by BSS inclusion, where 0.33% BSS decreased A:P compared with 0.00% BSS ($P = 0.050$). Including BSS at 0.66% and 1.00% of the diet DM had negative effects on in vitro fermentation of bahiagrass hay. However, when BSS was included at 0.33%, A:P was decreased and total VFA concentrations were unaffected. Nitrate inclusion reduces methane production without negatively affecting fermentation. A combination of BSS and CAN may favorably affect ruminal fermentation while decreasing methane emissions.

Key Words: bismuth subsalicylate, nitrate, fermentation

1371 The effect of a monensin controlled release capsul at prepartum on betahydroxy butyrate, milk yield, fat, protein, postpartum diseases, rectal temperature, and body condition in Holstein cows. P. Melendez[*1], A. Arevalo[2], P. J. Pinedo[3], and M. Duchens[2], *[1]University of Missouri, Columbia, [2]University of Chile, Santiago, Chile, [3]Colorado State University, Fort Collins.*

The objective was to evaluate the effect of a monensin controlled release capsule given prepartum on blood BHB, milk yield, fat and protein, incidence of postpartum diseases, rectal temperature, and BCS in confined Holstein cows. The study was conducted in a 400-cow dairy operation (ME 305 12,500 kg). Cows were housed in a free-stall system, fed a TMR and milked 3X. Eighty cows of parity $\geq$ 2 were randomly assigned either a treatment (n = 40) or a control group (n = 40) at 30 d before expected parturition. Treatment group received a capsule of monensin orally (Rumensin®, ELANCO, Chile, releasing 300 mg of monensin daily for 95 d). Control cows were randomly matched by parity and expected due date. The outcome variables were blood BHB at 7, 14, 21, and 28 d postpartum, rectal temperature up to 3 d postpartum, incidence of retained fetal membranes, metritis, endometritis, monthly test day milk yield, fat (%) and protein (%) and changes in BCS from prepartum (~ 30 d before calving) to calving and from parturition to 30 DIM. Continuous variables over time were analyzed by repeated measure ANOVA. Postpartum disorders were analyzed by logistic regression. BCS changes were analyzed by ANOVA. Monensin group had lower rectal temperature at Day 1 postpartum (40.3 vs. 38.9°C; P = 0.08) and higher protein % on test Day 1 (3.51% vs. 3.20%) than controls (P = 0.0007). There were no differences for milk yield, blood BHB, fat % over time and incidences of postpartum disorders (P > 0.05). The change in BCS from prepartum to parturition was 0.01 and 0.17 for controls and treated cows, respectively (P = 0.01). The change in BCS from parturition to 30 DIM was –0.31 and –0.13 for controls and treated cows, respectively (P = 0.008). It is concluded that monensin improved milk protein on test Day 1, decreased rectal temperature on Day 1 postpartum and modulated positively the changes in BCS both prepartum and postpartum.

Key Words: monensin, milk yield, diseases

1372 Effects of essential oils and exogenous enzyme in low starch diets for finishing feedlot cattle. T. S. Acedo[1], L. F. M. Tamassia[1], C. S. Cortinhas[1], V. N. D. Gouvea[*1], V. R. M. Couto[2], and J. J. D. R. Fernandes[3], *[1]DSM Nutritional Products SA, Sao Paulo, Brazil, [2]Universidade Federal de Goiás, Goiânia, Brazil, [3]UFG, Goiania, Brazil.*

The objective of this study was to evaluate the effects of the combination of essential oils (Crina® Ruminants) and α-amylase (Ronozyme® RumiStar™) on performance of Nellore bulls finished in feedlot. One hundred twelve Nellore bulls (initial BW = 349 kg ± 33) were fed during 90 d with diets containing 54.5% ground corn, 8.5% sugarcane bagasse, 16% soybean hulls, 12% whole cottonseed, 5% soybean meal, 3% minerals and vitamin supplement and 1% urea. Animals were blocked based on initial BW and randomly allocated in 14 pens. Treatments were: MON (Sodium Monensin, Tortuga®– 26 mg/kg DM) or CRINA-RUM (Crina® Ruminants, DSM®, 90 mg/kg DM and Ronozyme® RumiStar™, DSM®, 560 mg/kg DM). Response variables included: final body weight (FBW); dry matter intake (DMI), average daily gain (ADG), feed efficiency (G:F), hot carcass weight (HCW) and dressing percentage (dressing, %). Pen was considered the experimental unit. The data were analyzed using PROC MIXED of SAS and means were compared by Tukey test considering the block as random effect and treatments as fixed effects. Animals fed with CRINA-RUM had 9.9% greater DMI (10.30 *vs*. 9.28 kg; P < 0.001) and a tendency for greater FBW (529 vs. 523 kg*; P* = 0.07) compared with animals fed MON, respectively. There was no effect of treatments on ADG (1.65 and 1.72 kg, for MON and CRINA-RUN respectively, P = 0.14). Animals fed MON had greater G:F compared with CRINA-RUN (0178 vs. 0166, P < 0.01). The combination of essential oils and α-amylase increased HCW and dressing percentage. Animals fed CRINA-RUM had 6.4 kg more carcass compared with MON (298.2 vs.291.8 kg respectively, P = 0.015) and dressing percentage were 56.3 *vs* 55.8% for CRINA-RUM and MON respectively (P < 0.01). In conclusion, the use of essential oil combined with α-amylase improved intake, carcass dressing and weight in animals fed low starch diets combined with coproducts and can be an alternative to monensin.

Key Words: beef, coproducts, starch

1373 Optimal blood sampling time points to determine bioavailability of rumen-protected Met products using the plasma free AA dose–response method.

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Determination of bioavailability of rumen-protected AA products using the plasma free AA dose–response method has relied on blood sampling 2, 4, 6, and 8 h after the morning feeding the last 3 d of each period in Latin square experiments with cows fed every 8 h. The objective of this study was to determine if this sampling protocol captured the diurnal variation in plasma Met concentrations that exists and adequately measures the bioavailability of Met in Smartamine M (SM; Adisseo Inc., Alpharetta, GA). Five multiparous lactating Holstein cows were used in a 5 × 5 Latin square design with 7-d periods. Treatments were: 1) control diet with no supplemental Met; 2) 12 g/d of abomasally-infused Met; 3) 24 g/d of abomasally-infused Met; 4) 15 g/d of fed Met from SM; and 5) 30 g/d of fed Met from SM. Blood samples were collected via jugular catheters every 2 h starting at 0700 h on d 5, 6, and 7 of each period. Plasma Met analysis was conducted using gas chromatography after chloroformate derivatization (EZ:-faast, Phenomenex). Data were analyzed using the MIXED procedure of SAS. Plasma Met concentrations (μ*M*) increased with infused Met or supplemental SM ($P < 0.001$). There was no diurnal variation in plasma Met concentrations ($P = 0.18$). Plasma Met concentrations were averaged across days for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h blood sampling periods. Plasma Met concentrations were regressed on 0, 12, and 24 g of infused Met and 0, 15, and 30 g of fed Met using the REG procedure of SAS. Slopes for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h sampling periods for infused Met were 1.356 (SE = 0.145), 1.369 (SE = 0.147), 1.329 (SE = 0.120), and 1.346 (SE = 0.123), respectively. Slopes for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h sampling periods for fed Met were 1.148 (SE = 0.038), 1.156 (SE = 0.059), 1.197 (SE = 0.038), and 1.140 (SE = 0.030), respectively. There was no effect of sampling period on the slopes for infused ($P \geq 0.91$) or fed Met ($P \geq 0.26$). The bioavailabilities of Met in SM averaged 84.7, 84.4, 90.0, and 84.6% for the 2 to 8, 10 to 16, 18 to 24, and 2 to 24 h sampling periods, respectively. The similarity in estimates of bioavailability for SM for the 2 to 8 and 2 to 24 h sampling periods indicates our blood sampling protocol is adequate for determining the bioavailability of RP-Met products.

Key Words: bioavailability, methionine, sampling

1374 Effects of prophylactic supplementation with oral calcium boluses on peripartum calcium, urine pH and health in a commercial Jersey herd supplemented with anionic salts.

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The objectives of this study were to evaluate the effect of prophylactic supplementation with oral calcium boluses after calving on peripartum serum calcium and urine pH levels, as well as the prevalence of ketosis and endometritis. Multiparous Jersey cows from a 3,500 herd were randomly assigned to control (no calcium supplementation [$n = 67$]) or treatment (2 oral calcium boluses [$n = 64$], [QuadriCalMINI, Bio-Vet, Barneveld, WI]). The first calcium bolus was given at 2:30 h after calving (SD ± 1:54 h) and the second at 18:21 h after calving (SD ± 11:56 h). Coccygeal blood and midstream urine were collected immediately before the first and second bolus administration and 1 h after each bolus was administered. Serum samples were analyzed for total calcium. Urinary pH was measured cow-side with a handheld meter (LAQUAtwin B-712, Horiba, Montpellier, FR). Blood Beta-hydroxybutyrate (BHBA) concentrations were determined at 5, 8, and 11 d postpartum, using a handheld meter (Precision Xtra; Abbot, Alameda, CA). Ketosis was defined as ≥ 1.4 mmol/L of BHBA in blood at least once during the sampling period. Clinical endometritis was evaluated based on the observation of purulent or mucopurulent vaginal mucus retrieved with Metricheck (Simcro, NZ) from 28 to 40 d postpartum. Treatment effects on serum calcium and urine pH were evaluated with linear mixed models with repeated measures using the MIXED procedure of SAS (Cary, NC). The prevalence of ketosis and endometritis was evaluated with the chi-square option of the FREQ procedure (SAS). Subclinical hypocalcemia (≤ 8.5 mg/dL) before treatment administration was 58% for control and treatment ($P = 0.96$). One hour after bolus administration, serum calcium concentration was significantly greater in treated cows at first (8.65 vs. 8.01 mg/dL; $P < 0.0001$) and second (8.71 vs. 8.23 mg/dL; $P < 0.001$) bolus administration. However, no significant differences were observed before second bolus administration (8.23 vs. 8.01 mg/dL; $P = 0.12$). There was a treatment effect on urine pH (7.0 control vs. 6.1 treatment; $P < 0.0001$) and a significant treatment by time interaction ($P = 0.02$). No treatment effects were observed on ketosis (26.7%; $P = 0.97$) or endometritis (47%; $P = 0.93$). These results suggest that postpartum total serum calcium levels can be increased with oral bolus administration; however, serum calcium levels might not be maintained by the time the second bolus is administered.

Key Words: oral calcium supplementation, urine pH, serum calcium

1375 Effects of supplemental zinc sulfate concentrations on growth performance and carcass characteristics of feedlot heifers, and in vitro ruminal fermentative activity. C. L. Van Bibber-Krueger*, C. I. Vahl, and J. S. Drouillard, *Kansas State University, Manhattan.*

Effects of supplemental Zn as Zn sulfate on feedlot performance and carcass characteristics were evaluated using 480 crossbred heifers (BW = 385 kg ± 13.08) in a randomized complete block design. Heifers were blocked by BW and randomly assigned within block to receive 0, 30, 60, or 90 mg supplemental Zn/kg diet DM. Heifers were housed in dirt-surfaced pens (20 animals/pen; 6 pens/treatment) equipped with fence-line feed bunks and automatic water fountains. Heifers were fed once daily ad libitum. Plasma was collected Days 0, 63, and 115 from 4 or 5 heifers/pen to determine changes in plasma Zn concentrations. Heifers were transported on d 144 to a commercial abattoir where HCW and incidence of liver abscesses were recorded at harvest and carcass data were recorded after 36 h of refrigeration. Plasma Zn concentration increased linearly in response to increasing concentrations of dietary Zn ($P = 0.02$). Final BW and ADG were not affected by supplementation ($P \geq 0.29$). Increasing supplemental Zn concentrations tended to decrease DMI (linear effect, $P = 0.07$), resulting in a linear improvement in feed efficiency with increasing Zn concentration ($P = 0.03$). No differences were detected for HCW, dressing percentage, LM area, 12th rib fat, percentages of carcasses grading Select or Choice, or yield grade ($P > 0.53$). There was a tendency for a quadratic effect of Zn concentration on percentage of carcasses graded as USDA Prime, with percent Prime peaking at 60 mg/kg added Zn. Carcasses from heifers supplemented 60 mg Zn/kg diet DM yielded the greatest numerical increase ($25/carcass) in carcass value compared to other treatments ($P = 0.32$). In vitro fermentations were performed using ruminal fluid cultures containing 0, 30, 60, 90, 120, 150 mg Zn/kg substrate DM to determine impact of Zn on gas production, VFA concentrations, and IVDMD. There was no Zn × time interaction or effect of Zn on in vitro gas production ($P \geq 0.59$). Zinc supplementation tended to reduce acetate (quadratic effect; $P = 0.07$), and decreased isovalerate (linear effect; $P = 0.05$), but did not affect other VFA ($P \geq 0.17$) or IVDMD ($P \geq 0.20$). Overall, Zn supplementation up to 150 mg/kg substrate weight minimally affected in vitro fermentation. Supplementing up to 60 mg Zn/kg diet DM improves feed efficiency of feedlot cattle.

Key Words: feedlot cattle, feed efficiency, gas production, zinc

1376 Evaluating the effects of an injectable trace mineral product on steers raised in a natural beef feedlot program. E. K. Niedermayer*, O. N. Genther-Schroeder, and S. L. Hansen, *Iowa State University, Ames.*

To determine effects of an injectable trace mineral (TM) on growth and TM status of steers fed in a natural program 168 certified natural Angus steers (359 ± 36.6 kg), blocked by BW (6 steers per pen), received an injection of sterilized saline (SAL) or Multimin90 (MM) on d 0 at 1 mL/68 kg BW (n = 14 pens, 84 steers per treatment). Multimin90 contains 15 mg Cu, 60 mg Zn, 10 mg Mn, and 5 mg Se/mL. Steers received a growing diet for 56 d, followed by 3 wk of transition. On d 84 steers started a corn-based finishing diet and received a second injection of SAL or MM, creating 4 treatments (n = 7 pens, 42 steers per treatment): 1) d 0 Saline, d 84 Saline (SAL/SAL); 2) d 0 Saline, d 84 Multimin90 (SAL/MM); 3) d 0 Multimin90, d 84 Saline (MM/SAL); and 4) d 0 Multimin90 and d 84 Multimin90 (MM/MM). Blood and liver mineral concentrations were determined (n = 7 per treatment) on d −5, 14, 79, and 98. Steers were harvested on Day 162. Data were analyzed in SAS with the fixed effects of block and treatment (2 treatments for growing, 4 treatments for finishing), with mineral data as repeated measures. Steer was experimental unit except for DMI and G:F, where experimental unit was pen. Treatment did not affect growing or finishing ADG, DMI, or G:F ($P \geq 0.14$). There was a treatment × day interaction for finishing period ADG ($P = 0.01$), where ADG was similar across treatments from d 84 to 113, and greatest in SAL/SAL from d 113 to 144; however, MM/MM was greatest from d 140 to 161. There was a treatment × day interaction for liver Se ($P < 0.001$), where concentrations increased on d 14 in MM-treated steers, were similar across treatments on d 79, but increased on d 98 in SAL/MM and MM/MM. Liver TM concentrations tended ($P = 0.08$) to display treatment × day interactions where MM/MM had greater Mn and Cu on d 14, tended to have greater liver Mn and Cu than MM/SAL and SAL/SAL on d 79, and had greater liver Cu compared to SAL/SAL and MM/SAL on d 98. Adequate steer TM status at onset of this trial likely negated any potential benefits of injectable minerals and injectable TM can be utilized safely in natural finishing programs.

Key Words: beef, natural, mineral

1377 Interactive effects of supplemental Zn sulfate and ractopamine hydrochloride on growth performance, carcass traits, and plasma urea nitrogen in feedlot heifers. C. L. Van Bibber-Krueger[*1], J. M. Gonzalez[1], R. G. Amachawadi[2], H. M. Scott[3], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]Kansas State Univeristy, Manhattan, [3]Texas A&M University, College Station.*

Interactive effects of supplemental Zn and ractopamine hydrochloride (RH) were evaluated using 156 crossbred heifers (initial BW = 527 kg ± 6.61; gross BW × 0.96) to determine impact on feedlot performance, plasma urea nitrogen (PUN) and carcass characteristics. The study was conducted as a randomized complete block design with a 2 × 2 factorial arrangement. Factors consisted of: 1) 30 or 100 mg supplemental Zn/kg diet DM (30Zn or 100Zn) as Zn sulfate, and 2) 0 or 200 mg RH/animal daily. Heifers were blocked by BW and, assigned randomly within block to treatments. Heifers were housed in partially covered feeding pens (3 heifers/pen; 13 pens/treatment), fed once daily ad libitum, and RH was fed for 42 d and removed from the diet until cattle were harvested on d 43. Plasma samples were collected on d 0 and 36 to assess changes in plasma Zn and PUN. On d 43, heifers were transported to a commercial abattoir where HCW and incidence of liver abscesses were recorded. Carcass data were collected after 32 h of refrigeration. No Zn × RH interactions were observed for plasma Zn or PUN ($P \geq 0.58$); however, there was a tendency for RH × d interaction for PUN ($P = 0.08$). Supplementing 100Zn increased plasma Zn concentration ($P = 0.02$) compared to 30Zn. No interactions were observed for feedlot performance ($P \geq 0.24$). Final BW and ADG increased with RH supplementation ($P \leq 0.02$), but DMI was not affected ($P = 0.63$), thus feed efficiency improved ($P < 0.01$) when cattle were fed RH. Supplementing 100Zn tended to reduce ADG ($P = 0.07$), but did not affect other measures of feedlot performance or incidence of liver abscesses ($P \geq 0.12$). Zinc × RH interactions were observed for LM area and yield grade ($P \leq 0.01$); LM area decreased and yield grade increased when cattle were supplemented 100Zn with no RH compared to other treatments. A tendency for Zn × RH interaction was detected for dressing percentage ($P = 0.08$), but no other interactions or effects of Zn were observed for carcass traits ($P \geq 0.11$). Supplementing RH increased HCW ($P = 0.03$), but did not affect other carcass traits ($P \geq 0.13$). In conclusion, supplemental Zn had little impact on feedlot performance or PUN concentration, but may alter muscle and fat deposition when fed in conjunction with RH.

Key Words: feedlot cattle, urea nitrogen, ractopamine, zinc

1378 SafeGain™ (ruminally-protected lysine) for growing beef cattle. V. De Aguiar Veloso[*1], C. L. Van Bibber-Krueger[1], K. Karges[2], and J. S. Drouillard[1], *[1]Kansas State University, Manhattan, [2]H.J. Baker, Animal Health and Nutrition Division, Little Rock, AR.*

Crossbred heifers ($n = 448$; 287 ± 14.1 kg initial BW) were used in a randomized complete block experiment to assess growth response to SafeGain, a lipid-encapsulated, ruminally-protected form of lysine sulfate. The basal diet consisted of (DM basis) of 45% brome hay, 25% steam-flaked corn, 25% wet corn gluten feed, and supplement. Based on Level 2 estimates from the Nutrient Requirements of Beef Cattle Update 2000, heifers were projected to consume 134% of their lysine requirement with the basal diet alone. Treatments consisted of dietary additions of 0, 15, 30, or 45 g/d of SafeGain. Heifers were blocked by initial BW; implanted with Component TE-IH; allocated within strata to 64 partially-shaded, concrete-surfaced (4.3 m × 8.6 m) pens with 7 heifers/pen and 16 pens/treatment; and fed once daily for 112 d. At the end of the 112-d growing trial, a subset of 12 blocks was consolidated, such that 2 pens from each growing treatment were combined to make one finishing pen. Cattle were weighed, re-implanted with Component TE-200, relocated to finishing pens, and fed a common finishing diet (no supplemental lysine) for 94 d until harvest to evaluate possible carryover effects of SafeGain. At the end of the finishing period pens of cattle were weighed, loaded onto trucks, and transported 450 km to a commercial abattoir for harvest. Liver abscess incidence and HCW were collected the day of harvest, and carcass traits were evaluated following 32 h of refrigeration. Growing phase performance and resulting HCW are summarized in the table, below. SafeGain was effective for improving performance of cattle fed roughage-based backgrounding diets.

Key Words: lysine, growing cattle, SafeGain™

1379 Effects of rotating antibiotic and ionophore feed additives on enteric methane and rumen microbial populations of steers consuming a high forage diet. W. L. Crossland[*1], L. O. Tedeschi[1], T. R. Callaway[2], M. D. Miller[1], and W. B. Smith[3], *[1]Texas A&M University, College Station, [2]USDA-ARS, College Station, [3]Texas A&M AgriLife Research, Overton.*

Ionophore and antibiotic feed additives have been shown to decrease ruminal methanogenesis, but evidence of long-term mitigation is lacking. We proposed a rotation of feed additives as an alternative to reduce methane (CH_4) production. Rumen-cannulated steers ($n = 12$) were fed a basal high forage diet at 2% of BW (DM) for 13 wk in a Calan gate facility receiving 1 of 6 treatments (trt): 1) control (Con) no additive, 2) bambermycin (B) = 20 mg B/hd/d, 3) monensin (M) = 200 mg M/hd/d, 4) B7M = rotating B and M treatments weekly, 5) B14M

= rotating B and M treatments every 14 d, and 6) B21M = rotating B and M treatments every 21 d. Steers were blocked by weight in a RCBD with repeated measures. Rumen fluid was collected weekly for analysis (n = 13) and results were normalized according to organic matter intake (kg OMI). Trt did not significantly affect CH_4 production (P = 0.60), but tended to affect CH_4 to Propionate ratio (CH_4:Pro) (P = 0.06) being highest for Con and lowest for M, B21M, and B14M (0.42 vs. 0.36, 0.36, and 0.33, respectively). Week affected both CH_4 and CH_4:Pro ($P < 0.05$) with significant reductions by wk 3 but this effect was not sustained beyond wk 6. Microbial analysis revealed rotationally treated steers had greater populations of gram positive (G^+) bacteria than continuously fed steers and Con ($P < 0.01$) and wk 0 populations were different from wk 5 and 6 but similar to wk 12 (51.1 vs. 37.5 and 35.1 vs. 44%, respectively; $P < 0.01$). A class of G^- bacteria (*Sphingobacteriia*), phylum *Bacteroidetes,* was not affected by trt or wk but was positively correlated with CH_4 production (r = 0.24, P = 0.04). Archaeal populations of *Methanobrevibacter spp.* and *Methanosphaera sp.*correlated with CH_4 production (r = 0.22 and r = 0.37, respectively) and were not affected by trt. Wk tended to affect *Methanobrevibacter spp*. populations being lowest during week 3 and highest during week 12 (53.64% vs. 68.89% of Archaea; P = 0.06). *Methanosphaera sp*. populations were lowest during week 5 and higher during week 0 and 12 (0.02% vs. 1.31 and 0.53% of Archaea respectively; $P < 0.05$). Our results suggest microbial adaptation to trt between 4 and 6 wk. Rotating monensin and bambermycin did not reduce CH_4 or delay microbial adaptation, more than continuously fed steers.

Key Words: CH_4, feed additives, microbes

1380 Effects of supplementing lactating dairy cow ration with sodium sesquicarbonate on reticulorumen pH, rumination, and dry matter intake. M. L. Jones*[1], J. D. Clark[1], N. A. Michael[2], and J. M. Bewley[1], [1]*University of Kentucky, Lexington,* [2]*Arm & Hammer Animal Nutrition, Princeton, NJ.*

The objective of this study was to assess the effects of sodium sesquicarbonate (SQ-810), a reticulorumen buffer, on rumen pH, rumination time, and dry matter intake (DMI). Sixteen early lactation multiparous, Holstein cows were housed in a tie-stall barn and milked twice daily at the University of Kentucky Coldstream Dairy from October 31, 2015 to January 1, 2016. Cows were balanced by parity and milk production then split into 2 treatment groups for a crossover study with a low buffer (LB, n = 8) group and a high buffer (HB, n = 8) group. The base TMR contained 16kg/d sodium bicarbonate. The LB group did not receive any SQ-810 while the HB group received 0.30 kg of SQ-810 as fed. Eight cows proceeded through sequence 1: three, 21 d periods receiving the LB diet in period 1, HB diet in period 2, and the LB diet in period 3. The remaining 8 cows proceeded through sequence 2: three, 21 d periods receiving the HB diet in period1, LB diet in period 2, and the HB diet in period 3. Each group was fed ad-libitum and dry matter intake (DMI) was collected. All cows were administered an iNovotec Animal Care (iNovotec Animal Care, Austria) reticulorumen pH and temperature bolus. Daily rumination time was recorded using HR tags (SCR Engineers Ltd., Netanya, Israel) and CowManager SensOor (SENRUM) tags (Agis Automatisering, Harmenlen, Netherlands). Low pH was calculated as the total time where pH was < 5.80. The MIXED procedure of SAS (SAS Institute, Inc., Cary, NC) was used to evaluate the effects of cow, sequence, treatment and period on each parameter measured. Rumen pH and low pH time (pH < 5.80) were significantly influenced by treatment ($P < 0.01$). Rumen pH was 5.82 ± 0.07 for LB cows and 5.85 ± 0.07 for HB cows. Low pH time (pH < 5.80) was greater ($P < 0.01$) for LB Days 10.70 ± 0.23 h/d than for HB days, 9.40 ± 0.23 h/d. Dry matter intake was 25.68 ± 0.61 kg/d with LB cows and 26.53 ± 0.61 kg/d for HB cows. Treatment affected SCR rumination times ($P < 0.01$) LB 457.84 ± 19.15 min/d and HB 435.02 ± 19.15 min/d. However, the rumination time measured using SENRUM was not significantly different between treatments. The addition of SQ-810 to the TMR increased reticulorumen pH and DMI significantly ($P <$ 0.01). This research demonstrates the positive effects of SQ-810 rumen buffer in a lactating cow diet.

Key Words: sodium sesquicarbonate, rumen pH

1381 Comparison of Titanium® 5 PH-M versus Titanium® 5 plus NUPLURA® PH with the presence or absence of monensin on health and performance of newly received feedlot calves fed RAMP®. R. M. Jones*[1], C. J. Bittner[1], F. H. Hilscher[1], R. A. Stock[2], and G. E. Erickson[1], [1]*University of Nebraska, Lincoln,* [2]*Cargill, Blair, NE.*

Crossbred steers (n = 704; initial BW = 269; SD = 22 kg) were utilized in a randomized block designed experiment with a 2 × 2 factorial arrangement of treatments. Factors included vaccine type and the presence or absence of monensin (Elanco Animal Health, Greenfield, IN) in the receiving diet. Vaccines were, Titanium® 5 PH-M (VacPH-M, Elanco Animal Health) or Titanium® 5 plus NUPLURA® PH (VacPH, Elanco Animal Health). VacPH-M is labeled to deliver effective immune response against bacteria (*Mannheimia haemolytica* and *Pasteurella multocida*) and viruses (BVD types 1 and 2, IBR, PI_3 and BRSV). VacPH is labeled similar to VacPH-M excluding protection against *Pasteurella multocida*. All steers were fed RAMP® product (Cargill Corn Milling, Blair, NE) with monensin included at 0 or 27.6 mg/kg. Steers were weighed on d 1 to establish initial BW. Steers were assigned to pen based on processing order, with every fourth steer being assigned to 1 of 4 treatments. Once a pen replicate was filled, new pen replicates were started until all steers were assigned to 40 pens (10 pens per simple effect treatment). The receiving trial lasted 28

d. Ending BW was an average of 2 consecutive day weights collected after limit feeding for 5 d. There were no significant monensin × vaccine interactions ($P > 0.27$) observed for growth performance or morbidity. Vaccine treatments (VacPH-M or VacPH) did not affect DMI ($P = 0.52$), ADG ($P = 0.95$), or G: F ($P = 0.79$). Monensin level (0 or 27.6 mg/kg) did not affect DMI ($P = 0.28$), ADG ($P = 0.94$), or G: F ($P = 0.65$). The number of steers pulled and treated for bovine respiratory disease one or more times was not different ($P = 0.17$) for VacPH-M compared to VacPH. Furthermore, no difference ($P = 0.34$) was observed when comparing second pull rates between vaccine types. There was a tendency ($P = 0.09$) for steers fed 27.6 mg/kg of monensin to have a lower percentage of first and second pulls as compared to steers receiving 0 mg/kg of monensin. We concluded that neither vaccine type nor monensin concentration affected steer growth performance or morbidity rate for the first 28 d of receiving.

Key Words: monensin, receiving, vaccine

1382 Effect of Bovamine® on performance of lactating dairy cows.

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The objective of this study was to determine if feeding Bovamine® has an effect on the production performance of dairy cows. Bovamine® (Nutritional Physiology Company, LLC, Overland Park, KS) is a direct-fed microbial consisting of *Lactobacillus acidophilus* and *Propionibacterium freudenreichii*. Thirty lactating Jersey cows (147 ± 49 d in milk) were used in a randomized complete block design for 12 wk with a 2-wk covariate period and 10-wk experimental period. The cows were blocked by parity, calving date, and milk yield. There were 2 treatments: a control group and cows that were fed Bovamine®. As a top dress, control cows received 454 g/d of ground corn and the cows fed Bovamine® were given 1 g/d of Bovamine® and 453 g/d of ground corn. All cows were milked and fed the same TMR twice daily. DMI and milk yield were recorded each day. DMI for the control cows (20.3 kg/d) was similar ($P > 0.10$) to that for the Bovamine®-fed cows (20.5 kg/d). There was a trend ($P = 0.07$) for greater milk yield in cows fed Bovamine® (25.3 kg/d) compared to control cows (24.4 kg/d). Percentage of fat and protein in the milk was similar ($P > 0.10$) between the 2 treatments, with control cows averaging 4.58% fat and 3.67% protein compared to 4.65% fat and 3.69% protein by the Bovamine®-fed cows. Milk urea nitrogen (MUN) was greater ($P < 0.05$) in the Bovamine®-fed cows (15.9 mg/dL) compared to the control cows (15.1 mg/dL). Fat corrected milk (FCM) and energy corrected milk (ECM) also tended to be greater ($P = 0.08$ and 0.07, respectively) in the Bovamine®-fed cows, averaging 29.8 kg/d for FCM and 30.5 kg/d for ECM compared to 28.6 and 29.3 kg/d for FCM and ECM by the control cows, respectively. BW was greater ($P = 0.02$) for the control cows with an average of 426.7 kg compared to 418.1 kg for the Bovamine®-fed cows. FCM/DMI and ECM/DMI were not different between the two treatments ($P > 0.10$) with the control cows averaging 1.42 and 1.45 and the Bovamine®-fed cows averaging 1.46 and 1.50, respectively. With a trend for increased milk yield, FCM, and ECM, results from this study indicate that Bovamine® may be a viable option to increase production in dairy cows without an increase in DMI.

Key Words: Bovamine®, direct-fed microbial, production

1383 Effects of rumen-protected choline (RPC) supplementation to periparturient dairy cows did not depend on prepartum energy intake.

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Objectives were to evaluate the effect of prepartum energy intake on performance of dairy cows supplemented without or with RPC (0 or 60 g/d ReaShure, Balchem Corp., New Hampton, NY). At 48 d before calculated calving date, 93 multiparous Holstein cows were assigned to 1 of 4 treatments. Cows were fed prepartum high energy (HE; 1.63 Mcal NEL/kg DM; 58% corn silage) or controlled energy (CE; 1.40 Mcal NEL/kg DM; 43% wheat straw) diets in ad libitum amounts with or without RPC. The RPC was top-dressed daily from 21 d prepartum to 21 d postpartum. After calving, cows were fed the same diet balanced for methionine, apart from RPC supplementation, through 15 wk. Liver tissue was collected for biopsy at −14, 7, 14, and 21 d relative to calving. Data were analyzed by ANOVA for repeated measures using the MIXED procedure of SAS. Cows fed the HE diet consumed energy at 24% above requirement whereas cows fed the CE-based diet consumed energy at 0.7% above requirement during the last 15 d prepartum. Cows fed RPC tended ($P < 0.10$) to produce more milk (43.5 vs. 41.3 kg/d) and energy-corrected milk (44.2 vs. 42.0 kg/d) without increasing DM intake (23.7 vs. 23.2 kg/d) and tended to have greater mean body condition (3.32 vs. 3.24) during the first 15 wk postpartum. Over the first 40 wk postpartum, feeding RPC in transition increased milk yield of cows ($n = 91$) fed HE (37.4 vs. 33.4 kg/d) or CE diets (36.5 vs. 36.1 kg/d) prepartum (RPC by prepartum energy diet interaction, $P = 0.16$). Cows fed the CE compared with the HE diet consumed more feed postpartum (24.0 vs. 22.9 kg/d, $P < 0.01$) but did not produce more milk (43.1 vs. 41.6 kg/d). Thus, postpartum cows fed the CE diet prepartum were in less mean negative energy balance ($P < 0.05$) and tended to have lower ($P = 0.10$) mean NEFA and had lower ($P < 0.01$) mean BHBA concentrations in plasma compared with cows fed HE diets prepartum. Mean postpartum concentration

of liver triacylglycerol was greater ($P < 0.05$) for cows fed the HE compared with the CE diet (10.7 vs. 8.3% DM) whereas RPC had no effect on hepatic triacylglycerol (Control = 9.0 vs. RPC = 9.9%DM). Compared with an HE diet, feeding a CE diet prepartum improved energy balance and DM intake postpartum. Feeding RPC during the transition period increased yield of milk for 40 wk regardless of prepartum energy intake.

Key Words: choline, transition, wheat straw

1384 Effects of Peptein supplementation on ruminal microbiota and feed digestibility in dairy cows.

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The aim of this study was to evaluate the performance of Peptein (APC Europe, Spain), a protein hydrolysate derived from red blood cells with 2 degrees of hydrolysis, either high (HDH) or low (LDH) as a N source for rumen microbial growth in comparison with other N supplements including urea, pork peptone, fish peptone, soy peptone, and spray dried red blood cells (SDRBC), and to determine the potential consequences on feed degradation. In experiment 1, four replications of Tilley Terry incubations with all N sources providing an isonitrogenous supply of 0.3% N were performed from rumen aliquots obtained from 3 cows. Growth of Gram positive and Gram negative bacteria was estimated by quantitative RT-PCR. In experiment 2, 4 cows (2 dry and 2 lactating) received 320 g/d of Peptein HDH via a rumen cannula split in 2 doses of 160 g for 12 d, and 4 other cows (2 dry and 2 lactating) received an equivalent amount of N in the form of 100 g/d of urea per day via a rumen cannula, split in 2 daily doses. On Day 10, in situ bags containing 0.8 ± 0.06 g of corn, soybean hulls, alfalfa, or beet pulp were placed in the rumen for 2, 4, 8, 12, 16, 24, and 48 h. Each sample was run in duplicate bags at each time point on two consecutive days. Data were analyzed using a mixed-effects model. In Experiment 1, Peptein HDH and LDH and pork peptone increased ($P < 0.05$) the growth of Gram negative bacteria in comparison with the other peptones and SDRBC, but contrarily, fostered ($P < 0.05$) a slight decrease in the growth of Gram positive bacteria. In Experiment 2, the effective rumen degradation of DM from beet pulp in dry cows supplemented with Peptein HDH (68.1 ± 1.11%) tended ($P = 0.07$) to be greater than when incubated in unsupplemented dry cows (64.6 ± 1.11%). The effective rumen degradation of CP and NDF from corn was greater ($P < 0.05$) in lactating cows supplemented with Peptein HDH (52.7 ± 0.96 and 44.8 ± 0.23%, respectively) than in unsupplemented lactating cows (44.6 ± 0.96 and 37.5 ± 0.23%, respectively). It is concluded that Peptein fosters the growth of Gram negative and decreases that of Gram positive bacteria in the rumen and improves degradation of CP and NDF from corn.

Key Words: bacteria, nitrogen, rumen

1385 Effects of different doses of sodium monensin on nutrient digestibility on feedlot Nellore cattle.

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The objective of this research was to examine the effects of different doses of sodium monensin (MON) on digestibilities of DM, NDF and starch of feedlot Nellore cattle. This study, conducted at the São Paulo State University feedlot, Dracena campus, Brazil, was designed as a completely randomized block, replicated 12 times, in which 60 20-mo-old yearling Nellore bulls (402.52 ± 33.0 kg) were fed in individual pens for 84 d according to the different doses of MON (DM basis): 1) 0 ppm (D0); 2) 9 ppm (D9); 3) 18 ppm (D18); 4) 27 ppm (D27), and 5) 36 ppm (D36). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 68% to 84% of diet DM. The finishing diet contained: 71.5% cracked corn grain, 16.0% sugarcane bagasse, 7.7% soybean meal, 3.0% supplement, 1.2% urea, and 0.6% limestone (DM basis). Diet samples were collected just after morning delivery (0830) on Days 7, 8, 19, and 20 of experimental period, and composite samples were made per pen for Days 7 and 8, and 19 and 20. Samples of orts and feces were collected just before morning (0800) meals on Days 8, 9, 20, and 21 of experimental period, and composite samples were made per pen for Days 8 and 9, and 20 and 21. The digestibility of DM, NDF and starch was determined by using chromium dioxide as an external marker. Orthogonal contrasts were used to evaluate linear, quadratic, and cubic relationship between doses of MON and the dependent variable. The use of different doses of sodium monensin did not affect ($P > 0.10$) DM and starch digestibility in the adaptation period; however, NDF digestibility increased ($P = 0.01$) linearly (D0: 56.77%; D9: 59.39%; D18: 65.75%; D27: 63.22%; D36: 70.74%) as doses of MON increased. In the finishing period (d-21), as doses of MON increased, NDF digestibility decreased ($P = 0.01$) linearly (D0: 74.00%; D9: 65.35%; D18: 69.83%; D27: 64.50%; D36: 52.30%) and starch digestibility was affected ($P = 0.03$) cubically (D0: 91.38%; D9: 95.05%; D18: 90.32%; D27: 94.63%; D36: 96.03%). Thus, based on the results of this study, increasing doses of MON affected nutrient digestibility of feedlot Nellore cattle. Also, the dose of 36 ppm per kilogram of DM seemed to be the best option.

Key Words: ionophore, NDF, starch

1386 Effects of carbohydrases on the digestibility of fibrous feed ingredients using a rumen simulation model. V. R. Vasconcelos[1], K. G. Arriola[2], A. F. Campos[3], F. Amaro[4], M. C. Walsh[5], and A. T. Adesogan[*2], *[1]Universidade Federal do Piaui, Piaui, Brazil, [2]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [3]IFC (Instituto Federal Catarinense), Videira, Brazil, [4]Federal University of Vicosa, Vicosa, Brazil, [5]Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, UK, United Kingdom.*

The objective of this experiment was to determine the effect of an enzyme mixture on the digestibility of fibrous feed ingredients under simulated rumen conditions. Feed ingredients evaluated included 1) ground corn, 2) corn distillers dried grains (cDDGs), 3) Corn stover (CS), 4) dilute ammonia pretreated CS (DACS), 5) caustic delignified CS (DCS), 6) caustic delignified switchgrass (DSG), and 7) enzyme-treated CS (ECS), 8) DACS (EDACS), 9) DCS (EDCS), and 10) DSG (EDSG). Each substrate was incubated in duplicate in Ankom bags (0.5 g) within 250-mL gas-tight culture bottles. The enzyme was a mixture of a cellulase/hemicellulose enzyme preparation and β1–4, endoxylanase (Danisco, UK) at respective rates of 15 and 1 g/kg on as fed basis. Enzymes were diluted in 2 mL of 0.1 M citrate-phosphate buffer (pH = 6.0) and added with 52 mL of buffered-rumen fluid to the substrate in culture bottles sealed with screw-on caps on which a pressure sensor-syringe assembly was fitted. Bottles were incubated for 24 h at 39°C in a forced-air incubator. Rumen fluid was collected from 2 non-lactating, non-pregnant ruminally-cannulated Holstein cows 3 h after feeding. The experiment had a completely randomized design with ten treatments, two replicates/treatment and five runs. Data were analyzed with the GLIMMIX procedure of SAS and the model included treatment, run and treatment × run. Ground corn was more digestible than all other feed ingredients. The DM digestibility (DMD) of cDDGs was greater than those of CS and DSG (42.2 vs. 19.8 and 25%). Ammonia pretreatment (35.7 vs. 44.9%) and caustic delignification (35.7 vs. 46.2%) increased the DMD of CS ($P < 0.0001$). Enzyme treatment also increased the DMD of DSG (25.0 vs. 33.8%). Enzyme treatment increased total gas production during fermentation of DCS and DSG but did not affect those of other substrates. Pretreatment of CS by either delignification or dilute ammonia increased the NDF and ADF digestibility compared to untreated CS but addition of enzymes did not further enhance the digestibility of the pretreated CS. Dilute ammonia pretreatment of CS had no effect on ammonia-N concentration compared to CS, however caustic delignification resulted in a reduction in ammonia-N concentration ($P < 0.01$). Enzyme treatment had no effect on total VFA concentration but decreased acetate proportion of DCS and increased the propionate proportion from both DCS and ACS. Enzyme treatment decreased the acetate to propionate ratio of all substrates except untreated CS.

Key Words: corn stover, enzyme, in-vitro

1387 Microbial and chemical additives inhibit the growth of *Escherichia coli* O157:H7 in corn silage. I. M. Ogunade*, D. Kim, Y. Jiang, A. A. P. Cervantes, K. G. Arriola, D. Vyas, and A. T. Adesogan, *Dep. of Animal Sciences, IFAS, University of Florida, Gainesville.*

This study examined if adding bacterial inoculants or propionic acid to corn silage contaminated with *Escherichia coli* O157:H7 at ensiling, at silo opening, or after aerobic exposure would inhibit the growth of the pathogen. Corn forage was harvested at approximately 35% dry matter, chopped to 10-mm lengths, and ensiled after treatment with one of the following: 1, distilled water (Control); 2, 1×10^5 cfu/g of *E. coli* O157:H7 (EC); 3, EC and 1×10^6 cfu/g of *Lactobacillus plantarum* (ECLP); 4, EC and 1×10^6 cfu/g of *Lactobacillus buchneri* (ECLB); and 5, EC and 2.2 g/kg of propionic acid (ECA). Each treatment was ensiled in quadruplicate in laboratory silos for 0, 3, 7, and 120 d and analyzed for EC counts, pH, and organic acids. Samples from d 120 were also analyzed for chemical composition, ammonia-N, yeasts and molds, and aerobic stability. Data were analyzed with the GLIMMIX procedure of SAS. The pH of silages from all treatments decreased below 4 within 3 d of ensiling and remained low until d 120. Consequently, the pathogen was eliminated within 3 to 7 d of ensiling. The ECLB and ECA silages resulted in fewer ($P < 0.05$) yeast counts, and greater ($P < 0.05$) acetate and propionate concentrations, respectively, and hence increased ($P < 0.05$) aerobic stability compared to the control, EC and ECLP silages. Subsamples of d 120 silages were reinoculated with 5×10^5 cfu/g of *E. coli* O157:H7 either immediately after silo opening on d 120 or after 168 h of aerobic exposure (d 127), and the pathogen was enumerated after 6 and 24 h, respectively. All silages had similar low pH values and no EC was detected after 6 h of aerobic exposure. Twenty-four h later, the EC and ECLP silages reinoculated with the pathogen after 168 h of aerobic exposure had relatively higher ($P < 0.05$) pH values (5.50 and 6.13) and EC counts (5.39 and 5.3 log cfu/g), respectively. Whereas those treated with *L. buchneri* or propionic acid had low pH values (4.24 or 3.96, respectively), and lower (1.32 log cfu/g) or no EC count, respectively. *Escherichia coli* O157:H7 was eliminated during ensiling of corn within 7 d of ensiling across treatments. Application of propionic acid or *L. buchneri* at ensiling suppressed the growth of the pathogen in aerobically exposed silage

Key Words: corn silage, *Escherichia coli* O157:H7, propionic acid

Table 1388.

		pH	DM	DM loss	Prolamin	Deg 3 h	Deg 7 h	Deg 18 h
			% of as fed	% of ensiled	% DM	% of incubated		
Glucoamylase	Control	4.45	69.9	2.3	3.97	14.0	26.4	55.4
	GAM	4.09	68.1	4.4	4.04	16.6	30.6	56.3
Particle size	584 µm	4.09	69.6	2.7	4.00	16.4	28.5	57.1
	844 µm	4.46	68.4	3.9	3.99	17.1	28.5	54.6
Duration	30 d	4.37	68.2	3.2	4.28	16.3	26.9	50.5
	250 d	4.18	69.8	3.4	3.73	17.3	30.1	61.1
SEM		0.02	0.13	0.19	0.13	0.02	0.02	0.02
					P-value			
G		<0.01	<0.01	<0.01	0.69	0.01	0.13	0.76
PS		<0.01	<0.01	<0.01	0.95	0.74	0.99	0.36
D		<0.01	<0.01	0.44	<0.01	0.65	0.25	<0.01
G*PS		<0.01	0.42	<0.01	0.09	0.27	0.36	0.48
G*D		<0.01	0.83	0.68	0.82	0.56	0.66	0.50
PS*D		0.12	0.31	0.08	0.38	0.70	0.92	0.69
G*PS*D		0.32	0.29	0.30	0.62	0.64	0.56	0.74

1388 Effect of glucoamylase, particle size, and duration of silage storage on dry matter loss and digestibility of ground corn rehydrated and ensiled. N. M. Lopes[1], P. C. Cardoso[2], and M. N. Pereira[*1,3], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]University of Illinois, Urbana, [3]Better Nature Research Center, Ijaci, Brazil.*

Storing mature corn grain by rehydration and ensiling can improve digestibility by prolamin degradation in the silo. Particle size (PS) can determine the rate of grinding during ensiling and the duration of silage storage (D) determines farm cash flow. We evaluated the digestibility and DM loss of rehydrated and ensiled corn (REH) in response to PS, D, and glucoamylase addition at ensiling (G). Treatments were formed by a 2 × 2 x 2 factorial combination of PS (584 vs. 844 µm geometrical mean PS), D (30 vs. 250 d), and G (CTL vs. GAM. Sanferm Yield, 120 AGU/g, Novozymes. 0.35 mL/kg of corn). Particle distribution of fine and coarse corn were (% above screen): 2360 µm: 0.2 and 9.9. 2000 µm: 0.5 and 10.6. 1180 µm: 2.2 and 14.4. 850 µm: 21.3 and 21.8. 425 µm: 57.9 and 24.8. 300 µm: 4.7 and 3.9. Bottom pan: 13.1 and 14.5. Mature corn (86.8% DM, 49.2% vitreous endosperm, 4.3% prolamin/starch) was hydrated to a targeted DM concentration of 65%. Approximately 1 kg of corn DM was ensiled in heat sealed, nylon-polyethylene vacuum pouches, 5 silos per treatment combination. At opening, silages were frozen, dried at 55°C for 72 h, and ground through a 1 mm mesh diameter screen for determination of ruminal in vitro DM degradation in 3, 7, and 18 h. Coarse corn had higher pH and DM loss and lower DM concentration than fine corn. There was no effect of PS on digestibility and prolamine concentration. Longer D reduced pH and prolamine concentration, increased DM concentration and degradation in 18 h, and had no effect on DM loss. Glucoamylase reduced pH and DM concentration and increased DM loss and degradation in 3 h, and also induced greater decrease in silage pH and greater increase in DM loss when added to coarse (4.20 vs. 4.71 and 5.65 vs. 2.25% of ensiled) than to fine corn (3.98 vs. 4.19 and 3.09 vs.2.34% of incubated). The increase in DM loss induced by GAM was smaller when D was 30 d (4.21 vs. 2.25% of ensiled) than 250 d (4.52 vs. 2.35% of ensiled). Glucoamylase increased the proportion of rapidly degradable fraction in corn grain, but at the expense of increased DM loss, especially with coarse grinding. Longer storage increased prolamin degradation and the potentially degradable grain fraction.

Key Words: amylase, corn ruminal degradation, corn grain silage.

1389 Effect on a crude fermentation extract derived from *Trichoderma* on the performance of early lactation primiparous cows. N. D. Walker[*1] and G. Povey[2], *[1]AB Vista Feed Ingredients, Marlborough, United Kingdom, [2]ADAS, Stratford on Avon, United Kingdom.*

Research has demonstrated that pre-treating rations with fermentation extracts (FE) derived from Trichoderma sp., may improve the digestibility of the ration. The aim of the current study was to evaluate the effect of pre-treating a ration with FE on the performance of early lactation primiparous cows. Fifty early lactation primiparous cows (DIM 55 ± 15) were fed a diet containing (on a DM basis), grass silage (26%), corn silage (24%), and concentrate (50%). The trial was split into a 3 wk co-variate pre-period, followed by a 12 wk test period. Individual milk yield was measured daily, averaged weekly; BW and BCS were measured every 3 wk and fertility and health records were maintained throughout. Animals were placed into 25 blocks on the basis of DIM, milk production during the pre-period. Within each block, cows were randomly assigned to either Control (CTL) or treated (TRT) groups. Either water (750 mL/T DM, CTL) or FE (750

mL/T DM, TRT) were sprayed onto each group's TMR. Every week, CTL and TRT TMR samples were analyzed by NIR to determine whether there was any effect of pre-treatment on TMR composition (%DM, %CP, %Starch, %NDF, %ADF, theoretical D-value and theoretical ME value). The statistical model included effects of FE, week, their interactions, as well as covariate milk production and analyzed by ANOVA. Significance was declared at $P < 0.05$, while numerical trends were discussed at $0.05 < P < 0.1$. NIR analysis of the CTL and TRT TMR samples indicated that digestibility was affected by FE, with an average increase in the predicted D-value from 63% to 67% and in predicted ME value from 10.5 to 11.1 MJ/kg DM. Over the entire test period, milk yield tended ($P = 0.09$) to be increased in the TRT versus CTL group, 28.2 vs. 27.6 kg/day. In the last 3 wk of the trial, the effect of FE on milk yield reached significance ($P < 0.05$), 27.7 vs. 26.3 kg/day. Fertility was also significantly ($P < 0.05$) improved in the TRT group, with higher confirmed pregnancy rates (84% vs. 64%), and less inseminations required (2.3 vs. 3.2). Body weight change was also higher in the FE group. To conclude, pre-treating the ration with FE led to an increase in the predicted digestibility and ME of the ration as determined by NIR. Milk yield tended to be increased and fertility improved.

Key Words: pre-treatment, digestibility, Trichoderma

1390 Whey protein-based composite gels fed to Jersey cows to protect β-carotene from rumen degradation. K. P. Ortega*, M. Rosenberg, J. G. Fadel, and E. J. DePeters, *University of California, Davis, Davis.*

Cow's milk has a low concentration of β-carotene (BC) due in part to low BC concentrations in feedstuffs, limited absorption of BC in the small intestine, and metabolism by and storage in tissues. There is also a phenomenon not well understood where dietary BC appears to be degraded in the rumen. Previously, a whey protein-based composite gel was demonstrated to increase the omega-3 concentrations in cow's milk by protecting the unsaturated fatty acids from biohydrogenation in the rumen. Our hypothesis was that the same technology if applied to BC would increase the BC concentration in the milk of Jersey cows. Jersey cows were used because this breed tends to have a higher concentration of BC in their milk than Holstein cows. The objective was to test the efficacy of a whey protein-based composite gel to protect BC from rumen degradation and increase the BC concentration of Jersey milk. Four primiparous and four multiparous Jersey cows were fed a basal total mixed-ration with 500 mg BC fed in 2 physical forms, either in a whey protein-based composite gel (GEL) or as free, rumen available BC (CTL) in a crossover design. The BC was fed once daily at the morning feeding. Periods were 21 d with a 2-wk interval between periods to minimize carryover effects. Concentrations of BC were measured in blood plasma and milk. Feeding the GEL significantly increased BC concentration in plasma by 0.6619 μg/ml in primiparous cows 0.6620 μg/ml in multiparous cows ($P < 0.0001$), but no significant increase in BC concentration occurred in milk. The WPI gel was effective in increasing the BC concentration of plasma; however, further research should address the transfer of BC from blood into milk.

Key Words: β-carotene, whey protein, Jersey, plasma, milk

1391 Rumen morphometrics of Nellore cattle fed different combinations of sodium monensin and virginiamycin. M. C. Pereira*[1,2], A. L. Rigueiro[3], A. C. J. Pinto[3], A. M. Silvestre[2], A. Perdigao[2], L. V. Toledo[2], L. D. Miranda[2], F. P. Luiz[2], M. D. Arrigoni[2], C. L. Martins[2], and D. D. Millen[3], *[1]Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu campus, Brazil, was designed to evaluate the effect of the combined use of monensin (MON) and virginiamycin (VM) in high-concentrate diets during adaptation and finishing periods on rumen morphometrics and rumenitis of Nellore cattle. The experiment was designed as a completely randomized block, replicated 6 times (3 animals/pen), in which 72 26-mo-old yearling Nellore bulls (388.0 ± 31.1 kg) were fed in 24 pens for 90-d according to the treatments: MON (30 mg per kg of diet DM) during both adaptation and finishing periods (MON-MON); MON (30 mg/kg of DM) plus VM (25 mg/kg of DM) during the adaptation period, and only VM (25 mg/kg of DM) during the finishing period (MONVM-VM); MON (30 mg/kg of DM) plus VM (25 mg/kg of DM) during both adaptation and finishing periods (MONVM-MONVM); and only VM (mg/kg of DM) during the adaptation period, and MON (30 mg/kg of DM) plus VM (mg/kg of DM) during the finishing period (VM-MONVM). The adaptation program consisted of ad libitum feeding of three diets over adaptation period of 19 d with concentrate level increasing from 69% to 84% of diet DM. The finishing diet contained: 72.2% high-moisture corn grain, 14.0% sugarcane bagasse, 8.0% peanut meal, 2.0% coast cross hay, 3.0% supplement, and 0.8% urea (DM basis). Also, cattle were fed ad libitum twice daily throughout the study. At harvest, rumenitis incidence was determined, on the entire washed rumen, using a scale of 0 (no lesions noted) to 10 (severe ulcerative RUM). Likewise, a 1-cm^2 fragment of each rumen was collect from cranial sac. The number of papillae per cm^2 of rumen wall (NOP) was determined, as well as the mean papillae area (MPA). The rumen wall absorptive surface area (ASA) in cm^2 was calculated as follows: 1 + (NOP*MPA)–(NOP*0.002). No significant ($P > 0.10$) treatment effects were observed for any of the variables evaluated in this study:

Table 1392.

	G		A			D		*P*-value		
	Sorghum	Corn	CTL	AMG	GAM	30	180	G	A	D
DM, % of as fed	65.0	65.2	66.1	64.7	64.5	66.7	63.6	0.34	<0.01	<0.01
DM loss, % of ensiled	5.3	6.8	3.8	7.7	6.5	3.1	8.9	<0.01	<0.02	<0.01
Prolamin, % of starch	9.2	9.8	9.3	9.8	9.4	11.6	7.4	0.13	0.44	<0.01
Starch, % of DM	64.7	70.9	67.8	70.7	64.8	80.4	55.2	<0.01	0.06	<0.01
pH	3.99	3.92	3.92	3.94	4.01	4.17	3.74	0.02	0.03	<0.01
kd of Fraction B, %/h	3.14	3.33	3.30	3.20	3.21	3.17	3.30	0.01	0.42	0.05
Degradation 0 h, % of DM	39.8	32.5	33.7	38.2	36.6	32.9	39.4	<0.01	0.02	<0.01
Degradation 3 h, % of DM	47.7	41.2	43.7	44.7	44.9	39.9	49.0	<0.01	0.80	<0.01
Degradation 6 h, % of DM	51.5	47.1	50.3	48.5	49.2	43.8	54.8	0.03	0.76	<0.01
Degradation 12 h, % of DM	56.8	55.4	55.2	55.9	57.2	52.3	59.9	0.42	0.66	<0.01
Degradation 18 h, % of DM	62.1	60.6	61.3	61.2	61.5	57.6	65.0	0.28	0.98	<0.01
Degradation 48 h, % of DM	86.8	86.3	86.8	86.5	86.3	85.1	88.0	0.51	0.89	<0.01
ERD6, % of DM	60.3	56.5	57.1	59.6	58.5	56.0	60.8	<0.01	0.17	<0.01

rumenitis incidence (MONVM-VM = 1.00, MON-MON = 1.11, MONVM-MONVM = 1.00, VM-MONVM = 1.22; P = 0.92), NOP (P = 0.34), MPA (P = 0.46), and ASA (MON-VM-VM = 38.9 cm^2, MON-MON = 38.3 cm^2, MONVM-MONVM = 41.8 cm^2, VM-MONVM = 36.5 cm^2; P = 0.57). Thus, based on the results of this study, the combined use of monensin and virginiamycin in high-concentrate diets during adaptation and finishing periods did not negatively impact rumen morphometrics and rumenitis incidence of Nellore cattle.

Key Words: adaptation, additive, papillae

1392 Effect of glucoamylase and duration of silage storage on ruminal degradation and dry matter loss of corn and sorghum grain rehydrated and ensiled. T. Fernandes[1], K. T. Silva[1,2], D. R. Gomide[2], R. A. N. Pereira[2,3], C. L. S. Avila[1], and M. N. Pereira[*1,3], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, Brazil, [3]Better Nature Research Center, Ijaci, Brazil.*

Flint corn and sorghum grain are slow rumen degradable starch sources. Storing grain by rehydration and ensiling can improve ruminal degradability, by prolamin degradation in the silo. We evaluated the ruminal degradation and DM loss of rehydrated and ensiled grains of sorghum and flint corn (G) and the interaction of G with glucoamylase addition at ensiling (A) and duration of silage storage (D). Treatments were a 2 × 3 × 2 factorial combination of G (Sorghum, 129 µm geometrical mean particle size vs. Corn, 211 µm geometrical mean particle size), A (CTLvs. AMG vs. GAM), and D (30 d vs. 180 d). Dosage of glucoamylases AMG (AMG, Novozymes) and GAM (Sanferm Yield, Novozymes) was 0.35 mL/kg of grain. Mature grain was rehydrated to a targeted DM concentration of 65%. Approximately 4 kg of rehydrated grain was ensiled in 10 cm diameter × 60 cm length PVC silos with Bunsen valves (6 silos/treatment combination). At opening, silages were frozen and dried at 55°C for 72 h for determination of ruminal in situ DM degradation in 0 (bag wash), 3, 6, 12, 18, and 48 h of incubation (3 rumen cannulated cows). Time 0 DM disappearance was the fast degrading Fraction A. The slowly degradable Fraction B was 100– Fraction A (a 2 pool model). The fractional rate of Fraction B degradation (kd) was calculated as the slope of the linear regression over time of the Ln of bag residue/incubated. Effective ruminal degradation (ERD6) was calculated as: A + B [kd/(kd + kp)], kp at 6%/h. Glucoamylases increased Fraction A, but had no effect on DM degradation at other incubation times and ERD6, and increased DM loss, especially in longer storage (P < 0.01 for the interaction of A and D). Corn had greater DM loss and kd than sorghum, but lower DM degradation up to 6 h of ruminal incubation and ERD6, the smaller particle size of ground sorghum may explain such response. Longer storage increased DM loss, kd, ruminal degradation at all incubation times, and ERD6. Glucoamylase increased the rapidly degradable grain fraction at the expense of increased DM loss. Longer storage increased ruminal degradation and DM loss. Rehydrated and ensiled sorghum was as degradable in the rumen as corn and had lower DM loss, but had lower starch concentration than corn.

Key Words: amylase in silage, corn grain silage, sorghum grain silage

Table 1393.

Variable	Optifeed® (n=76)	Control (n=78)	P-value
Feed intake (FI) days 1-21, g	2,798 ± 190.8	2,755 ± 186.6	0.87
FI,days 22-42, g	21,082 ± 690.2	19,544 ± 675.9	0.11
FI, days 35-42, g	11,200 ± 365.8	10,155 ± 358.2	0.04
FI, days 1-42, g	32,282 ± 1,045.4	29,700 ± 1,023.7	0.08
Live weight (LW) Day 1, kg	36.3 ± 0.19	36.1 ± 0.18	0.43
LW Day 14, kg	39.3 ± 0.33	38.6 ± 0.32	0.13
LW Day 28, kg	50.3 ± 0.44	49.8 ± 0.44	0.37
LW Day 42, kg	60.4 ± 0.61	58.8 ± 0.60	0.05
LW Day 56, kg	79.6 ± 1.08	77.3 ± 1.07	0.13

1393 Effect of Optifeed on feed intake and live weight of Holstein calves. D. A. Vermeire*, *Nouriche Nutrition, Ltd., Lake Saint Louis, MO.*

Effect of a plant extract-based additive (Optifeed®, OF, Phode Laboratoires, Albi, France) on feed intake and live weight was tested in 154 Holstein calves raised for dairy beef in a naturally ventilated barn for a 42 d trial. Calves were individually housed and fed, and were fed 1 of 2 treatment feeds. Calves in pens 1, 2, 5, 6, 9, 10, etc. (Optifeed®) were assigned to the pre-starter feed (Smart Starter, BABY DOLL Nutrition Ltd, Lake St. Louis, MO) containing OF which was incorporated into the supplement pellet to provide 1 kg OF/1,000 kg of complete feed. Calves in pens 3, 4, 7, 8, 11, 12, etc. (Control) were assigned to receive the same pre-starter feed without OF. On d 43, calves were moved into group pens and fed a common starter feed. Calves were weighed on arrival (d 1), and d 14, 28, and 42. Daily feed provision was monitored with plastic cups which held an average 165 g (blue cup, d 1 to 21) or 316 g (white cup, d 22 to 42) of textured pre-starter feed. Data were analyzed using Statistix 10.0 using ANOVA for completely randomized experiment with calf as the experimental unit. Estimated (using cups) differed from actual (by weight) feed consumption by < 3% demonstrating that the cup delivery model was a good method for measuring daily intake of pre-starter feed by young Holstein calves. Calves fed OF consumed more feed from Day 35 to 42 (11,200 ± 365.8 vs. 10,155 ± 358.2 g, $P = 0.04$), tended to consume more feed over the entire 42 d trial (32,282 ± 1045.4 vs. 29,700 ± 1023.7 g, $P = .08$), and had heavier LW (60.4 ± 0.61 vs. 58.8 ± 0.60, $P = 0.05$) than calves fed control. Optifeed® appears to be an efficient plant extract-based additive to enhance early pre-starter intake and growth of calves.

Key Words: calves, feed intake

1394 Dose-dependent effects of a sensory additive on the eating behavior of TMR-fed dairy cows. F. Bargo*[1,2], I. Guasch[3], G. Tedo[1], A. Bach[4,5], and I. R. Ipharraguerre[1,6], *[1]Lucta S.A., Barcelona, Spain, [2]FAUBA, Buenos Aires, Argentina, [3]Blanca, Lleida, Spain, [4]ICREA, Barcelona, Spain, [5]IRTA, Caldes de Montbui, Spain, [6]University of Kiel, Kiel, Germany.*

Forty four Holstein dairy cows (156 DIM, 28.9 kg/d of milk, 648 kg of BW) were assigned to a 4 × 4 Latin Square design with 25-d periods replicated 11 times to evaluate the dose response to a sensory additive (ProEfficient, PE; Lucta S.A.) on eating behavior of dairy cows fed a TMR. Cows were grouped in 11 blocks and, within blocks, randomly assigned to 4 doses of PE: 0, 15, 30, and 45 g/d. The TMR averaged 16.4% CP, 31.4% NDF, and 1.63 Mcal NE_L/kg. Cows were fed ad libitum on electronic scales and eating behavior and feed consumption were recorded automatically. Data were analyzed using a model with fixed effects of dose (treatment), period, block, and the random effect of cow within block using PROC MIXED of SAS. Treatments effects were evaluated using linear, quadratic, and cubic orthogonal contrasts. Dose of PE affected ($P < 0.05$) eating time, intake rate, dry matter (DM) intake, and energy corrected milk (ECM) of dairy cows. Eating time responded cubically ($P < 0.05$) to PE dose because cows fed 30 g/d dedicated more time to eat than cows fed the other doses. There was a quadratic effect ($P < 0.05$) of PE dose on intake rate given that cows fed 15 and 30 g/d had lower rates than cows fed 0 and 45 g/d. Lying time was not affected ($P > 0.05$) by PE dose. DM intake and ECM responded cubically ($P < 0.05$) to PE dose because cows fed 30 g/d consumed the most DM and produced the largest amount of ECM. In summary, cows fed a TMR supplemented with 30 g/d of PE spent more time eating but at a lower rate than cows receiving other PE doses. These results confirm the positive impact of the sensory additive PE on the eating behavior of dairy cows and indicate that such an effect is most pronounced at 30 g/d.

Key Words: dose response, eating behavior and sensory additive

Table 1394.

	Sensory additive dose, g/d					Contrast, $P <$		
	0	15	30	45	SEM	Linear	Quadratic	Cubic
Eating time, min/d	198	209	229	211	5.4	<0.01	<0.01	<0.01
Intake rate, g DM/min	204	190	194	227	5.4	<0.01	<0.01	0.45
Lying time, min/d	728	723	727	721	14.4	0.69	0.97	0.62
DMI, kg/d	22.2	21.7	23.1	23.1	0.35	<0.01	0.51	<0.01
ECM (3.5%F 3.2%P)	30.7	30.4	31.3	30.7	0.66	0.46	0.64	0.03
Milk fat, %	4.02	3.99	4.00	4.07	0.03	0.13	0.06	0.77
Milk protein, %	3.42	3.45	3.48	3.48	0.02	<0.01	0.38	0.54

1395 Effect of rumen-protected capsicum on milk production in early lactating cows in a pasture-based system.

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In monogastric animals capsicum affects insulin homeostasis, glucose metabolism and nutrient partitioning. Recent research has shown a beneficial response on milk production and glucose utilization in dairy cows fed rumen-protected *Capsicum* oleoresin. During early lactation, when cows are in negative energy balance, they are in a state of insulin resistance (IR), promoting increased lipolysis, decreased peripheral tissue sensitivity and making more glucose available for mammary milk synthesis (i.e., "glucose-sparing"). The hypothesis of the current study is that rumen-protected capsicum extract enhances milk production during early lactation. Multiparous New Zealand Holstein Friesian cows on a commercial farm were randomly assigned to a Control group (CON; $n = 25$) or a group receiving 100 mg/d per cow of rumen-protected capsicum oleoresin (Nexulin, Pancosma, NEX; $n = 25$) during the first 100d in milk to determine the effect of Nexulin on milk production and body weight during early lactation under pasture-grazing conditions. All cows were managed exactly the same, as a single group, and were milked using 3 automated milking systems, allowing daily measurements of milk yield and composition and body weight. Nexulin was provided in 0.22 kg/d concentrate to NEX cows. All cows received < 3kg concentrate, 0.5 kg molasses and ad libitum access to grass pasture. Data were analyzed by (multivariate) analysis of variance (M)ANOVA, using initial body weight as a covariate for production parameters. Average milk yield was increased in NEX cows (27.9 vs. 26.1 kg/d, ± 0.9, $P < 0.06$) during the first 100 d of lactation. However, the effect occurred after peak production (wk > 5; 27.7 vs. 25.7 kg/d, ± 0.9, $P < 0.04$). Milk composition did not differ, but yield of fat, protein and lactose were increased in NEX cows (respectively, g/d: 1,397 vs. 1,313, ± 60, $P < 0.17$; 1,118 vs. 1,014 ± 39, $P < 0.02$; 1,409 vs. 1,321 ± 48, $P < 0.07$). All cows maintained their body weights (no differences) and prevalence of subclinical ketosis, based on milk fat: protein > 1.5, was lower in the NEX group (1.7 vs. 10.2%, ± 1.0, $P < 0.02$; nonparametric analysis). Rumen-protected capsicum increased milk production during early lactation in cows on pasture, but not until after peak lactation (wk > 5). This delayed response is consistent with delayed glucose sparing and may be due to the previous observation that in the New Zealand pasture-adapted strain of Holstein Friesian cows, IR is lower and insulin levels are higher immediately post-partum compared to American Holstein cows.

Key Words: *Capsicum* oleoresin, early lactation, milkproduction

1396 Effects of Valkalor on feed intake and digestibility, rumen functions, milk yield and composition in mid lactating dairy cows.

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The inclusion of feeds with nutraceutical properties in the livestock diets has been proposed to modulate rumen fermentations, improve post rumen-digestive processes and physiological status. This approach is considered a new tool to improve animal health and to increase feed efficiency. The aim of this research was to assess the effects of Valkalor (Idena, Sautron, France), a dietary supplement which contains yeast cell wall, an extract from *Hibiscus sabdariffa*, and minerals, on the health status, feed intake and digestibility, rumen functions, milk yield and composition of mid-late lactating cows. 36 Italian Friesians were used in a change-over design with 2 treatments in two 35-d periods, with a 1 wk washout period in between. Each period started with 14 d of adaptation. Cows were divided into 2 homogeneous groups, each one further divided in 3 boxes of 6 subjects. The control group (CTR) received a standard total mixed ration (TMR) diet for lactating dairy cows whereas the treated group (TRT) received the same diet supplemented with Valkalor (TRT) at 50 g/cow/day, included in the TMR. Daily feed intake of each box, individual milk yield, health status, BW and rumination time were recorded daily. In each period, BCS was evaluated at Day 14 and 35. Individual samples of milk and blood were taken at Day 14 and 34 to assess milk composition and metabolic profile. Samples of feces and TMR were collected at Day 33 and 34 to estimate the feed digestibility, using AIA as indigestible marker. At Day 35, rumen samples were taken 6h after the morning feeding, to assess the VFA profile. Treated

cows showed higher feed intake ($P < 0.05$), feed digestibility ($P < 0.05$ for DM, OM, CP and starch), rumination time (interaction treatment × day: $P < 0.05$) and total VFA concentration (CTR 121 vs. TRT 129 mmol/L; $P < 0.01$); BW showed a slight increase ($P < 0.05$) in TRT compared to CTR. Milk yield was higher in TRT (31.7 vs. 30.5 kg/d in TRT and CTR, respectively; $P < 0.01$), whereas milk composition was only slightly affected and the lactose and total protein yield were higher in TRT ($P < 0.01$ and NS respectively). At metabolic level, treated cows showed a better liver functionality (higher albumin, paraoxonase and lower ceruloplasmin; $P < 0.05$). Positive effects of the supplementation became progressively more evident during the treatment. Results suggest the effectiveness of Valkalor on the improvement of the production and the health status of dairy cows.

Key Words: nutraceutic, rumen fermentation, milk yield

1397 Screening for effects of live yeast or yeast derivative on dry matter disappearance in batch culture. P. X. Jiao[*1,2], F. Liu[2], Z. X. He[1,3], S. Ding[1], N. D. Walker[4], K. A. Beauchemin[1], T. W. Alexander[1], and W. Z. Yang[1], *[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Northwest Agriculture and Forestry University, Yangling, China, [3]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Hunan Research Center, The Chinese Academy of Sciences, Changsha, China, [4]AB Vista Feed Ingredients, Marlborough, United Kingdom.*

The objective of this study was to screen for the effects of live yeast (LY) or yeast derivative (YD) on DM disappearance (DMD) in batch culture varying yeast products, media pH and dosage of yeast. The study was arranged in a 5 yeasts × 2 pH × 4 dosages + monensin (positive control) factorial design. Substrate was a high-grain diet containing 10% barley silage and 90% concentrate (DM basis). Five yeast products were 3 LY (LY1, LY2, LY3) and 2 YD (YD4, YD5). The buffer pH was low (5.8) and high (6.5). Doses of LY (cfu/ml) were control (no LY), 4×10^6, $8 \times 10^6$and 1.6×10^7, and doses of YD (mg/bottle) were control (no YD), 15, 30, and 60. The dose of monensin was 0.17 mg/bottle. Inoculum was obtained from 2 ruminally fistulated beef heifers fed the same diets to the substrate. Substrate (0.75 g) ground through a 1-mm sieve was weighed into a filter bag and incubated for 24 h in a gas-tight culture bottle in 3 replications by each combination of treatments. The culture was repeated at different day. Data were analyzed using mixed procedure of SAS with a model that includes fixed effects of yeast, pH, dosages, and 2 way interactions, and the random effects of day. There was interaction ($P < 0.05$) of LY2, LY3, YD4 and YD5 with media pH or yeast with its dosage. Supplementation of LY1 had higher ($P < 0.01$) DMD (61%) at pH 6.5, whereas the DMD was lowest ($P < 0.05$) for YD5 (54%) and medium for other yeasts (averaged 57%). Increased media pH from 5.8 to 6.5 improved ($P < 0.01$) DMD (low vs. high pH; averaged 47 vs. 59%). Increasing the dose of LY3 and YD5 linearly ($P < 0.05$) increased the DMD at pH 6.5 with no dose effect of other yeasts. Adding monensin overall improved ($P < 0.05$) the DMD (62 vs. 57%) compared with yeasts at pH 6.5; whereas, at pH 5.8, the DMD was lower with monensin (44%) vs. LY2 (47%; $P < 0.05$), LY3 (47%; $P < 0.05$) or YD5 (49%; $P < 0.01$). These results suggest that in vitro DMD of high-grain diet varied with source and dosage of yeast and media pH. The improved DMD at pH 5.8 with LY2, LY3 and YD5 over monensin would be beneficial to high-grain fed cattle.

Key Words: dry live yeast, yeast derivative, batch culture, fermentation pH

1398 Supplementation of β-mannanese (CTCZYME) tends to improve immune traits in early lactating dairy cows. M. L. C. B. Azevedo[1], T. Tewoldebrhan[2], R. Appuhamy[2], G. C. Reyes[2], K. J. Bolek[2], S. Seo[3], J. J. Lee[4], and E. Kebreab[*2], *[1]Wageningen University, Wageningen, Netherlands, [2]University of California, Davis, Davis, CA, [3]Chungnam National University, Daejeon, The Republic of Korea, [4]CTC Bio Inc, Seoul, The Republic of Korea.*

Early lactating dairy cows typically face metabolic and immune challenges. Therefore, improving health status, besides feed conversion efficiency, can affect their productivity and welfare positively. β-mannanase is a fibrolytic enzyme that breaks down the non-structural carbohydrate mannan. It is currently used in pig and poultry production to increase nutrient digestion and may also improve their immune status. However, information about the effects of β-mannanase on ruminants is scarce. In a previous experiment, β-mannanese supplementation improved feed conversion efficiency and reduced somatic cell count of mid-lactating dairy cows. The objective of this study was to examine immune responses to β-mannanese supplementation in early-lactating cows. Fourteen early-lactating Holstein cows, paired by parity and milk production, were allocated to 2 treatments; control (50:50 forage:concentrate) and β-mannanese supplemented (0.1% of concentrate DM) diet. Acute phase protein, haptoglobin, and Immunoglobulin G (IgG) levels in blood were measured weekly from 14 to 50 d in milk. The CD4 and CD8 lymphocytes percentages in blood drawn at one time point were also evaluated by flow cytometry. Absolute numbers of CD4 and CD8 lymphocytes, total white blood count and the differential count of the 5 major white blood counts (neutrophils, lymphocytes, monocytes, eosinophils and basophils) were measured. Significance of β-mannanese supplementation on the blood immune traits were analyzed using linear mixed effects model including fixed effects of treatment, parity and days in

milk, and random effect of cow. Blood haptoglobin concentration tended to decrease ($P = 0.088$) in cows fed β-mannanese supplemented diet (0.373 ± 0.042 mg/ml) compared to those receiving control diet (0.498 ± 0.048 mg/ml). Higher concentrations of plasma haptoglobin may indicate a response to inflammation. Blood IgG concentrations and CD4:CD8 ratio were numerically higher in cows fed β-mannanese, but not significantly different ($P = 0.376$ and $P = 0.181$, respectively). Results for total white blood count and the five major white blood counts were also not significantly different. Dietary supplementation of β-mannanase has a potential to improve immunity of early-lactating cows.

Key Words: β-mannanase, immune traits, lactating cows

1399 To guarantee its threshold concentration in the rumen, live yeast *Saccharomyces cerevisiae* (CNCM I-4407) needs to be supplemented daily to dairy cows. C. Julien[1], M. Rey[*1], J. P. Marden[1], E. Auclair[1], and C. Bayourthe[2], *[1]Phileo Lesaffre Animal Care, Marcq-en-Baroeul, France, [2]Université de Toulouse, INRA, INPT UMR1388 GenPhySE, Castanet-Tolosan, France.*

It has already been stated that live yeast (LYSc47, 10^{10} CFU/g DM, *Saccharomyces cerevisiae* CNCM I-4407, Phileo Lesaffre Animal Care, France) is unable to colonize the digestive tract of cows. But, is the LY ruminal concentration stable after few days of distribution and how does it change within the day? Four early-lactating Holstein cows fitted with permanent ruminal cannulas were assigned to 4 treatments in a 4 × 4 Latin square design: 2 control diets consisting of a corn-silage-based TMR with ground corn (CD) or ground wheat (WD) top dressed at 0 to 5.10^{10}CFU/cow/day of LYSc47 in the morning meal (YCD and YWD, respectively). Each 14-d experimental period consisted of 9 d of adaptation to the diet, 3 d of measurement (d 1 to d 3) and a 2-d transition phase. During d 1 to d 3, ruminal fluid of cows was individually sampled −1 h, +0.5 h and +7 h around the morning meal. The concentration of live LYSc47 was determined by the method for counting the CFU (CFU/mL of ruminal fluid) on YM agar containing 1% chloramphenicol. Data were analyzed using general mixed model procedure of SPSS (IBM SPSS Statistics V22) including fixed effect of day, diet and hour nested in day and cow as random effect. No LySc47 was detected in ruminal fluid of cows receiving WD or CD. For cows receiving LYSc47, ruminal concentration of LYSc47 was affected ($P < 0.001$) by time of sampling during the day: 3.91, 4.94 and 4.16 log CFU/mL at −1 h, +0.5 h and 7 h around morning meal, respectively. LYSc47 content significantly increased 30 min after ingestion of the daily dose: +1.03 log CFU/mL and then decreased significantly toward lower level (−0.78 log/mL over 7 h whatever is the diet). LYSc47 content at +7 h remained significantly higher than at −1 h, but after 9 d of daily supplementation, LYSc47 ruminal concentration remained similar ($P = 0.432$) over the 3 d of sampling whatever was the diet. It clearly showed that LYSc47 had a quick revival capacity in ruminal content and that its daily supplementation is essential to maintain a threshold concentration in ruminal ecosystem.

Key Words: live yeast, rumen, dairy cow

1400 Feedlot performance and carcass traits of Nellore cattle fed different combinations of sodium monensin and virginiamycin. A. L. Rigueiro[*1], F. P. Luiz[2], M. M. Squizatti[1], A. H. Assumpção[1], M. M. Ferreira[1], C. P. Garcia[2], L. R. Muller[2], A. P. D. Bueno[2], C. L. Martins[2], M. D. Arrigoni[2], and D. D. Millen[1,3], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]SÃ£o Paulo State University (UNESP), Dracena campus, Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu campus, Brazil, was designed to evaluate the effect of the combined use of monensin (MON) and virginiamycin (VM) in high-concentrate diets during adaptation and finishing periods on feedlot performance and carcass characteristics of Nellore cattle. The experiment was designed as a completely randomized block, replicated 6 times (3 animals/pen), in which seventy-two 26-mo-old yearling Nellore bulls (388.0 ± 31.1 kg) were fed in 24 pens for 90-d according to the treatments: MON (30 mg per kg of diet DM) during both adaptation and finishing periods (MON-MON); MON (30 mg per kg of diet DM) plus VM (25 mg per kg of diet DM) during the adaptation period, and only VM (25 mg per kg of diet DM) during the finishing period (MONVM-VM); MON (30 mg per kg of diet DM) plus VM (25 mg per kg of diet DM) during both adaptation and finishing periods (MONVM-MONVM); and only VM (25 mg per kg of diet DM) during the adaptation period, and MON (30 mg per kg of diet DM) plus VM (25 mg per kg of diet DM) during the finishing period (VM-MONVM). The adaptation program consisted of ad libitum feeding of three diets over adaptation period of 19 d with concentrate level increasing from 69% to 84% of diet DM. The finishing diet contained: 72.2% high-moisture corn grain, 14.0% sugarcane bagasse, 8.0% peanut meal, 2.0% coast cross hay, 3.0% supplement, and 0.8% urea (DM basis). Also, cattle were fed ad libitum twice daily throughout the study. Cattle fed the combination of MON and VM during the adaptation period and only VM during the finishing period had greater ($P < 0.05$) final BW in kg (MONVM-VM = 536.1^{a}, MON-MON = 516.0^{b}, MONVM-MONVM = 512.7^{b}, VM-MONVM = 518.2^{b}), DMI in kg (MONVM-VM = 9.62^{a}, MON-MON = 8.73^{bc}, MONVM-MONVM = 8.47^{c}, VM-MONVM = 9.09^{b}), ADG in kg (MONVM-VM = 1.65^{a}, MON-MON = 1.42^{b}, MONVM-MONVM = 1.38^{b}, VM-MONVM = 1.44^{b}), as well as heavier HCW in kg (MONVM-VM = 284.2^{a}, MON-MON

= 266.4[b], MONVM-MONVM = 264.1[b], VM-MONVM = 270.8[b]) and increased dressing percentage (MONVM-VM = 53.0[a], MON-MON = 51.7[b], MONVM-MONVM = 51.5[b], VM-MONVM = 52.2[b]). No treatment effect on G:F ratio was observed ($P = 0.32$). Thus, Nellore yearling bulls should be fed high concentrate diets containing MON and VM during the adaptation period and only VM during the finishing period.

Key Words: adaptation, additive, ionophore

1401 Effects of supplementation of isoquinoline alkaloids and monensin on microbial protein synthesis, ruminal fermentation and nutrient digestibility in steers fed a finishing diet.

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Four Holstein steers with ruminal and duodenal cannulas were used in a 4 × 4 Latin square design to examine the effect of different treatments on ruminal fermentation and digestive function. Treatments consisted of a steam-flaked corn-based finishing diet supplemented with Sangrovit® RS (IQs) and monensin sodium (MS) as follows: 1) no additives (Control), 2) 1.35 mg IQs/kg diet, 3) 30 mg MS/kg diet, and 4) 1.35 mg IQs/kg diet plus 30 mg MS/kg diet. Experimental periods consisted of a 10-d adjustment period followed by a 4-d collection period. Between each experimental period, steers were allowed a 7-d recovery period during which all steers were fed the control diet. There were no differences ($P > 0.05$) between controls and IQs on ruminal digestion of OM, starch and NDF, but ruminal microbial efficiency and protein efficiency increased ($P < 0.05$) 7.6 and 9.1%, respectively with IQs supplementation. IQs increased (6.1%, $P = 0.02$) postruminal digestion of N and tended (3.7%, $P = 0.06$) to increase total tract digestion of N. Compared to the control, duodenal flow of feed N was greater (14.7%, $P = 0.04$) for steers which were supplemented with MS and tended to be greater in the IQs group (11.9%, $P = 0.09$). There was no difference ($P = 0.17$) between IQs and the MS group. Duodenal flow of microbial N was lower ($P \leq 0.01$) in the MS group compared to control and IQs. Microbial efficiency and protein efficiency were greater in the IQs group (13.8 and 10%, respectively, $P < 0.01$) compared to the MS group. IQs supplementation increased ruminal molar proportion of acetate 11.9% ($P = 0.05$) with no differences ($P > 0.12$) in molar proportions of propionate or acetate:propionate molar ratio. Compared to the control diet, MS did not affect ($P > 0.80$) ruminal pH, molar concentrations of total VFA, ruminal VFA molar proportions or estimated methane production. Combining IQs + MS did not improve the responses on digestion nor ruminal fermentation compared to the IQs or the MS group. IQs represent a tool to improve N utilization in ruminants.

Key Words: isoquinoline alkaloids, steers

1402 Effect of pelleted feed products and bambermycins on performance when fed to cattle grazing corn residue.

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Two corn residue grazing trials (84 and 85-d) were conducted from November to January in successive years to evaluate the effects of a corn byproduct pellet and bambermycins (Gainpro) on growing cattle performance. Both trials were arranged as a 2 × 3 factorial, inclusion of bambermycins (0 or 10 mg/d and 0 or 20 mg/d for years 1 and 2, respectively) was the first factor. The second factor was level of supplemental pellet (year 1) and amount of RUP supplied in the supplemental pellet (year 2). Supplement was delivered daily via Calan gates. In year 1, 60 steers (initial BW = 254 kg; SD = 26) were supplemented a pellet consisting of 54% corn stover treated with calcium oxide, 32% dried distillers grains, and 14% solubles at 0.3, 0.7, or 1.1% of BW. In year 2, 60 steers (initial BW = 222kg; SD = 14) were supplemented a pellet consisting of 44.5% corn stover treated with calcium oxide, 40% Soypass, soybean meal (SBM), or processed SBM, and 15.5% solubles at 1.82 kg/d. In year 1, steers were dosed with 10 g of titanium dioxide daily to measure residue intake. Steers were limit fed 5-d and weighed on 2 consecutive days for beginning and ending BW. There was no interaction between bambermycin inclusion and level of supplement on ending BW, ADG, or DMI in year 1 ($P \geq 0.82$). Bambermycin inclusion did not affect ending BW, ADG, or DMI ($P \geq 0.78$). There was a linear increase ($P < 0.01$) for ending BW and ADG as pellet supplementation increased. For steers supplemented at 0.3, 0.7 and 1.1% of BW, ADG was 0.01, 0.28 and 0.56 kg/d, respectively. There was a quadratic decrease in DMI as the trial progressed and supplement increased ($P < 0.01$). In year 2, there was no interaction between inclusion of bambermycins and RUP supplied in the pellet for ending BW or ADG ($P \geq 0.61$). Bambermycin inclusion at 20 mg/steer daily did not affect ending BW or ADG ($P \geq 0.79$). Likewise, there was no main effect of pellet type on ending BW or ADG ($P \geq 0.57$). For steers receiving pellet with supplemental protein provided by SBM, Soypass, or processed SBM, ADG was 0.35, 0.35, and 0.33 kg/d, respectively. Neither bambermycins nor increased amounts of RUP in the supplemental pellet affected performance of steers grazing corn residue.

Key Words: growing, pellet, corn residue

1403 Mineral-glycinate supplementation improves the systemic immune response to lipopolysaccharide challenge in lactating dairy cows. E. H. Wall*[1], K. Tran[2], C. Wallinger[2], J. S. Hogan[2], and W. P. Weiss[2], *[1]Pancosma, Geneva, Switzerland, [2]Department of Animal Sciences, OARDC, The Ohio State University, Wooster.*

Previously, it was observed that supplementation of growing steers with a Zn-glycinate complex improved immunity compared to an inorganic Zn source. The objective of this experiment was to test the hypothesis that supplementation of dairy cows with minerals in glycinate form would improve immune responses. Twelve mid-lactation Holstein cows were fed either a diet (UNSUP) void of supplemental Cu, Zn, and Mn (containing approximately 8, 30, and 30 ppm of each mineral, respectively in inorganic form) or a diet (GLY) containing Cu, Zn, and Mn in the glycinate form (B-TRAXIM® 2C, Pancosma; 16, 60, and 60 ppm, respectively) for 30 d. After 30 d, blood samples were collected for measurement of Cu in the serum as well as isolation of neutrophils to assess function. Cows were then exposed to intramammary infusion with lipopolysaccharide (LPS) of*Escherchia coli* O111:B4 (10 mL of a 10 μg/mL solution infused into the teat canal) to compare host defense responses, which were monitored for 7 d. Milk samples were collected for analysis of SCC and visual characterization. Clinical scoring (1 = normal; 5 = severe) was conducted and rectal temperature was monitored to estimate the systemic response to the LPS challenge. As expected, concentrations of Cu in the serum were increased with GLY (0.77 vs. 0.91 μg/g; $P < 0.05$). Percentage of intracellular kill and phagocytic neutrophils were not affected by treatment ($P > 0.05$); however, the phagocytic index (number of bacteria ingested per phagocyte) was decreased in GLY cows (2.47 vs. 1.85; $P < 0.05$). Before, during, and after the LPS challenge there was a trend for decreased SCC in GLY cows ($P < 0.15$). By design, the LPS challenge elicited a marked increase in clinical score (peak score = 4) and this was not affected by supplementation ($P > 0.70$). Rectal temperature during the first 24h post-LPS challenge was lower in the GLY cows, characterized by a lower area under the curve (933.8 vs. 927.7; $P < 0.05$) and a lower peak temperature (40.5 vs. 40.0°C; $P < 0.05$). The decreased body temperature combined with the lower SCC in GLY cows indicates that mineral-glycinate supplementation influences immune responses in dairy cows and may improve the ability to fight off infection. This has implications for mammary health; however, additional research is needed to distinguish the role of each metal, and their form, in this response.

Key Words: glycinates, immunity, mastitis

1404 Effects of replacing soybean meal with canola meal or treated canola meal on ruminal digestion, and omasal nutrient flow in lactating dairy cows. E. Marostegan de Paula*[1], M. A Camargo Danes[2], N. E Lobos[3], F. L. Drago[4], G. I. Zanton[5], G. A. Broderick[6], and A. Faciola[1], *[1]University of Nevada, Reno, [2]Federal University of Lavras, Lavras, Brazil, [3]Kemin Industries, Des Moines, IA, [4]University of Sao Paulo, Piracicaba, Brazil, [5]USDA-Agricultural Research Service, U.S. Dairy Forage Research Center, Madison, WI, [6]Broderick Nutrition & Research, LLC, Madison, WI.*

Treated canola meal (TCM) was produced as an attempt to increase the RUP fraction of canola meal (CM) with the goal of increasing AA availability for absorption in the small intestine. The objective of this study was to measure nutrient and microbial omasal flow when CM and TCM replaced soybean meal (SBM) in the diet of dairy cows. Six rumen-cannulated

Table 1404.

Table 1. Intake, DM flow, and flow of N fractions at the omasal canal in dairy cows

	Diet				Contrasts *P* -value	
Item	SBM	CM	TCM	SEM	SBM vs. CM+TCM	CM vs. TCM
DM intake, kg/d	25.4	26.0	26.7	1.62	0.28	0.48
DM Flow, kg/d	18.9	19.3	19.8	1.33	0.34	0.52
OM truly digested in the rumen, kg/d	15.1	15.5	15.1	0.91	0.81	0.72
Dietary N intake, g/d	625	668	679	39	0.04	0.64
Total NAN[1], g/d	669	688	671	50	0.82	0.76
N truly digested in the rumen, g/d	413	472	471	29	0.10	0.97
RDP supply, kg/d	2.58	2.96	2.95	0.18	0.10	0.81
RUP flow, kg/d	1.33	1.28	1.30	0.18	0.78	0.92
NMNAN flow[1], g/d	187	200	183	21	0.72	0.31
FAB-NAN flow[1], g/d	185	176	190	7.89	0.82	0.20
PAB-NAN flow[1], g/d	298	306	298	35	0.89	0.84
Total microbial NAN flow, g/d	482	482	488	41	0.94	0.90
Microbial efficiency, g of NAN/kg of OMTDR[1]	32.2	30.5	32.8	1.95	0.81	0.38

[1]NAN = non-ammonia-N, NMNAN = nonmicrobial NAN; FAB - and PAB-NAN = fluid- and particle-associated bacterial NAN; OMTDR = OM truly digested in the rumen.

cows were blocked into 2 blocks of 3 cows and randomly assigned within blocks to 3 dietary sequences in a replicated, 3 × 3 Latin square design with 21 d of adaptation and 7 d of sampling. Treatments differed only in CP source, which were: SBM, CM, or TCM. The TCM was treated by extrusion, with added molasses to promote the browning reaction. All diets contained (DM basis) 30% alfalfa silage, 30% corn silage, 4% soy hulls, 2.4% mineral-vitamin premix and 16% CP. The SBM diet contained 25% high moisture corn (HMC) and 8.6% SBM; the canola diets contained 22% HMC and 11.4% CM or TCM. Omasal sampling was performed during the last week of each period. Data were analyzed using the MIXED procedure of SAS. Orthogonal contrasts were used to compare effects of different protein sources (SBM vs. CM + TCM) and (CM vs. TCM). Partial data are presented in Table 1. Compared to SBM, CM and TCM increased N intake ($P = 0.04$) and there was a trend ($P = 0.10$) to increase RDP supply (kg/d), and N truly digested in the rumen (kg/d). There were no differences in DMI, ruminal digestibility, efficiency of ruminal microbial synthesis, and flows of: RUP, non-microbial-non-ammonia-N, and total microbial-non-ammonia-N among diets. Results indicate that both canola diets may increase N intake and RDP supply. Treating CM by extrusion did not affect microbial N flow at the omasal canal. Under the conditions of the present study, treating CM by extrusion was not effective in increasing RUP flow in dairy cows.

Key Words: nitrogen metabolism, rumen undegraded protein, omasal flow

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1405 Growth performance of dairy heifers limit-fed distillers dried grains with ad libitum forage.

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Most previous research on feeding distillers dried grains with solubles (DDGS) to dairy heifers has been conducted using a set forage to concentrate ratio in total mixed rations. Our objective was to determine the growth performance and DMI of heifers when fed DDGS or a corn and soy products concentrate mix with ad libitum grass hay. Our hypothesis was that heifers fed DDGS would have improved G:F because of slightly greater dietary fat, but growth performance would be maintained. A 16-wk randomized complete block design study was conducted using 24 heifers (18 Holstein and 6 Brown Swiss; 219 ± 2 d of age; 230 ± 4 kg BW). Heifers were blocked based on age and breed. Treatments were: 1) a control corn and soy products concentrate mix (CON) and 2) DDGS based concentrate mix (DG). Both concentrate mixes were fed at 0.8% of BW (DM basis) and grass hay was fed ad libitum. Heifers were individually fed respective concentrate mixes at 0800 h and hay was offered at 0900 h using a Calan gate feeding system. Orts were recorded daily before feeding. Frame sizes, BW, and BCS were measured at 4 h post feeding on 2 consecutive d during wk 0 and then every 2 wk thereafter throughout the feeding period. Data were analyzed using the MIXED procedures of SAS 9.4 with means compared using Tukey's test. Significance was declared at $P < 0.05$ and tendencies were declared at $0.05 \leq P < 0.10$. There were no significant interactions of treatment by wk. Heifer DMI (6.18 and 6.31 kg/d; SEM = 0.276 for the CON and DG, respectively), BW (269.8 and 266.9 kg; SEM = 9.86), and ADG (0.99 and 0.96 kg/d; SEM = 0.050) were similar ($P > 0.05$) between treatments. The G:F (0.168 and 0.156 kg/kg; SEM = 0.0099) was also similar ($P = 0.38$) between treatments. There were no differences ($P > 0.05$) in hip height (123.3 and 122.8 cm; SEM = 0.38), heart girth (140.6 and 139.9 cm; SEM = 0.40), or hip width (36.6 and 36.2 cm; SEM = 0.71) between treatments. Body condition scores (3.10 and 3.11; SEM = 0.026) were similar ($P = 0.68$) between treatments. Feeding heifers DDGS at 0.8% of BW with ad libitum forage maintained frame growth, ADG, DMI, and G:F compared to the CON concentrate mix.

Key Words: distillers grains, dairy heifer, growth performance

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1406 Effects of roughage inclusion and particle size on performance and rumination behavior of finishing beef steers.

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This experiment was conducted to determine the effects of feeding 5 or 10% corn stalks at various grind sizes with 30 or 25% wet corn gluten feed (WCGF), respectively, on rumination behavior, animal performance, and carcass characteristics of finishing beef steers. Fifty-one crossbred beef steers (BW = 881 ± 8 lbs), outfitted with rumination monitoring collars, were used in a randomized complete block design. Corn stalks were either passed through a commercial tub grinder once (large grind; LG) or twice (short grind; SG). Steam-flaked corn-based finishing treatment diets included: 10% SG with 25% WCGF (10%SG), 5% SG with 30% WCGF (5%SG), and 5% LG with 30% WCGF (5%LG). Animals were fed once daily at 0900 h using Calan head gates for an average of 155 d (heavy block = 148 d, light block = 162 d). Particle size of individual ingredients and treatment diets were quantified using the Penn State Particle Separator. Data were analyzed using the MIXED procedure of SAS with animal as the experimental unit. Means were separated using LSMEANS with the PDIFF option. There were no differences ($P = 0.52$) in final shrunk body weight between 5%SG, 5%LG, and 10%SG (1401, 1393, and 1373 ± 25.46 lbs, respectively), ADG (3.8, 3.8, and 3.7 ± 0.08 lbs, respectively; $P = 0.14$), or G:F (0.180, 0.175, and 0.176 ± 0.003, respectively; $P = 0.27$). However, DMI was greater ($P = 0.03$) for steers consuming the 5%LG

diet compared to the 10%SG (21.9 and 21.0 ± 0.31 lbs, respectively). Dressing percent also was greater ($P = 0.05$) for steers consuming 5%LG compared to 5%SG and 10%SG (64.3, 63.1, and 62.5 ± 0.007%, respectively). Hot carcass weight tended ($P = 0.10$) to be greatest for steers fed 5%LG. Steers consuming 10%SG had the greatest daily minutes of rumination ($P < 0.001$) followed by 5%LG, and 5%SG being the least (310, 288, and 244 ± 2.98 min/d, respectively). Steers consuming a longer particle size had increased dry matter intake and dressing percent, and tended to have greater carcass weights. With similar roughage inclusion rate, steers consuming a longer particle size also had increased daily rumination minutes. Therefore, increasing roughage particle size has the potential to allow a decrease in roughage inclusion without sacrificing feedlot performance and rumen function.

Key Words: rumination, corn stalks, corn gluten feed

1407 Automation of statistical procedures to screen raw data and construct feed composition databases.

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Millions of feed composition records have been generated from feed testing laboratories annually, providing high-valued assets that could be leveraged to benefit the animal nutrition community. Unfortunately, managing, handling, and processing feed composition data that originate from multiple resources are challenging, due in part to inconsistencies of how data are reported and the time needed to develop databases. Methods that consolidate and utilize these data are needed to develop accurate and precise feed composition databases. The objectives of this project were to: 1) develop automated statistical procedures to screen for outliers of feed composition data obtained from multiple resources; and 2) evaluate the efficiency of these procedures on classifying feedstuffs. A published statistical procedure (Yoder et al., 2014) was employed, modified, and programmed to operate using Python (Python Programming Language, v. 2.7) and SAS. A total of 2.761×10^6 records received from four commercial feed testing laboratories were used to develop the procedures and to construct tables summarizing feed composition. Briefly, feed names and variables across laboratories were standardized before the erroneous datapoints and duplicated samples were removed. Histogram, univariate, and principal component analyses were used to identify and remove outliers having key nutrients outside of the mean ± 3.5×SD. Clustering analyses were conducted to identify groups of feeds within a named feedstuff. Aside from the clustering step that was programmed in Python to automatically execute SAS, all steps were programmed and automatically conducted using Python followed by a manual evaluation of the resulting Pearson correlation matrixes and clusters. The input data contained 94, 162, 270, and 42 feeds, respectively, for laboratories 1 through 4 and were composed of 28 to 37 nutrients. The resulting database included 173 feeds (1.489×10^6records) with 111 feeds having more than 1 cluster. The developed procedures effectively classified byproducts (bakery byproducts, brewers grains, distillers grains and solubles, rice bran), forage (legume vs. grass, mature vs. immature and mid-maturity), and oilseeds vs. meal (cottonseed, canola seed, linseed/flaxseed, soybeans, sunflower) into distinct sub-populations. Results from these analyses provide a robust tool for the National Animal Nutrition Program (A National Research Support Project supported by USDA-NIFA and the State Agricultural Experiment Stations) to efficiently and consistently construct and update large feed datasets in an accurate, precise, and timely manner. This approach may also be used by commercial laboratories, feed manufacturers, animal producers, and other professionals to process feed composition datasets.

Key Words: automation, feed composition database, statistics

1408 Effect of pelleting at different temperatures and times on nutrient supply of co-products form canola oil processing.

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The objective of this study was to evaluate effects of conditioning temperatures (70, 80, and 90°C) and conditioning time (50s and 75s) and their possible interaction during pelleting on predicted truly absorbed protein supply of canola meal. Truly absorbed protein supply were measured for dairy cows according to DVE/OEB system and NRC-2001 model. The treatments were designed in 3 × 2 factorial arrangement and experiment design was RCBD. Statistical analysis was performed using the PROC MIXED of SAS 9.3. The results showed that conditioning time had a quadratic effect ($P < 0.05$) on total protein supplied to the small intestine (TPSI), microbial protein synthesized in the rumen based on available nitrogen (N_MCP), truly absorbed microbial protein in the small intestine (AMCP),rumen bypass feed crude protein (BCP) and truly absorbed bypass protein(ABCP). Samples conditioned at 80°C were highest in AMCP and N_MCP while lowest in TPSI and ABCP between pellets. Pelleting decreased ($P < 0.01$) TPSI, BCP and ABCP (261.39 vs. 241.66 g/kg DM, 195.68 vs. 174.20 g/kg DM and 55.49 vs. 41.61 g/kg DM, respectively) but increased AMCP of canola meal (55.86 vs. 57.34 g/kg DM). Pelleting induced decreased truly digested protein in the small intestine (DVE; 99.26 vs. 86.77

g/kg DM) and increased degradable protein balance (OEB; 115.26 vs. 135.27 g/kg DM) were observed ($P < 0.01$). In NRC-2001 model, affected by quadratic effect of conditioning temperature ($P < 0.05$), samples conditioned at 80°C between pellets were lowest in rumen undegradable feed crude protein (RUP), truly absorbed rumen undegradable protein in the small intestine (ARUP) and metabolizable protein (MP). Rumen endogenous protein (ECP) and truly absorbed rumen endogenous protein in the small intestine (AECP) were decreased by increasing conditioning time (10.58 vs.10.21 g/kg DM and 4.23 vs. 4.08 g/kg DM, respectively; $P < 0.01$). Pelleting decreased ($P < 0.01$) MP, AECP and ECP of canola meal (107.09 vs. 94.65 g/kg DM, 4.43 vs. 4.16 g/kg DM and 11.08 vs. 10.39 g/kg DM, respectively). RUP and ARUP of canola meal were decreased by pelleting as well (176.29 vs. 156.94 g/kg DM and 49.99 vs. 37.49 g/kg DM, respectively; $P < 0.01$). Summarily, pelleting changed potential protein supply of canola meal; alteration of pelleting conditions caused differences between pellets in predicted protein supply profiles.

Key Words: co-products from oil processing, nutrient supply and pelleting conditions

Table 1409.

1409 Okara meal can completely replace soybean meal in diets of early to mid-lactation dairy cows.

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Okara meal is a byproduct from the production of soy milk and tofu that can potentially replace soybean meal due to its high CP concentration. We aimed to evaluate the effects of okara meal as a replacement for soybean meal on performance and plasma concentration of metabolites in lactating dairy cows. Twelve multiparous (65 ± 33 DIM; 451 ± 45 kg of BW) and 8 primiparous (100 ± 35 DIM; 370 ± 51 kg of BW) Jersey cows were used in a crossover design with 21-d periods (14 d for diet adaptation and 7 d for data and sample collection). Diets were fed as TMR and formulated to be isonitrogenous and isofibrous and contained (DM basis) 50% grass-legume baleage, 2% liquid molasses, 2% minerals-vitamins premix, and: 1) 8.1% soybean meal, 10% soyhulls, and 27.9% corn meal (SBM treatment); 2) 15% okara meal, 8% soyhulls, and 23% corn meal (OKM treatment). The dietary nutrient composition averaged 15.4 vs. 15.9% CP, 35.3 vs. 36.3% NDF, and 24.1 vs. 24.1% ADF for SBM and OKM, respectively.

Table 1. Effects of a soybean meal (SBM)- or a okara meal (OKM)-based diet on performance and plasma metabolites in dairy cows

	Treatments			
Item	SBM	OKM	SEM	*P*-value
DMI, kg/d	18.1	17.9	0.58	0.30
Milk yield, kg/d	20.5	20.8	1.08	0.44
4% FCM, kg/d	24.1	24.2	1.05	0.73
ECM, kg/d	25.9	26.1	1.15	0.63
Milk fat, %	5.24	5.16	0.12	0.37
Milk fat, kg/d	1.05	1.06	0.04	0.59
Milk true protein, %	3.81	3.76	0.09	0.02
Milk true protein, kg/d	0.77	0.78	0.04	0.71
MUN, mg/dL	9.47	8.51	0.40	<0.01
PUN, mg/dL	22.2	21.1	0.41	0.03
Plasma Met, μ*M*	21.6	23.0	0.91	0.27
Plasma Lys, μ*M*	99.5	95.5	4.24	0.44
Plasma His, μ*M*	37.7	35.8	2.81	0.52
Plasma Leu, μ*M*	152	140	4.18	0.02
Plasma total EAA, μ*M*	109	103	3.03	0.09

Cows were fed and milked twice daily, and milk (d 15 to 16) and blood (d 16 to 17) samples were collected and analyzed for components and plasma metabolites [AA, urea-N (PUN)], respectively. Results are shown in Table 1. No significant differences were observed for DMI (mean = 18.0 kg/d), milk yield (mean = 20.7 kg/d), 4% FCM (mean = 24.2 kg/d), and ECM (mean = 26.0 kg/d) in cows fed SBM or OKM. Whereas milk fat concentration was not affected by treatments, milk true protein concentration was greater ($P = 0.02$) in cows fed SBM than OKM. Yields of milk fat and true protein did not differ significantly between treatments and averaged 1.06 and 0.78 kg/d, respectively. However, MUN ($P < 0.01$) and PUN ($P = 0.03$) were greater in cows fed SBM compared with those fed OKM suggesting an improvement in N use efficiency. Plasma concentrations of Met, Lys, and His did not differ significantly in cows fed SBM or OKM. Conversely, the plasma concentration of Leu was greater ($P = 0.02$), and that of total EAA tended ($P = 0.09$) to be greater in cows offered SBM vs. OKM, which may explain the observed increase in milk true protein concentration when feeding SBM. Overall, replacing soybean meal with okara meal maintained animal performance and appeared to improve N use efficiency.

Key Words: dairy cows, okara meal, soybean meal

1410 Effect of flax meal supplementation on oxidative stress and metabolic status of early lactation dairy cows infused with flax oil in the abomasum.

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The addition of flax oil (FO) to the diet of high-yielding dairy cows is a good strategy to improve the energy balance during early lactation. Although polyunsaturated fatty acids have numerous healthy attributes, they are easily oxidized and promote oxidative stress. In this project, we tested if the inclusion of natural antioxidants, flax meal (FM) rich in plant lignans, in cow's diet could decrease oxidative stress and optimize the potential of FO as a source of energy. This experiment was conducted using twenty (20) multiparous high-yielding Holstein cows fitted with ruminal cannulas. Cows were assigned to two dietary treatments: (1) 250 g flax oil/d infused in the abomasum ($n = 10$, FO) and (2) FO + 15% flax meal (FM) in the dry matter ($n = 10$, FMFO). Treatments were administered over a 21 d (d) period from d 7 to d 28 post calving. Plasma and urine samples were collected on d 7 (before treatment initiation), 14, 21, 28 (end of treatment) and 49 (for carryover effect) to evaluate systemic oxidative damage to proteins (carbonyls) and DNA (8-hydroxy-2'-deoxyguanosine), and to determine the enzymatic activity of the antioxidants glutathione peroxidase (GPx) and superoxide dismutase (SOD), and diet had no effect ($P > 0.05$). Biopsies were taken from the liver and mammary gland tissue on d 7, 28, and 49 to measure the activity and mRNA expression of antioxidants and evaluate energy production in the form of adenosine triphosphate (ATP), and diet had no effect ($P > 0.05$) on activity of GPx and SOD. The mRNA expression of *SOD1* in mammary tissue was lowered by the addition of FM to the diet ($P < 0.01$). In the liver, *SOD1* mRNA levels remained stable throughout the experimental period in the FMFO group while it was higher on d 49 in cows infused with FO (interaction treatment × day, $P < 0.05$). Analysis of hepatic levels of ATP revealed that the addition of FM suppressed the increase in energy production observed on d 49 in the FO group (interaction treatment × day, $P < 0.05$). Infusion of FO in the abomasum decreased the level of proteins carbonyls in mammary gland tissue from d 7 to d 49, and this effect was counteracted by the addition of FM (interaction treatment × day, $P < 0.05$). Taken altogether, these results suggest that the oxidative status of early lactating cows infused with FO is not significantly affected by the addition of FM to the diet.

Key Words: dairy cows, oxidative stress, antioxidant

1411 The effect of by-product inclusion and concentrate feeding level on milk production and composition, pasture dry matter intake, body weight and body condition score of mid-late lactation spring calving grazing dairy cows.

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There is growing interest in the use of by-products (or co-products) as economical sources of nutrients that complement grazed grass when grass supply is not sufficient to meet the nutritional demands of lactation. The objective of this research was to investigate the effect of by-product inclusion and concentrate feeding rate on milk production and composition, pasture dry matter intake (DMI), body weight (BW) and body condition score (BCS) of mid-late lactation spring calving grazing dairy cows. Forty eight (41 multiparous, 7 primiparous) Holstein Friesian dairy cows were blocked according to parity, balanced for days in milk, predicted 305 d milk yield, BCS and pre-experimental milk yield and randomly assigned to one of four dietary treatments in a 2 × 2 factorial design. All cows were grazed in one group on a perennial ryegrass based sward. The dietary treatments (T) were: concentrate containing 35% by-products offered at either 3 kg (T1) or 6 kg (T2)/d or a concentrate containing 95% by-products offered at 3 kg (T3) or 6 kg (T4)/d. The by-products used were maize dried distillers grains (DDG), palm kernel expeller (PKE) and soybean hulls (SH), included in equal proportions on a DM

basis. The experimental diets were offered for 63 d. Pasture DMI (14.5 kg/d) was not affected by feeding rate ($P = 0.37$) or by-product inclusion level ($P = 0.27$). Similarly, there were no effects of treatment on BW change (−9.3 kg, $P = 0.20$) or BCS change (+0.07, $P = 0.94$). By-product inclusion level had no effect on milk yield (27.33 kg/d, $P = 0.65$) or fat and protein yield (2.00 kg/d, $P = 0.54$). However, cows offered 6kg of concentrate produced more milk (+1.94 kg/d, $P = 0.08$) and milk fat (+0.10 kg/d, $P = 0.02$) than cows offered 3kg of concentrate. In conclusion, the results of this research show that by-products (DDG, PKE and SH) can be included at up to 95% of the concentrate fed to pasture based cows without impacting on milk production or composition, pasture DMI, BW or BCS. Cows offered 6kg of concentrates produced more milk and milk fat yield than cows offered 3kg, however, this response is unlikely to yield an economic return.

Key Words: by-products, dairy cow, milk production.

1412 Evaluating the feeding value of field peas for growing and finishing cattle. H. L. Greenwell*[1], K. H. Jenkins[2], and J. C. MacDonald[1], [1]*University of Nebraska-Lincoln, Lincoln,* [2]*University of Nebraska, Scottsbluff.*

A two year experiment was conducted to determine the effects of field pea (FP) supplementation during grazing and finishing phases on animal performance and carcass characteristics. In year one, 110 steers (initial BW = 348 kg; SD = 22 kg) and in year 2, 113 heifers (initial BW = 249 kg; SD = 11 kg) were arranged in a 3 × 2 factorial. The first factor was supplementation during grazing, consisting of three treatments: 1) FP; 2) mixture of dry rolled corn (70.8%), solubles (24%), and urea (5.2%); (DRC); (mixture was used to ensure RDP was not limiting); 3) control group receiving no supplement (CON). The second factor was finishing treatment, cattle were fed a DRC-based finishing diet with or without 20% FP (DM basis). Cattle grazed crested wheatgrass pastures and were supplemented at a rate of 0.5% BW (DM basis). During the growing phase ending BW and ADG ($P < 0.01$) were greatest for calves supplemented DRC (413 ± 11 kg, 0.89 ± 0.05 kg, respectively) followed by FP (399 ± 11 kg, 0.78 ± 0.05 kg, respectively) and the CON treatment (379 ± 11 kg, 0.62 ± 0.05 kg, respectively). In the finishing phase there was an interaction between growing and finishing treatments for G:F ($P = 0.03$), a result of cattle supplemented with FP during the growing phase and with no FP in the finisher performing better than cattle supplemented with FP during growing and with FP also included in their finishing diet (0.142 ± 0.004 kg vs. 0.132 ± 0.004 kg, respectively). There were no other interactions of finishing and growing treatments on other variables ($P \geq 0.10$). Feedlot ADG was affected by growing treatment ($P < 0.01$), where cattle in the CON treatment had greater ADG (1.95 ± 0.04 kg) than cattle that were supplemented DRC (1.80 ± 0.04 kg) and FP (1.78 ± 0.04 kg), which were not different. Final BW and HCW tended ($P = 0.07$) to be affected by growing treatment in a similar manner to feedlot ADG. Inclusion of FP in the finishing diet had no impact on carcass characteristics. In conclusion, cattle supplemented DRC during grazing had greater ADG than cattle supplemented FP or CON. However, in the finishing phase CON cattle compensated in feedlot ADG. Inclusion of FP in grower supplement or finishing diets may be advantageous if appropriately priced.

Key Words: cattle, field peas, finishing, grazing

1413 Cotton burrs as alternative roughage to adapt beef steers to steam-flaked corn-based finisher diet. L. A. Ovinge*[1], J. O. Sarturi[1], P. R. B. Campanili[1], B. J. M. Lemos[2], B. C. Bernhard[1], and D. Pettit[1], [1]*Texas Tech University, Lubbock,* [2]*Universidade Federal de Goiás, Goiânia, Brazil.*

Effect of cotton burrs as a roughage source during the transition of beef cattle (hay to finisher diet) was evaluated on intake, ruminal characteristics, nutrient digestibility, and feeding behavior. Ruminally cannulated steers ($n = 6$; BW = 235 ± 81 kg) were assigned using a complete randomized design to 1 of 2 adaptation strategies: Alfalfa hay-based or cotton burrs-based. In both strategies, roughage sources decreased as steam-flaked corn gradually increased. Steers were fed ad libitum once daily, a series of six diets (7-d period each): wheat hay; 4 step-ups; and a finisher. In situtechnique was used to assess ruminal fiber degradability (substrate = wheat hay). Wireless rumen pH probes were used. A 3-d spot fecal collection (twice daily, last 3 d of each period) and AIA were used to estimate total tract apparent nutrient digestibility. Rumen fluid samples (0, 4, 8, and 16 h post-feeding) were taken (d-6 of each period) for VFA and NH_3. Data were analyzed using Glimmix procedure of SAS (wheat hay period used as a covariate). Intake was not affected by adaptation strategies ($P \geq 0.16$), except for a tendency ($P = 0.10$) for steers adapted with alfalfa-strategy to ruminate more per kg of NDF consumed during finisher diet, than those adapted with cotton burrs-strategy. Steers fed cotton burrs-strategy showed lower ruminal pH average on step-3 and finisher periods (5.62 and 5.51 vs. 6.04 and 5.83; $P < 0.01$ and $P = 0.05$, respectively) compared with alfalfa-strategy. A greater area of pH below 5.6 (200 vs. 15 min*pH; $P < 0.01$); lower ruminal NH_3 concentration (5.1 vs. 8.8 mg/L; $P < 0.01$); and lower digestibility (OM, ADF, and hemicellulose; $P \leq 0.02$) during step-3 were also observed for steers fed cotton burrs-strategy compared to alfalfa-strategy, respectively. However, cotton burrs-strategy steers showed greater ($P = 0.01$) NDF digestibility during step-4; greater ($P < 0.01$) OM digestibility during finisher diet; and lower acetate/propionate ratio ($P = 0.04$) with a tendency ($P = 0.08$) to have greater propionate molar proportion during step-2, compared to alfalfa-strategy steers. Ruminal fiber degradability was not affected by adaptation strategies ($P \geq 0.36$), neither was dietary starch digestibility during common

finisher ($P = 0.73$). Cotton burrs adaptation strategy induced an improved ruminal fermentation environment during finisher diet, although with riskier ruminal pH and rumination than alfalfa-strategy. Further evaluation must consider cattle growth performance and economic aspects.

Key Words: adaptation, cotton burrs, alfalfa

1414 Temporal effects of ruminal propionate infusion on feeding behavior of Holstein cows In the postpartum period.

1415 Evaluation of five cool season grasses and alfalfa-grass mixtures. J. Paulson*[1], D. Holen[2], D. Nicolai[3], and B. J. Heins[4], *[1]University of Minnesota Extension, Rochester, [2]University of Minnesota, Morris, [3]University of Minnesota, Farmington, [4]University of Minnesota West Central Research and Outreach Center, Morris.*

Our increased knowledge of NDF digestibility has shown a benefit to feeding grasses in ruminant diets. However, data on the yield and nutrient analysis of alfalfa/grass mixtures with modern grass varieties and harvest management are lacking. The objective of this study was to determine the yield and nutritional value of selected alfalfa-grass mixtures and grass monocultures. At 2 MN locations, plots of grasses alone, alfalfa alone, and alfalfa-grass mixtures were planted using a forage plot seeder. Four randomized replications were planted of all plot variables. Each location was seeded with 1 alfalfa (A) variety and each of 5 grass species. Grass species included smooth brome (SB), meadow brome (MB), orchard (OG), tall fescue (TF), and meadow fescue (MF). Forage samples were sent to Dairyland Laboratories, St. Cloud, MN and analyzed by NIRS for DM, CP, NDF, and TDN. Data were analyzed using the MIXED procedure of SAS. Independent variables for analyses were the fixed effects forage, and replicate was a random effect. Nutrient analysis for Otter Tail forage showed no significant differences for CP, NDF or $NDFD_{30}$ for any of the forage species or mixtures evaluated. However, at Lanesboro, the mixture of A × MF × MB was significantly higher ($P < 0.05$) in CP than the mixture of A x MF and A or MF in pure stands. NDF tended to be higher in pure grass but was significantly lower ($P < 0.05$) in the A × MF × MB mixed stand. In conclusion, high quality alfalfa/grass forage can compare favorably with alfalfa for both yield and nutrient analysis.

Key Words: alfalfa, grasses, meadow fescue, forage

Table 1415.

Table 1. LANESBORO	Nutrient analysis, % of DM					
species	CP	NDF	NDFD30	RFV	RFQ	Yield t/a
A	18.68^{a}	44.63^{ab}	43.32	130	125	4.03^{c}
MF	18.24^{a}	47.67^{b}	45.01	121	120	4.06^{c}
TF	19.76^{ab}	44.25^{ab}	43.52	133	121	5.62^{d}
SB	19.99^{ab}	43.59^{ab}	39.15	131	120	4.51^{cd}
OG	20.03^{ab}	42.82^{ab}	41.05	136	128	4.48^{cd}
MB	18.92^{ab}	47.81^{b}	46.36	121	110	4.39^{c}
A MF	18.64^{a}	45.75^{ab}	43.98	128	123	3.89^{c}
A MF TF	19.24^{ab}	45.51^{ab}	44.61	128	125	3.85^{c}
A MF SB	19.98^{ab}	42.71^{ab}	42.27	138	131	4.07^{c}
A MF OG	20.17^{ab}	42.63^{a}	41.22	138	127	4.01^{c}
A MF MB	20.62^{b}	43.18^{ab}	44.79	138	136	4.04^{c}

Uncommon superscripts (a,b)differ P<.01. Uncommon superscripts (c,d) differ P<.1

1416 A novel bm3 corn silage hybrid with floury kernel genetics improves lactational performance and feed efficiency in Holstein cows. E. M. Remick*[1], S. M. Fredin[1], K. W. Cotanch[1], H. M. Dann[1], C. S. Ballard[1], J. P. Brouillette[2], and R. J. Grant[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Dow AgroSciences, Mycogen Seeds, Indianapolis, IN.*

Dry matter intake, lactation performance, feed efficiency and chewing behavior of multiparous Holstein cows ($n = 15$) fed diets containing a novel *bm3* corn silage (CS) hybrid with floury kernel genetics were compared to diets containing commercially available conventional and *bm3* hybrids using a replicated 3 × 3 Latin square design with 28-d periods. Cows were housed in tie-stalls, milked 3×/d, and fed a diet containing (DM basis) 49.0% of 1 of 3 CS hybrids (Mycogen Seeds, Dow AgroSciences, LLC): 1) a conventional CS hybrid (CON); 2) a brown midrib hybrid (BMR); and 3) a *bm3* hybrid with floury kernel genetics (BMRFL). All diets contained 6.3% hay crop silage and 44.7% concentrate. Diet nutrient composition averaged 14.8 ± 0.3% CP, 2.7 ± 0.5% NDF, and 26.3 ± 0.5% starch. Dry matter intake and milk yield were measured on d 22 to 28. Milk composition was measured on d 25 to 26. Cow behavior was monitored for 48 h over d 24 to 26. Data were analyzed by ANOVA using the MIXED procedure in SAS. Dry matter intake was increased ($P = 0.01$; SE = 0.5)

for cows fed BMR (28.0 kg/d) compared to CON (26.8 kg/d); DMI for cows fed BMRFL was intermediate (27.6 kg/d). Energy-corrected milk yield was increased ($P < 0.01$; SE = 1.5) for cows fed BMR (50.3 kg/d) and BMRFL (51.8 kg/d) compared to CON (47.2 kg/d). Milk fat yield was increased ($P \leq 0.05$; SE = 0.06) for cows fed BMRFL (1.87 kg/d) compared to CON (1.74 kg/d) and BMR (1.80 kg/d). Milk protein yield was increased ($P < 0.01$; SE = 0.06) for cows fed BMR (1.49 kg/d) and BMRFL (1.54 kg/d) compared to CON (1.36 kg/d). Milk urea-N was reduced ($P < 0.01$; SE = 0.3) for cows fed BMR (11.61 mg/dL) and BMRFL (11.16 mg/dL) compared to CON (13.60 mg/dL). Feed efficiency (Energy Corrected Milk/DMI) was increased ($P \leq 0.03$; SE = 0.04) for cows fed BMRFL (1.87) compared to CON (1.76) and BMR (1.79). Milk N efficiency ($P = 0.001$; SE = 1.2) was greatest for cows fed BMRFL (40.4%) followed by BMR (38.1%) and CON (35.3%). Cows fed CON chewed 5 min more per kg NDF consumed than cows consuming either *bm3* hybrid ($P < 0.01$). Lactational performance was increased for cows fed diets containing both *bm3* CS. Greater feed efficiency indicates that a *bm3* CS hybrid containing floury kernel genetics improves lactational performance and energy utilization compared to *bm3* and conventional CS. Additionally, improved milk N efficiency indicates greater ruminal carbohydrate fermentability can be achieved when feeding a BMRFL diet.

Key Words: brown midrib, floury corn, feed efficiency

1417 Alternative forage crops modify the composition and content of bovine milk fatty acids.

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Bioactive fatty acids (FA) found in milk have been linked to human health benefits. Alternative forage crops (AFC) include small grains, warm-season grasses and legumes that can potentially enhance forage production. The objective of this study was to determine if traditional pasture strip-tilled with AFC (treatment, TRT) would alter the composition (g/100 g FA) and content (g/kg milk) of milk FA compared with traditional grass-legume pasture (control, CON). Two 21-d experiments, spring (SPR) and summer (SUM), were conducted using 16 lactating Jersey cows (SPR, 85 ± 46 DIM; SUM, 143 ± 58 DIM). Cows were divided into 2 groups and offered 60% TMR (DM basis) and 40% pasture as AFC or traditional. SPR AFC included barley, wheat, rye, triticale, and hairy vetch (2.4% diet DM), while SUM AFC included buckwheat, chickling vetch, and oat (10.0% diet DM). From d 19 to 21 of each experiment, milk samples were collected during four consecutive milkings. Forage and milk FA were analyzed via gas-liquid chromatography. Differences between least-squares means were evaluated using the student's *t* test (JMP Pro 12). SPR forage FA (% total) included CON (total n-3 FA: 30.1%; total n-6 FA: 35.2%) and TRT (total n-3 FA: 46.2%; total n-6 FA: 21.5%), whereas the SUM forage FA included CON (total n-3 FA: 44.4%; total n-6 FA: 22.6%) and TRT (total n-3 FA, 45.7%; total n-6 FA, 22.0%). No differences in the milk content of total PUFA, branched-chain FA, or biohydrogenation intermediates (e.g., *trans*-11 18:1) were observed in either experiment. Milk proportions of total odd-chain FA were higher ($P < 0.01$) in SPR TRT (2.07 g/100 g) than in SPR CON (1.96 g/100 g). Milk proportions of n-3 FA and *trans*-18:1 were respectively lower ($P < 0.01$) in SPR TRT (0.64 g/100 g; 20.5 g/100 g) than in SPR CON (0.71 g/100 g; 22.8 g/100 g), but the contents of these FA were not different between groups. Milk content of 12:0 was higher ($P < 0.05$) in SPR TRT (1.86 g/kg milk) than in SPR CON (1.56 g/kg milk) ($P < 0.05$). Total milk SFA content was higher ($P < 0.05$) in SUM TRT (33.7 g/kg) than in SUM CON (29.1 g/kg). Milk content of de novo FA (CON: 11.6 g/kg milk; TRT: 13.2 g/kg milk) and mixed FA (CON: 13.0 g/kg milk; TRT: 16.2 g/kg milk) were higher ($P < 0.01$) in SUM AFC-fed cows. In conclusion, AFC altered the composition and content of milk FA.

Key Words: dairy, organic, pasture

1418 Effects of post-ethanol extraction sorghum silage as an alternative forage in growing and finishing diets on steer performance, carcass characteristic and nutrient digestibility.

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Two experiments evaluated use of post-ethanol extraction sorghum silage as an alternative forage to hay in feedlot diets. In experiment one (Exp1), 72 crossbred steers (397 ± 23, SD) were used to evaluate growth and carcass characteristics. Steers were blocked by BW into pens of 6 steers and randomly assigned to growing diets containing 40% (DM basis) of sorghum silage (SS; 57.6% NDF) or grass hay (CON; 63.3% NDF) for 56d ($n = 6$ pens per treatment). Within each treatment steers transitioned to dry-rolled corn-based finishing diets (fed for 56d) containing 6% effective NDF contributed by the forage source, resulting in forage inclusions of 16% for SS and 13.1% for CON. Experiment two (Exp2), utilized a subsample of steers ($n = 12$ per treatment) housed in pens equipped with Growsafe bunks for determination of growing phase diet total tract digestibility. From d28- 42, steers received titanium dioxide at approximately 10 $g^{-1} \cdot steer^{-1} \cdot d^{-1}$. Fecal samples were collected on d 41 and 42. Fecal and total mixed ration samples were dried, and ground for analysis of DM, OM, NDF, ADF, CP, ether extract (EE), and starch. Data were analyzed using PROC MIXED of SAS with the fixed effects of treatment and block (Exp1) or treatment (Exp2); significance was determined at $P \leq 0.05$ and tendencies at $P \leq 0.10$. Growing phase DMI and ADG did not differ due to treatment ($P \geq 0.19$); however, SS-fed steers had improved

G:F compared to CON ($P = 0.04$). Finishing period ADG or G:F did not differ ($P \geq 0.15$), despite SS-fed steers having lesser ($P = 0.008$) DMI than CON-fed steers. No differences in DMI, ADG, or G:F over the whole trial were noted between treatments ($P \geq 0.12$), nor were any carcass traits affected ($P \geq 0.23$). Growing phase total tract apparent digestibility of DM and starch did not differ ($P \geq 0.19$), due to treatment; however, OM digestibility tended to be greater ($P = 0.09$) in SS-fed steers. During the digestibility assessment period DMI was lesser ($P = 0.003$) in SS-fed steers. Steers fed the SS diet had greater ($P \leq 0.03$) digestibility of EE, CP, NDF, hemicellulose, and cellulose than CON-fed steers. Interestingly, CON-fed steers had greater ($P < 0.0001$) ADF digestibility than SS-fed steers. These data suggest that post-extraction sorghum silage can be effectively utilized in feedlot diets as an alternative forage.

Key Words: sorghum silage, cattle performance, digestibility

1419 Effect of lactic acid bacterial inoculants on the fermentation parameters and aerobic stability of sorghum-sudangrass silage. X. Li[*1,2], Y. Zhu[2], D. Vyas[1], and A. T. Adesogan[1], [1]*Dep. of Animal Sciences, IFAS, University of Florida, Gainesville,* [2]*Institute of Grassland Science, China Agricultural University, Beijing, China.*

Sorghum-sudangrass (*Sorghum vulgare* × *Sorghum sudanense*) has great potential to be widely used for silage making because of its rapid growth, high yields and nutritional value, and acceptability to cattle. However, it is prone to aerobic spoilage, which reduces its nutritional value. The aim of this study was to examine the effect of lactic acid bacterial inoculants on fermentation quality and aerobic stability of sorghum-sudangrass silage. Sorghum-sudangrass was harvested at 20% DM, chopped to approximately 20-mm lengths and treated in triplicate with 10^6 cfu/g of fresh weight of *Lactobacillus buchneri* (LB), *L. plantarum* (LP), and *Enterococcus fecalis* (EF) or distilled water (Control). Samples were stored at room temperature (about 25°C) for 264 d in polyethylene bags. Silage chemical composition was analyzed, and aerobic stability was determined by measuring the number of hours the temperature in the silages remained stable before rising more than 2°C above room temperature. Data were analyzed using the General Linear Model procedure of SAS and means were separated using Duncan's test. Silage treated with LB had greater pH compared to Control, LP, and EF silages (3.78 vs. 3.75, 3.73, 3.75, respectively; $P \leq 0.05$). Similarly, acetic acid concentration was greater for the silage treated with LB compared to Control, LP and EF silages (2.59 vs. 2.05, 1.59, 2.20, % DM, respectively, $P \leq 0.05$); however, no effects were observed on butyric or propionic acid concentration. The NH_3–N/TN concentration was greater in EF silage and lower in LB silage compared to that of the Control silage (6.92, 5.13 vs. 5.90%, $P \leq 0.05$). The lactic acid concentrations were 15 and 13% greater in LP and EF silages, respectively compared to the Control silage (12.30, 12.04 vs. 10.70, % DM, $P \leq 0.05$). Silages treated with LB and EF took longer to heat than untreated silage when exposed to air (169, 166.5 vs. 133.5, h, $P \leq 0.05$). In contrast, silages inoculated with LP had lower aerobic stability compared to the Control silage (99.5 vs. 133.5, h, $P \leq 0.05$). Inoculating sorghum-sudangrass silage with LB and EF improved aerobic stability, whereas inoculating the silage with LP improved fermentation parameters.

Key Words: aerobic stability, fermentation, inoculants

1420 Effects of feeding triticale and wheat silages on feed intake, milk production and composition, and enteric methane production in lactating dairy cows. M. T. Harper*, J. Oh, F. Giallongo, G. Roth, and A. N. Hristov, *The Pennsylvania State University, University Park.*

The objective of this experiment was to evaluate the production effects of replacing corn silage (serving as the control) with either triticale or wheat silage in a total mixed ration fed to lactating dairy cows. Twelve Holstein cows (days in milk 38 ± 5.6, BW 632 ± 101.6kg) were used in a replicated 3 × 3 Latin square design experiment with 3, 28 d periods. Feeding was ad libitum for 5 to 10% refusals. The control diet consisted of (DM basis): 44% corn silage, 8% alfalfa haylage, 5% hay/straw mixture, 9% ground corn, 8% canola meal, 7.5% whole roasted soybeans, 7% SoyPLUS, 4.5% molasses, 4% cottonseed hulls, and 3% mineral premix. For the triticale diet, 22.7% (DM basis) of the corn silage was replaced with triticale silage. Similarly, 22.7% of the corn silage in the wheat diet was replaced with wheat silage. Diets met or exceeded the MP and NE_lrequirements of the cows. The triticale (Hyoctane) and wheat (Malabar) were harvested May 13 and 20, 2015, respectively, at the boot stage. The silages had DM of 30.7 and 40.7%, pH 4.48 and 4.46 and (DM basis): lactic acid, 7.03 and 6.43%; NDF, 51.1 and 51.0%; and CP, 17.3 and 14.6%, respectively. Diet did not affect DMI (27.5 kg/d; SEM = 1.8, $P = 0.37$), enteric methane emission (470 g/d; SEM = 23.4, $P = 0.16$), or milk fat yield (1.55 kg/d; SEM = 0.11, $P = 0.35$). Milk yield was higher in control versus triticale or wheat diets (42.7, 41.2, and 41.4 kg/d, respectively; SEM = 5.2, $P = 0.01$). Energy corrected milk yield was also higher ($P = 0.05$) in control (40.9 kg/d) versus triticale (38.6 kg/d) or wheat (38.5 kg/d) diets. Triticale and wheat diets increased ($P < 0.001$) milk urea nitrogen concentration compared with the control (12.7 and 13.1 vs. 10.8 mg/dL, respectively). Milk true protein and lactose yields were lower for both triticale and wheat diets compared with the control: 1.20, 1.20, and 1.27 kg/d (SEM = 0.096, $P = 0.02$) and 2.00, 1.98, and 2.14 kg/d (SEM = 0.173, $P = 0.01$), respectively. The results indicate that a 22.7% replacement of corn silage DM with either triticale or wheat silage in the diet of lactating dairy cows did not affect enteric methane emission

or DMI, but decreased milk yield.

Key Words: triticale, wheat, silage

1421 Effects of feeding sorghum and oat silages on feed intake, milk production and composition, and enteric methane production in lactating dairy cows. M. T. Harper*, J. Oh, F. Giallongo, J. C. Lopes, G. Roth, and A. N. Hristov, *The Pennsylvania State University, University Park.*

The objective of this experiment was to evaluate the production effects of replacing corn silage (serving as the control) with either sorghum or oat silage in the total mixed ration fed to lactating dairy cows. Twelve Holstein cows (days in milk 81 d ± 24; BW 615 kg ± 49.6) were used in a replicated 3 × 3 Latin square design experiment with 3, 28 d periods. Feeding was ad libitum for 5 to 10% refusals. The control diet consisted of (DM basis): 44% corn silage, 7.5% alfalfa haylage, 4% hay/straw mixture, 11% ground corn, 7.5% SoyPLUS (West Central Cooperative, Ralston, IA), 7.5% whole roasted soybeans, 7% canola meal, 4.5% molasses, 4% cottonseed hulls, and 3% mineral premix. For the sorghum diet, 22.7% (DM basis) of the corn silage in the diet was replaced with sorghum silage. Similarly, 22.7% of the corn silage in the oat diet was replaced with oat silage. The MP balance of the control, sorghum, and oat diets was 199, 238, and 290 g/d, respectively, whereas the balance of NE_l was 2.8, 2.4, and 2.8 Mcal/d. The forage sorghum (Alta AF 7202) was harvested on November 11, 2014 with the harvester set to 1 inch total chop length. The oats (Forage Plus) were mowed in a vegetative state and harvested on November 14, 2014. Sorghum and oat silages had DM of 30.5 and 30.8% and (DM basis): lactic acid, 2.89 and 7.27%; NDF, 62.7 and 54.7%; and CP, 9.5 and 11.7%, respectively. Enteric methane emission measurements were collected with the GreenFeed system. Control and oat diets resulted in higher DMI and milk yield than sorghum: 26.7, 27.1, vs. 26.0 kg/d (SEM = 1.68, $P = 0.02$) and 39.6, 40.2, vs. 38.7 kg/d (SEM = 3.57, $P < 0.01$), respectively. Methane emission (502 g/d; SEM = 26.7, $P = 0.59$) and milk fat yield (1.41 kg/d; SEM = 0.07, $P = 0.78$) were not affected by diet. The sorghum silage diet decreased milk true protein concentration ($P = 0.03$) compared with the control or oat silage (2.78 vs. 2.85 and 2.83%, respectively). Similarly, milk protein yield was decreased ($P = 0.05$) by the sorghum diet (1.04 vs. 1.13, and 1.13 kg/d, respectively). The results indicate that a 22.7% replacement of corn silage DM with oat silage is a viable alternative for dairy producers in the Northeast U.S.

Key Words: sorghum, oats, silage

1422 Effect of harvest method on digestibility of corn residue. T. M. King*[1], M. L. Jolly-Breithaupt[1], J. L. Gramkow[2], J. C. MacDonald[1], and T. J. Klopfenstein[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Lincoln.*

Advanced techniques of harvesting corn residue has led to improved residue quality by reducing proportion of stem in the bale. The objectives of this study were to determine 1) the effect of harvest method on the digestibility and quality of corn residue and 2) the effect of drying method used to process feces on digestibility estimates. An 85 d digestion study was conducted utilizing 9 crossbred wethers (initial BW = 42.4 kg; SD = 7 kg) blocked into 3 blocks based on initial BW. Residue based diets contained corn residue harvested with 1 of 3 methods (low-stem, high-stem, and conventional) at 70:27:3 residue: Sweet Bran®: bromegrass hay (DM basis). Five periods of 17 d provided 10 d for adaption and 7 d for total fecal collection. Sweet Bran® and bromegrass hay were fed at a 9:1 ratio in the fourth period for determination of residue digestibility by difference. Feces were collected twice daily, composited at the end of the period, and dried using 1 of 3 methods (60°C forced air oven, 100°C forced air oven, and freeze dry technique). No differences in DM intake, OM intake, or NDF intake were observed among residue type ($P > 0.05$). Low-stem had greater DM digestibility (DMD) than conventional ($P = 0.02$) and had a tendency to be greater than high-stem ($P = 0.06$). There were no differences in DMD ($P = 0.63$) or OM digestibility (OMD; $P = 0.86$) between high-stem and conventional. Low-stem had greatest OMD and NDF digestibility (NDFD, $P < 0.05$). High-stem had a NDFD which was greater than conventional ($P < 0.01$). Drying method had no effect on digestibility determination by lab assays for both OMD and NDFD ($P = 0.99$). Overall low-stem had the greatest digestibility with high-stem being intermediate and conventional having the lowest digestibility. Reducing the proportion of stem in the bale through changes in the harvest method can lead to an increased quality of corn residue.

Key Words: corn residue, digestibility, harvest method

Table 1422.

Table 1. Digestibilities of Residues from 3 Harvest Methods

	Conventional	High-stem	Low-stem	SEM	P-value
DMD, %	46.05^{c}	47.22^{bc}	51.74^{ab}	2.3	0.05
OMD, %	51.41^{b}	51.05^{b}	55.56^{a}	2.0	0.06
NDFD, %	44.46^{c}	52.37^{b}	58.53^{a}	2.1	< 0.01

^{abc}Means with differing superscripts are different

1423 Supplementing Corn on Alfalfa Pasture to Alter Growth Performance, Carcass, and Quality Traits. Chloe Gresel, Cheryl Campbell, Lisa Duizer, Brian McBride, and Ira Mandell. *University of Guelph, Guelph, ON, Canada.*

Pasture finishing of beef cattle can be used to improve the fatty acid composition of beef (omega 3s and CLA) but at the possible expense of deleteriously affecting palatability traits. While pasture finished beef can command a premium in the marketplace, increased time on feed relative to finishing on a high grain diet can lead to production challenges due to much slower rates of gain for grass-fed beef. Supplementing corn on pasture may increase cattle gains and beef palatability attributes without necessarily deleteriously affecting beef fatty acid composition. The objective of this study was to examine how corn grain supplementation on alfalfa pasture alters carcass, meat quality, and fatty acid traits in an attempt to increase cattle performance and beef palatability. Fifty black Angus and Angus cross steers were randomly assigned to one of four management regimens: 1) 85.4% corn-based concentrate/14.6% forage diet fed in a drylot as a TMR (n = 12); 2) pastured cattle supplemented with corn at 1% BW (n = 13); 3) pastured cattle supplemented with corn at 0.5% BW (n = 12); 4) pastured cattle with no corn supplementation (n = 13). Pastured steers were rotationally grazed through 20 acres of predominantly alfalfa pasture while high concentrate-fed steers were housed in 2 drylot pens equipped with Calan gates to measure individual feed intakes. Cattle were fed for 111 d with BW taken every 14 d to track performance. Steers were harvested at a commercial packing plant where a rib section from each animal was shipped back to the University of Guelph Meat Lab for evaluation. Management regimen effects on performance, carcass, meat quality, trained taste panel and fatty acid data were evaluated using a Proc Mixed procedure in SAS. Average daily gain differed ($P < 0.0001$) across most management regimens. While grain feeding decreased ($P < 0.01$) dissectible lean, backfat and marbling were generally similar ($P > 0.14$) across management regimens. Grain feeding decreased ($P < 0.0001$) n-3 fatty acids without affecting ($P > 0.27$) CLA concentrations. Taste panel assessment of tenderness, juiciness, and beef flavor attributes were similar ($P > 0.30$) between beef from grain-fed cattle and beef from cattle that only consumed alfalfa pasture.

Key Words: beef cattle, grass-fed, fatty acids

1424 Effect of harvest method and ammoniation on apparent digestibility and intake of baled corn residue in lambs. A. C. Conway*, T. M. King, M. L. Jolly-Breithaupt, J. C. MacDonald, T. J. Klopfenstein, and M. E. Drewnoski, *University of Nebraska-Lincoln, Lincoln.*

The objective of this study was to assess the effect of three different harvest methods and ammonia treatment on the in vivo digestibility of baled corn residue. Nine wether lambs (49.2 ± 0.5 kg BW) were used in a 9 × 6 Latin Square design with a 3 × 2 factorial treatment structure; 3 harvest methods [conventional rake and bale (COV), New Holland Cornrower with 8 rows (high-stem; HS) or 2 rows (low-stem; LS) of corn stalks chopped into the windrow containing leaf, husk and upper stem] and ammoniation at 3% of DM of the resulting baled residue. Diets consisted of 64.2% corn residue, 29.8% Sweet Bran, 3.3% smooth-bromegrass hay, and 2.8% mineral mix (DM basis). Periods were 21 d (14 d adaptation and 7 d total fecal collection). Lambs were fed ad-libitum (110% of the previous day's DMI) during d 1 to 12 and reduced to 95% of ad-libitum intake for d 13 to 21. Treatment diets were fed over 6 periods, with the non-residue proportion of the diet (Sweet Bran, smooth-bromegrass hay, and mineral mix) fed alone in an additional period to determine the digestibility of the residue by difference. There was a harvest method by ammoniation interaction for ad-libitum DMI (d 7 to 12). Intake of non-ammoniated residue diets did not differ ($P \geq 0.92$) among harvest methods, however, ammoniation increased ($P \leq 0.05$) intake with LS having the greatest increase, COV

Table 1424.

Table 1. Effect of harvest method and ammoniation on *ad-libitum* DMI (% BW) and the DM and OM digestibility of the corn residue component of the diet.

	Non-ammoniated			Ammoniated			*P-value*			
	COV	LS	HS	COV	LS	HS	SEM	Harvest	Ammonia	Interaction
Diet DMI	2.6	2.6	2.6	3.6	4.1	3.1	0.15	<0.01	<0.01	<0.01
DMD,%	40.3	46.4	41.6	49.1	56.9	52.9	2.65	0.04	<0.01	0.89
OMD,%	45.9	50.6	45.6	55.1	60.1	57.4	2.43	0.12	<0.01	0.85

being intermediate and HS having the least increase. There was no harvest method by ammoniation interaction for DM or OM digestibility. Digestibility of DM (DMD) differed between harvest methods, with LS being greater than COV ($P = 0.01$) and tending ($P = 0.10$) to be greater than HS. Ammoniation increased DMD of the residues by 25% (10.2% units). Digestibility of OM (OMD) tended to be affected by harvest method with LS tending ($P = 0.06$) to be greater than COV. Ammoniation improved OMD of all harvest methods, resulting in a 22% (10.1% units) increase. Utilizing alternative harvesting technologies and ammoniation can improve the feeding value of baled corn residue.

Key Words: corn residue, digestibility, harvest method, ammoniation

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1425 Effects of growing system and silage type on feedlot growth performance, carcass characteristics, and nutrient digestibility of beef steers. P. R. B. Campanili*[1], J. O. Sarturi[1], S. J. Trojan[1], M. A. Ballou[1], B. J. M. Lemos[2], L. A. Ovinge[1], and J. B. G. Mayorquin[3], *[1]Texas Tech University, Lubbock, [2]Universidade Federal de Goiás, Goiânia, Brazil, [3]Zamorano, Tegucigalpa, Honduras.*

The effects of beef cattle growing systems (grazing vs. bunk) and silage type (corn vs. sorghum) on finishing phase growth performance, carcass characteristics, and nutrient digestibilities were evaluated. Steers ($n = 128$; BW = 394 ± 21 kg) were backgrounded by either grazing (forage sorghum AF7401, 104 d) or bunk fed (65% concentrate diet, 85 d). Following the backgrouding period, animals were blocked by BW, and randomly allocated to one of the two dietary treatments, corn (BH8895) or sorghum (AF7401) silage at 20%, DM basis, in a randomized complete block design. During the finishing phase, steers were fed once daily at approximately 0800 h. A 5-d spot fecal collection (twice daily) and acid insoluble ash were used to estimate total tract apparent digestibility. Slaughter was performed on 132, 146, or 174 d on feed. Data were analyzed using the Glimmix procedure of SAS, using pen as the experimental unit. No interaction (growing system × silage type) was observed ($P > 0.16$), except for a tendency ($P = 0.06$) of bunk backgrounded steers to consume more sorghum than corn silage diet, compared with grazing backgrounded steers. Steers that grazed forage sorghum had greater ADG (25%), DMI (23%), and greater gain:feed (5%) during the finishing phase, compared with bunk backgrounded steers ($P < 0.01$). A greater HCW (7.8%), lower dressing percent (0.8% unit), and lower fat thickness (18%) were observed for steers grown under sorghum grazing conditions compared to backgrounded bunk fed steers ($P < 0.01$). Steers fed the corn silage diet had lower DMI (7%), greater ADG (5%), and consequently greater gain:feed (10%) compared with steers fed sorghum silage diet ($P < 0.01$). A 0.5% unit greater ($P = 0.03$) dressing percent and 0.1% unit greater ($P = 0.04$) KPH were observed for steers fed corn silage compared to those fed sorghum silage. Steers fed the corn silage diet also had greater ($P < 0.01$) DM (11%), CP (9%), EE (1.9%), and starch (8%) digestibilities compared to steers fed sorghum silage diet. Digestibility of fiber components were not affected ($P \geq 0.12$) by silage type or growing system. Sorghum grazing backgrounded steers positively affected finishing phase, but such strategies must be further be evaluated considering economical aspects and water use. Replacing corn silage with sorghum silage in beef finishing diets even at low roughage inclusion requires adjustments to balance dietary energy.

Key Words: grazing, silage, sorghum

1426 Effects of feeding green chopped winter forages on digestibility, ruminal fermentation and blood parameters in beef steers. T. M. Schulmeister*, M. Ruiz-Moreno, M. E. Garcia-Ascolani, F. M. Ciriaco, D. D. Henry, J. Benitez, J. C. B. Dubeux Jr., G. C. Lamb, and N. DiLorenzo, *University of Florida, North Florida Research and Education Center, Marianna.*

An experiment was conducted in the winter over 2 consecutive yr to evaluate the effects of feeding green chopped winter forages on digestibility and ruminal fermentation parameters in beef steers. Each yr, 9 ruminally cannulated Angus crossbred steers (yr 1: 359 ± 79 kg; yr 2: 481 ± 105 kg) received fresh chopped forage ad libitum, from pastures planted with one of the following mixtures: 1) FL401 cereal rye (*Secale cereale* L.)/Prine annual ryegrass (*Lolium multiflorum* Lam.) (RYE); 2) Horizon 201 oats (*Avena sativa* L.)/Prine annual ryegrass (OAT); 3) Trical 342 triticale (*X Triticosecale* spp.)/Prine annual ryegrass (TRIT). Intake was measured throughout the study using GrowSafe, and any unconsumed forage was discarded before the next d feeding. After a 14 d adaptation period, feed and fecal samples were collected twice daily for 4 d, to determine apparent total tract nutrient digestibility using indigestible NDF as a marker. On d 19, blood and ruminal fluid samples were collected every 3 h during a 24 h period, to analyze blood urea nitrogen (BUN) and glucose in the plasma, as well as NH_3–N, pH, and VFA concentrations in ruminal fluid. Data were analyzed as a generalized randomized block design with repeated measures, using the Mixed Procedure of SAS, with treatment as a fixed effect and animal and yr as random effects. Treatments did not affect ($P > 0.05$) intake of DM, OM, CP, NDF, or ADF; however, apparent total tract digestibility of DM, OM, CP, NDF, and ADF was greater ($P < 0.05$) for OAT and TRIT, when compared with RYE. Steers fed OAT had greater concentrations of plasma glucose ($P < 0.05$) compared with TRIT and RYE. An effect of sampling time ($P < 0.01$) was observed for ruminal pH; however no treatment or treatment × sampling time interactions were observed ($P > 0.05$). Steers fed RYE had greater ($P < 0.05$) concentrations of NH_3–N,

BUN, and the least concentrations of total VFA ($P < 0.05$). Molar proportion of acetate, branched-chain VFA and acetate:-propionate were greater ($P < 0.05$) for RYE when compared with OAT and TRIT. In conclusion, OAT and TRIT resulted in greater digestibility of nutrients, and ruminal fermentation and blood parameters that are conducive to enhanced growth performance when compared with RYE.

Key Words: fermentation, ruminants, winter forage

1427 Effects of feeding steers extruded flaxseed and hay together (total mixed ration) or sequentially (non-total mixed ration) on animal performance and erythrocyte vaccenic, rumenic, and α-linolenic acid content.

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Considerable research has been conducted to try and increase PUFA and their biohydrogenation intermediates (BHI) in beef, mainly vaccenic acid (VA; *trans*-11 18:1) and rumenic acid (RA; *cis*-9, *trans*-11 18:2), due to their purported health benefits. There is often large between-trial variation, and the objective of the present trial was to determine if feeding steers extruded flaxseed (Linpro-R; O&T Farms Ltd., SK, Canada) and hay (25 and 75%, respectively, DM basis) together as a total mixed ration (TMR) or sequentially (non-TMR) could help explain differences in PUFA BHI. Forty-eight Continental crossbred steers (325 kg [SD 16]) were stratified by weight to 6 pens of 8 steers and pens were randomized to either TMR or non-TMR. Steers were fed ad libitum for 240 d, feed intake was recorded daily, and steers were weighed every 28 d. Blood was collected on 0, 112, and 228 d, and erythrocyte fatty acid compositions were analyzed (i.e., erythrocyte composition correlates well with other tissues). Blood was centrifuged, and erythrocytes were direct methylated with methanolic HCl and analyzed by GC using a 100-m CPSil 88 capillary column. Data were analyzed using PROC MIXED of SAS. For animal performance, diet was the main effect and pen was the experimental unit. For erythrocyte fatty acids, the experimental model included diet as a main effect, days on test as a repeated measure and the diet × day interaction, with individual animal as the experimental unit. Dry matter intake was lower for non-TMR vs. TMR steers (10.56 vs. 11.42 kg/d; $P = 0.019$), but final weight (286 kg), ADG (1.18 kg/d), and feed efficiency (7.95) did not differ ($P > 0.05$). At 0 d, percentages of VA, RA, and α-linolenic acid (ALA) in erythrocytes (0.93, 0.29, and 0.07%, respectively) did not differ between TMR and non-TMR steers ($P > 0.05$). At 112 d, percentages of VA, RA, and ALA increased and non-TMR (2.82, 0.53, and 7.87%, respectively) were greater than TMR (1.71, 0.36, and 6.36%, respectively). At 228 d, the VA, RA, and ALA percentages were still greater than 0 d but were less than 112 d. The non-TMR (1.24, 0.20, and 5.90%) were still, however, greater than TMR (2.01, 0.25, and 6.78%). Our results suggest that the method of feeding management of supplementary sources of PUFA has minimal effects on animal performance but can profoundly affect the content of PUFA and their BHI in erythrocytes during the feeding period.

Key Words: α-linolenic acid, flaxseed, rumenic acid, total mixed ration, vaccenic acid

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1428 Transcriptome responses to different forage allowance in the hypothalamus of grazing beef cows.

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The hypothalamus plays a major role in the response to changes in dietary nutrients supply. The aim of this study was to evaluate the effect of long-term nutrition at two different forage allowances (FA) of native pastures on the hypothalamic transcriptome of beef cows. Thirty-two multiparous cows (Angus, Hereford, and F_1 crossbreeds) were used, from May 2007 to May 2010, in a complete randomized block design with two FA throughout the year (4 vs. 2.5 kgDM/100 kg BW; HI vs. LO, respectively). At the end of the third experimental year and at 190 ± 10 d postpartum (45 d after calf weaning), cows were slaughtered and the hypothalami were collected. A subsample of 10 hypothalami ($n = 5$/treatment) from F_1 crossbreed cows was used. Total RNA extraction, amplification, library preparation, and sequencing were performed following the Illumina mRNA-Seq. Reads were mapped to the bovine reference genome using Tophat, and the resulting alignments were used to reconstruct transcript models using Cufflinks. Differential gene expression was evaluated using Cuffdiff. Additionally, gene set enrichment analysis was performed using goseq and meshr R packages. Overall, 217 genes were found to be differentially expressed at FDR < 0.05 and fold change ≥ 2 between HI vs. LO. Most differentially expressed genes were related to defense response and immune system, brain and neuronal development, neuronal regeneration and synaptic plasticity, neuronal communication, receptor and intracellular signaling, and metabolic hormone activity. The enrichment analysis using Gene Ontology (GO) and Medical Subject Headings (MeSH) databases revealed that GO biological process and MeSH terms related to defense response and immune system, negative regulation of proteolysis, chemotaxis, and regulation of JAK-STAT cascade were upregulated

in HI cows compared with LO cows. Meanwhile, GO biological processes and MeSH terms related to brain and neuronal development, synaptic plasticity, and neuronal communication were upregulated in LO cows compared with HI cows. These transcriptional changes in the hypothalamus would indicate a differential adaptation of grazing crossbreed cows to different nutritional environments. (This study was supported by CSIC Research Funds, UdelaR, Uruguay.)

Key Words: RNA-seq transcriptomic grazing

1429 Effects of feeding alfalfa stemlage or wheat straw for dietary energy dilution on growth performance and sorting behaviors of Holstein dairy heifers. H. Su*[1], N. M. Esser[2], W. K. Coblentz[3], K. F. Kalscheur[4], R. D. Hatfield[5], and M. Akins[1], *[1]University of Wisconsin, Madison, [2]University of Wisconsin, Marshfield, [3]U.S. Dairy Forage Research Center, Marshfield, WI, [4]USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI, [5]U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI*.

Feeding high-quality forage diets may lead to excessive weight gains and overconditioning for pregnant Holstein heifers. Restriction of energy density and DMI by heifers by using low-energy forages, such as straw, is a good approach for controlling this problem. Alfalfa stems containing high fiber and moderate protein content have the potential to be used to replace straw to reduce dietary energy. The objective of this study was to compare the growth performance and sorting behavior of dairy heifers offered an alfalfa silage/corn silage diet (CON; 13.1% CP, 67.4% TDN, and 39.7% NDF) with two energy-diluted diets replacing the corn silage and alfalfa silage with either alfalfa stemlage (STM; 12.6% CP, 60.1% TDN, and 46.4% NDF) or wheat straw (STW; 12.6% CP, 62.7% TDN, and 43.7% NDF) to get a similar diet composition. Seventy-two pregnant Holstein heifers (16.8 ± 1.3 mo) were stratified (24 heifers/block) by initial BW (light, 440 ± 18.0 kg; medium, 486 ± 18.6 kg; and heavy, 534 ± 25.1 kg) and then assigned to 1 of 9 identical pens (3 pens/block and 8 heifers/pen), where each of the 3 diets was randomly assigned to 1 pen within each block. Diets were offered in a 56-d feeding trial. Statistical analyses were performed using a MIXED procedure in SAS 9.3 with pen as the experimental unit. Daily DMI was greater for CON than for diluted diets (11.3 vs. 10.3 kg/d; $P = 0.01$), with no differences observed between STM and STW ($P = 0.61$). Average daily gains were greater for heifers offered the CON compared with heifers offered diluted diets (1.32 vs. 1.00 kg/d; $P = 0.02$). The feed:gain ratio tended to be less for heifers offered the CON relative to heifers offered diluted diets (8.6 vs. 10.7; $P = 0.08$). There were no differences detected across all growth measures within the diluted diets ($P > 0.05$). Physically effective fiber (pef) particle content was relatively static across sampling times for CON (overall sorting factor mean = 1.02), which indicates minimal sorting. Sorting against pef particles was observed for diluted diets and much more severely for the STM diet (overall sorting factor mean = 1.14 vs. 1.06; $P < 0.05$). These results indicate that diets diluted with low-energy forages (both STM and STW) were effective in reducing intakes of DM and energy and maintaining appropriate weight gains and body condition for pregnant Holstein heifers.

Key Words: alfalfa stemlage, dairy heifer, wheat straw

1430 Effect of partially replacing barley grain with liquid whey permeate in diets for finishing lambs on dry matter intake, average daily gain, and total tract digestibility. F. Joy* and G. B. Penner, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*.

The objective of this study was to evaluate the effect of partially replacing barley grain with liquid whey permeate in diets for finishing lambs on DMI, ADG, and apparent total tract digestibility. Eighteen wether lambs were individually housed and randomly allocated to 1 of 3 dietary treatments in a completely randomized design. The control diet (CON) consisted of 67.7% barley grain, 20% barley silage, and 12.3% mineral and vitamin supplement on a DM basis. For the moderate-sugar (MOD) and high-sugar (HIGH) treatments, whey permeate was included in the diet at 5 and 10% on a DM basis, respectively, by replacing an equal proportion of barley grain. Water was added to equalize dietary DM content among diets with a targeted DM content of 53.5%. Lambs were provided with a 12-d dietary transition protocol (2 dietary steps) to gradually adapt them to the finishing diet. Subsequently, a 28-d treatment period was imposed with the final 4 d used for measurement of DMI and total fecal collection. Data were analyzed using the mixed model of SAS with the fixed effect of treatment. Addition of whey permeate did not affect DMI ($P = 0.96$) or ADG ($P = 0.43$) with average values of 1.22 ± 0.148 and 0.19 ± 0.026 kg/d, respectively. Total tract digestibility of sugar in the MOD treatment was greater (95.1 vs. 69.5 ± 6.32%; $P = 0.04$) than for CON whereas the HIGH treatment did not differ from CON or the MOD treatment. The apparent digestibility coefficients for DM (74.7 ± 2.74%), OM (76.8 ± 2.55%), starch (98.7 ± 1.32%), CP (65.5 ± 3.47%), NDF (36.43 ± 7.07%), and ether extract (74.34 ± 3.57%) did not differ among treatments ($P > 0.10$). The results of this study indicate that liquid whey permeate can partially replace barley grain without negative effects on DMI, ADG, or digestibility. In addition, our results show that a low inclusion rate (5% DM) may improve sugar digestibility.

Key Words: lamb, sugar, whey permeate

Table 1431.

	Treatment				*P*- values		
Item, % DM	CS	CS:CPR	CS:SLV	SEM	Trt	d	Trt x d
Sinigrin, mg/g	0.00[c]	0.14[b]	1.72[a]	0.04	< 0.01	< 0.01	< 0.01
pH	4.25[b]	4.42[a]	4.40[a]	0.02	< 0.01	< 0.01	0.04
Acetic acid	0.63[c]	0.86[a]	0.76[b]	0.02	< 0.01	< 0.01	0.01
Lactic acid	3.66[a]	3.22[b]	3.47[b]	0.11	0.03	< 0.01	0.36
CP	7.3[b]	16.3[a]	16.4[a]	0.21	< 0.01	0.14	0.04
NDF	31.2[a]	25.9[b]	30.1[a]	0.59	< 0.01	< 0.01	0.34
EE	2.55[b]	7.59[a]	2.48[b]	0.09	< 0.01	< 0.01	0.02

[a-c]Means in the same row with unlike letters differ ($P < 0.05$).

1431 Evaluation of the fermentation characteristics and glucosinolate content of cold-pressed or solvent-extracted carinata meal ensiled with corn forage. K. Rodriguez-Hernandez*[1,2], J. L. Anderson[1], M. A. Berhow[3], and A. Garcia[1], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]CIRNOC-INIFAP, Matamoros, Mexico, [3]USDA, ARS, NCAUR, Peoria, IL.*

Carinata meal (CRM) is a quality protein source but contains high concentrations of sinigrin, a glucosinolate, which limits its use as a feedstuff. Previous research shows that CRM ensiled with forages reduces sinigrin content. Solvent extraction (SLV) or cold pressing (CPR) are methods used to extract oil from carinata seeds, leaving different residual oil content in the meals. We hypothesized that the oil content in CRM affects the fermentation when it is blended with forage for ensiling. The objectives were to determine the effects of CRM fat content when blended with corn forage on silage fermentation and sinigrin content. A micro-silo experiment was conducted with three treatments: 1) corn forage (CS), 2) CS and solvent-extracted CRM blend (CS:SLV), and 3) CS and cold-pressed CRM blend (CS:CPR). Both blends of CRM to forage were 25:75 on a DM basis. Micro-silos were packed at 86 kg of DM/m^3 in triplicate for 0, 7, 21, and 60 d of ensiling. Data were analyzed using MIXED procedures of SAS 9.4. The model included treatment, day, and treatment × day interaction, with significance declared at $P < 0.05$. The sinigrin content of CRM before blending was 15.3 vs. 16.2 mg/g for CPR and SLV meals, respectively. On d 0, within hours after mixing, the sinigrin content was reduced 94.8% in the CS:CPR blend but not in the CS:SLV blend. Compared with the original meal, by d 60, sinigrin content decreased 99.7% in CS:CPR and 99.4% in CS:SLV. Sinigrin was greater ($P < 0.01$) in CS:SLV compared with CS:CPR over time. Fat content as determined by ether extract was greater ($P < 0.01$) in the CS:CPR than in CS:SLV and CS. The pH decreased in all treatments over time but was greater in the blends. Acetic and lactic acids increased over time in all treatments. Acetic acid was less in the CS compared with the blends. Acetic acid was greater ($P < 0.01$) in CS:CPR than in CS:SLV. Lactic acid was less in CS:CPR. The CP was greater in both blends with CRM. Despite different fat contents, ensiling cold-pressed or solvent-extracted CRM with corn forage decreased sinigrin concentration without major detriment to silage fermentation.

Key Words: carinata meal, ensiling, glucosinolates

1432 Magnitude of difference in chemical and nutrient profiles, ruminal degradation kinetics, and intestinal digestion of three barley silages varieties in comparison with corn silage for dairy cattle. B. Refat*[1,2], W. Yang[3], J. J. McKinnon[4], J. Nair[1], A. D. Beattie[5], T. A. McAllister[6], D. A. Christensen[7], and P. Yu[1], *[1]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [2]Animal Production Department, Faculty of Agriculture, Zagazig University, Zagazig, Egypt, [3]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [4]Department of Animal and Poultry Science, College of Agricultural and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [5]Department of Plant Sciences, College of Agriculture and Bioresources, University of Saskatchewan, Saskatoon, SK, Canada, [6]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [7]University of Saskatchewan, Saskatoon, SK, Canada.*

Whole-crop barley (*Hordeum vulgare* L.) silage is the main forage source for dairy producers in western Canada. There are many varieties that are constantly being developed. However, there is limited knowledge on their nutritional quality. The main objective of this study was to assess the magnitude of difference among barley silage varieties in comparison with corn silage in terms of their 1) chemical composition and energy values, 2) protein and carbohydrates fractions, 3) rumen degradation kinetics, and 4) intestinal absorbed true protein supply to dairy cattle. The experiment was a complete randomized design with four treatments: corn silage (P7213R), CDC Cowboy barley silage, CDC Copeland barley silage, and Xena barley silage. Five cannulated lactating dairy cows were used for measuring the in situ rumen degradation kinetics. Intestinal digestibility of rumen undegraded feed protein was estimated

using a 3-step in vitro procedure. This study showed no significance difference in total carbohydrates (CHO; % DM) among the three varieties of barley silage. Corn silage showed a higher CHO when compared with barley silage varieties (82.6 vs. 78% DM; $P < 0.05$). Corn silage had the highest total digestible nutrient TDN_{1x} (71% DM) and energy content NEL_{p3x} (1.5 Mcal/kg DM), whereas Cowboy barley silage had the lowest NEL_{p3x} (1.3 Mcal/kg DM; $P < 0.05$). Studying the CNCPS system, predicted values showed no significant difference among the three barely silage varieties on rumen degradable of NDF RDCB3 (averaged 14% DM; $P > 0.10$) but Cowboy barley silage was lower in total rumen degradable of carbohydrates (TRDC) when compared with other barley silages varieties (32 vs. 38% DM; $P < 0.05$). Corn silage had the highest TRDC compared with all barley silage varieties (42.5% DM; $P < 0.05$). In terms of the in situ rumen degradation kinetics, Cowboy barley silage showed a significant high degradation rate Kd (%/h; $P < 0.05$). Cowboy and Copeland barley silages had higher effective degradability of CP, whereas Xena had an intermediate level and corn silage showed the significant lowest values ($P < 0.05$). The corn silage had the highest intestinal digestible protein (IDP), whereas Xena barley silage had the lowest values of IDP. In conclusion, among the three barley silages, Cowboy barley silage had the highest degradation rate of fiber and more effective degradability of protein when compared with the other barley silage varieties. Corn silage has a potential to be used as a good forage source in western Canada compared with barley silage.

Key Words: energy, ruminal degradation kinetics, silage

1433 Production of high-quality and digestible forages to increase milk production and nutrient supply for lactating dairy cows. J. P. Pretz*[1], C. Ramsier[2], and D. P. Casper[1], *[1]Dairy Science Department, South Dakota State University, Brookings, [2]Ag Spectrum, Inc., De Witt, IA*.

Two forage production programs based on soil amendments and foliar nutrition were used to produce corn silage and alfalfa haylage followed by a feeding study to evaluate the lactational performance of Holstein dairy cows. Thirty peak-lactation (58 DIM ± 2.9 and 38.9 kg/d milk ± 7.6) Holstein dairy cows (8 primiparous and 22 multiparous) were blocked by milk yield, DIM, and parity and randomly assigned to 1 of 2 treatments using a randomized complete block design. Treatments were 1) CONTROL, which is a normal forage (65%) ration formulated using alfalfa haylage and corn silage produced via standard soil and agronomy programs, and 2) TEST, which is the same forage inclusion rates (65%) using alfalfa haylage and corn silage produced on an enhanced soil (base saturations) and agronomy program (foliar applications). Cows were fed the CONTROL ration during the covariate period of 7 d followed by 12 wk of data collection when CONTROL and TEST diets were fed. Milk production was increased ($P < 0.04$) for cows fed TEST compared with cows fed CONTROL forage (32.6 and 36.9 kg/d for CONTROL and TEST, respectively, throughout results). Dry matter intakes (23.9 and 22.8 kg/d) were similar ($P = 0.46$). Milk protein (0.98 and 1.09 kg/d; $P < 0.04$), lactose (1.62 and 1.88 kg/d; $P < 0.04$), and total solids (3.77 and 4.25 kg/d; $P < 0.05$) yields were increased for cows fed TEST forages compared with cows fed CONTROL forages. Fat-corrected milk (4%) tended ($P < 0.09$) to be higher (33.6 and 39.0 kg/d) for cows fed the TEST forages compared with cows fed CONTROL forages. Energy-corrected milk was increased ($P < 0.05$) for the TEST-fed cows (33.0 and 36.8 kg/d). A decrease ($P < 0.01$) in ruminal butyrate percentage was found for cows fed the TEST diet. Ruminal propionate concentration ($P < 0.10$) and percentage ($P < 0.10$) tended to increase when cows were fed TEST forages. There was a trend ($P < 0.06$) for an increase in total tract starch digestibility for cows fed TEST forage compared with CONTROL-fed cows (97.9 and 98.4% digestible). Digestibility of NDF (48.5 and 54.7%; $P < 0.03$) and ADF (48.3 and 54.4%; $P < 0.03$) were increased for the TEST-fed cows compared with cows fed CONTROL forages. Feeding higher-quality forages obtained from enhanced agronomy procedures increased milk production, milk composition, and fiber digestibility when lactating dairy cows are fed a high-forage ration.

Key Words: dairy cattle, forage quality, high-forage diet

1434 Increased forage neutral detergent fiber digestibility (in vitro or in situ) is positively related to dry matter intake and milk yield both across and within forage type. D. Sousa*, M. J. VandeHaar, and M. S. Allen, *Michigan State University, East Lansing*.

Effects of laboratory measures of forage NDF digestibility (fNDFD) on DMI and milk yield (MY) were determined by meta-analysis using a database of 135 treatment means from 52 trials reported in 47 peer-reviewed articles published from 1979 through 2015. Trials must have been conducted comparing divergent fNDFD (measured in vitro or in situ) within the same forage type in experimental diets with cows past peak lactation (>60 d postpartum). Meta-analyses were performed with all forages together and also separated by forage type: alfalfa ($n = 29$), grass ($n = 22$), corn silage without BMR ($n = 26$), brown midrib corn silage (BMR; $n = 47$), and sorghum silage ($n = 11$). Data were analyzed by ANOVA including the random effect of trial, fixed effect of fNDFD, diet forage NDF, and their interaction as continuous variables. Treatment means were weighted by the inverse of their variance. Statistical significance was declared at $P \leq 0.05$ and a trend at $P > 0.05$ to $P \leq 0.10$, and the interaction of fNDFD with fNDF was kept in the model if $P \leq 0.30$. Enhanced fNDFD increased DMI and MY; a one-unit increase in fNDFD in vitro or in situ was associated with a 0.07 kg/d increase in DMI ($P < 0.01$) and a 0.08 kg/d increase in MY ($P < 0.01$) for all forages, a

0.07 kg/d increase in DMI ($P = 0.02$) and no effect on MY for alfalfa, a tendency of 0.08 kg/d increase in DMI ($P = 0.06$) and a 0.23 kg/d increase in MY ($P < 0.01$) for grass, 0.09 kg/d increase in DMI ($P = 0.04$) and a 0.20 kg/d increase in MY ($P < 0.01$) for all corn silage, a tendency of 0.13 kg/d increase in DMI ($P = 0.06$) and a 0.27 kg/d increase in MY ($P < 0.01$) for BMR corn silage, and a tendency of 0.06 kg/d increase in DMI ($P = 0.09$) and a 0.19 kg/d increase in MY ($P < 0.01$) for corn silage excluding BMR corn. The sorghum data included only 11 treatment means from 5 trials that showed a tendency of 0.12 kg/d increase in DMI ($P = 0.09$) and no effect on MY but, when combined with corn silages, resulted in a 0.12 kg/d increase in DMI ($P < 0.01$) and a 0.21 kg/d increase in MY ($P < 0.01$). Forage NDF digestibility is an important parameter of forage quality that is positively related to DMI and MY within or across forage families.

Key Words: fiber digestibility, forage quality, intake

1435 Lactation performance, in situ degradability, and rumen fermentation of Holstein cows fed BMR-6 sorghum silage versus corn silage based diets.

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The objectives of the study were to determine 1) the lactation performance, in situ degradability, and rumen fermentation of Holstein cows fed a bmr-6 sorghum silage (SS) vs. a leading non-bmr corn silage (CS) variety and 2) degradation kinetics of DM and starch from sorghum grain isolated from SS. In Experiment 1, four second lactation Holstein cows (578 ± 41 kg BW) in mid lactation, 101 to 113 DIM, were randomly assigned to diets containing SS or CS in a 2 × 2 crossover design with 14-d adaptation periods followed by 7-d collection periods. Cows were individually housed in open corrals (3.3 by 10 m) and fed once daily at 1000 h. Diets were formulated to supply 28% of the DM as each silage. Additionally, the diets were formulated to supply similar concentrations of NDF and total tract digestible starch, assuming 50% starch digestibility for SS. This was accomplished by replacing a portion of the steam-flaked corn (8% of diet DM) in the SS diet with 4% each of soy hull pellets and cottonseed hulls in the CS diet. All other dietary ingredients were similar between treatments. Milk production (32.6 vs. 31.4 ± 5.7 kg/d; $P > 0.725$) and percentages and yields of milk components did not differ ($P \geq 0.246$). In situ degradability of CS and SS were determined at 0, 6, 12, 18, 24, 36, 48, and 72 h. Cows fed CS had greater ($P \leq 0.001$) DM, OM, and NDF disappearances compared with cows fed SS at all incubation times. There was a treatment × time interaction ($P = 0.004$) for rumen pH recorded with greater pH at 1, 2, 3, 11, 12, 17, 23, and 24 h relative to feeding for SS. Total gas and methane produced from samples taken 3 h after feeding were greater ($P \leq 0.002$) for SS than for CS. The grain portion of SS was manually separated and ruminally incubated for 0, 3, 6, 12, 18, 24, 36, 48, and 72 h during Experiment 2. There were no differences ($P > 0.315$) between DM and starch disappearances of the sorghum grain until 18 h ($P \leq 0.001$). The DM disappearance continued to increase up to 72 h, but maximum starch disappearance, 55.7%, was reached at 18 h. Sorghum silage is an energy forage that may be used in lactating cow rations in areas where water availability may limit corn silage production; however, NDF and starch degradation should be improved.

Key Words: rumen, silage, sorghum

1436 Factors affecting methane production from ruminal fermentation of fiber isolated from dried distillers' grains and solubles.

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Ruminants produce more methane (CH_4) than any other livestock animal. Consequently, focus has been placed on developing mitigation strategies for ruminants in both the dairy and the beef industries. The objective of this study was to determine the effect of addition of fat or cellulose to fiber from dried distillers' grains and solubles (DDGS) on ruminal CH_4 production. Three representative samples of DDGS were obtained from different commercial biorefineries and NDF residue was isolated. The purified NDF residue was fermented 1) alone (control), 2) with feed-grade corn oil, or 3) with microcrystalline cellulose powder using the in vitro gas production technique. Both cellulose and corn oil were added along with NDF residue at a 4:1 ratio (DM basis). Inoculum was obtained by collecting a mixture of rumen fluid from two steers (BW = 543.3 ± 20.6 kg) consuming a diet containing 30% concentrate and 70% roughage. For each treatment within each run, gas production was measured in real time over a 48-h period. Using a paired but separate bottle, the concentration of CH_4 gas produced was measured using a gas chromatograph at 0, 4, 8, 18, 24, and 48 h. The volume of methane produced at each time point was calculated by multiplying total gas produced by the concentration of CH_4. Three separate runs ($n = 3$) were conducted and data were analyzed as a randomized complete block in which run and source of DDGS were considered random effects and treatment was considered a fixed effect. Compared with the control (74.0 ± 6.06 mL/g), addition of corn oil tended ($P = 0.11$) to reduce total gas production (58.0 ± 6.04 mL/g) whereas addition of cellulose increased ($P = 0.02$) gas production (85.7 ± 6.06 mL/g). Similarly, compared with the control (0.075 ± 0.0125 mL/g), the addition of corn oil tended ($P = 0.12$) to reduce CH_4 production (0.043 ± 0.0125 mL/g) whereas the addition of cellulose increased ($P = 0.02$) CH_4 production (0.099 ± 0.0125 mL/g). In an in vitro setting, the addition of oil or cellulose to NDF resulted in the decrease or increase of methane production, which suggests that dietary components can be used to mitigate methane in

ruminant livestock.

Key Words: gas production, in vitro, methane

1437 Effect of native and hybrid varieties of whole-plant corn silage on digestion in diets for cattle. L. Corona-Gochi*, *Universidad Nacional Autonoma de Mexico, Mexico City, Mexico*.

Whole-plant corn silage (WPCS) in many production systems is the main component of forage in the diets of cattle, due to its yield, cost, and nutritional quality. The objective of this study was to evaluate two native varieties (red and white) and two commercial hybrids ("A" and "B") commonly planted in the valley of Mexico on DM yield and nutrient digestibility in cattle through a metabolism trial. The corn was planted at a density of 80,000 plants/ha and row spacing of 0.8 m, harvested 135 d after sowing with chop length 2.17 inches, and stored in plastic bag silos (70 kg). Four bulls (489 kg average BW) were used in a 4 × 4 Latin square design on a diet containing 55.4% (DM) WPCS, with the following treatments: T1-red native (RN), T2- white native (WN), T3-A hybrid (AH), and T4-B hybrid (BH). Data were analyzed with the MIXED procedure in SAS and comparison of means by the following contrasts: RN vs. WN, AH vs. BH, and natives vs. hybrids. Dry matter yield was higher ($P = 0.04$; 18.6%) for native varieties than for hybrids (25.5 vs. 2,145 ton DM/ha, respectively), and total tract digestion (%) of DM (76–84 ± 8), OM (78–85 ± 7), NDF (73 to 79 ± 6), FDA (73 to 84 ± 11), starch (91 to 86 ± 6), nitrogen (61 to 75 ± 14), and DE (57 to 71) was higher ($P < 0.01$) for native varieties than for commercial hybrids. No differences ($P > 0.05$) between natives and between hybrids were observed. Digestibility was higher for native varieties than for hybrids for DM (7.4%; $P = 0.002$), OM (6%; $P = 0.003$), NDF (8.3%; $P = 0.003$), FDA (12.9%; $P < 0.001$), starch (5.9%; $P = 0.031$), N (15.6%; $P = 0.002$), and DE (16.5%; $P = 0.005$). Because the native varieties of corn plant showed higher DM yield and nutrient digestibility compared with the hybrids, they are advisable for planting and use in cattle diets.

Key Words: cattle, corn varieties, digestibility

1438 Evaluation of brown midrib sudangrass silage in the diets of lactating dairy cows. K. F. Kalscheur* and B. Geoff, *USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI*.

Forages that use less water but are high in digestibility are sought as alternatives to traditional forages such as corn silage. Brown midrib (BMR) sudangrass is a possible alternative that can provide high-quality forage as a replacement for corn silage. The objective of this study was to evaluate the replacement of corn silage and alfalfa silage with increasing concentrations of sudangrass silage in the diets of lactating dairy cows. Forty-eight Holstein cows in mid lactation were assigned to treatments in a randomized complete block design. Cows were fed a common covariate diet for 2 wk followed by 8 wk of experimental diets. Diets were formulated to contain 40% corn silage, 20% alfalfa silage, and 40% concentrate on a DM basis. Sudangrass silage was included in experimental diets at 0, 10, 20, and 30% of the diet DM. Proportionally, sudangrass silage replaced 2 parts corn silage and 1 part alfalfa silage. All other ingredients (high-moisture corn, canola meal, roasted soybeans, soyhulls, and minerals and vitamins) were included equally for all diets. Data were analyzed using MIXED procedures of SAS. Polynomial orthogonal contrasts were used to determine the effect of increasing BMR sudangrass silage in the diets of lactating dairy cows. Dry matter intake linearly decreased as sudangrass silage replaced corn silage and alfalfa silage ($P < 0.01$). Similarly, milk production decreased from 43.1 kg/d for cows fed 0% sudangrass silage to 39.2 kg/d for cows fed 30% sudangrass silage. Milk fat and lactose percentage were not affected by changes in forages; however, milk protein percentage was quadratically affected ($P = 0.02$). Yields of milk fat, protein, and lactose linearly decreased ($P < 0.05$) with increasing sudangrass silage. Similarly, energy-corrected milk (ECM) linearly decreased with increasing concentrations of sudangrass silage. Feed efficiency, defined as ECM/DMI, was not affected by changes in forage because milk production changes and DMI changes were the same. Although it was expected that increased digestibility of the BMR sudangrass silage would benefit the dairy cow, it is possible that the increased fiber in the sudangrass diets limited intake, resulting in a linear decrease in milk production.

Key Words: brown midrib sudangrass silage, dairy cows, forages

1439 Chemical composition and fermentation profile of corn silage ensiled for zero, thirty, ninety, or one hundred fifty days from corn treated with a foliar fungicide at different growing stages.

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Foliar fungicide application to the corn plant may reduce disease and provide developmental benefits to the crop. The objective of this study was to evaluate the effect of various applications of foliar fungicide on the nutrient composition and the energy and fermentation profile of corn silage ensiled for 0, 30, 90, or 150 d after harvest. Eight one-acre plots of corn were planted in April 2015. Treatments were replicated once and randomly assigned to one of the plots. Treatments were no foliar fungicide application (CON), one application of pyraclostrobin (Priaxor; BASF Corp.) foliar fungicide at corn vegetative growth stage V5 (V5), one application of pyraclostrobin and metconazole (Headline AMP; BASF Corp.) foliar fungicide at corn reproductive growth stage R1 (R1), and one application of pyraclostrobin foliar fungicide at V5 and one application of pyraclostrobin and metconazole foliar fungicide at R1 (V5/R1). At harvest, samples of the chopped corn silage were collected from each plot and immediately vacuum sealed. Corn silage ensiled for 0 d was frozen on the day of harvest, whereas corn silage ensiled for 30, 90, and 150 d was left in the vacuum-sealed bags for each respective time frame and frozen for later analysis. Statistical analysis was performed using the MIXED procedure of SAS. A treatment × time point interaction was observed for lignin ($P = 0.03$), water-soluble carbohydrate (WSC; $P = 0.02$) concentrations, and a tendency ($P = 0.07$) for VFA score. At 90 d of ensiling, R1 had lower lignin concentration (1.15 ± 0.21) than CON (2.55 ± 0.21), V5 (2.15 ± 0.21), and V5/R1 (2.55 ± 0.21) and higher concentrations of WSC (3.20 ± 0.49) than CON (2.45 ± 0.49), V5 (2.50 ± 0.49), and V5/R1 (2.60 ± 0.21). At 30 d of ensiling, CON tended to have a lower VFA score (8.18 ± 0.12) than V5 (8.92 ± 0.12), V5/R1 (8.73 ± 0.12), and R1 (9.05 ± 0.12). Corn silage from corn treated with foliar fungicide had improved chemical composition and fermentation and has the potential for increased milk production when fed to dairy cattle.

Key Words: corn silage, fermentation, foliar fungicide

1440 Chemical and energy profiles of value added pellet products based on combination of new coproducts from biofuel/bio-oil processing, low grade of peas, and lignosulfonate chemical compound at different levels for ruminants.

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The aim of this project was to test and develop eight high-value-added pellet products based on combination of coproducts from biofuel/bio-oil processing, low grade of peas, and lignosulfonate at different levels for ruminants. Statistical analyses were performed using PROC MIXED of SAS 9.3 with significance declared at $P < 0.05$. The results showed that BPP3 (high level of carinata meal, low level of peas, and no lignosulfonate), BPP4 (high level of carinata meal and low level of peas and lignosulfonate), and BPP7 (high level of canola meal, low level of peas, and no lignosulfonate) had the higher CP ($P < 0.05$), whereas both BPP3 and BPP4 also had the higher neutral detergent insoluble CP (NDICP; $P < 0.05$) and BPP6 (low level of canola meal and high level of peas and lignosulfonate) and BPP7 and BPP8 (high level of canola meal and low level of peas and lignosulfonate) had the higher acid detergent insoluble CP (ADICP; $P < 0.05$). BPP7 and BPP8 had the higher NDF, ADF, and ADL compared with the other blend pellet products ($P < 0.05$). Energy values using the NRC summative approach indicated that BPP1 (low level of carinata meal, high level of peas, and no lignosulfonate) and BPP6 (low level of canola meal and high level of peas and lignosulfonate) had the higher truly digestible nonfiber carbohydrate (tdNFC; $P < 0.05$); BPP3 and BPP4 had higher truly digestible CP (tdCP; $P < 0.05$); BPP1 was higher in truly digestible NDF (tdNDF; $P < 0.05$); and BPP7 and BPP5 (low level of canola meal, high level of peas, and no lignosulfonate) had the higher truly digestible fatty acids (tdFA; $P < 0.05$). However, BPP1 showed the higher level of total digestible nutrient (TDN; $P < 0.05$) and BPP1, BPP3, and BPP4 had the higher NE_L, NE_m, and NE_g ($P < 0.05$). In conclusion, carinata meal–based pellet products have more available protein (higher NDICP but lower ADICP) than canola meal–based blend pellet products. Canola meal–based blend pellet products have higher levels of NDF, ADF, and ADL than carinata meal–based pellet products. Pellet products based on carinata meal combined with peas has potential to be used as a good energy and good protein source compared with pellet products based on canola meal combined with peas.

Key Words: canola, carinata, lignosulfonate.

1441 Use of short-season hybrids may enable greater use of corn silage in western Canadian feedlot diets without decreasing animal performance.

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As a result of the overall trend for an increase in corn heat units and growing season precipitation in western Canada, early maturing corn hybrids are currently being introduced where previously barley silage (BS) was the main forage used in feedlot cattle production. We hypothesized that early maturing corn silage (CS) could replace BS in backgrounding (BKGN) feedlot cattle diets, and because of its greater starch content, dietary proportion of CS could be increased and duration of the BKGN phase could be extended without compromising animal performance. A total of 160 steers (mean BW ± SD: 272 ± 22.4 kg) were assigned to 16 pens and fed BKGN diets containing either 60% (DM basis) BS (CON) or 60 (60CS), 75 (75CS), and 90% CS (90CS; 4 pens/treatment) until they reached an average pen BW of 380 (SBKGN; 2 pens/treatment) or 430 ± 15 kg (LBKGN; 2 pens/treatment) in a split-plot design. All steers were finished (FIN diet; 9% CS, 86% barley grain, and 5% supplement) to an equal-BW end point (700 ± 15 kg LW). During BKGN and FIN, DMI, ADG, and G:F were measured for all pens. Carcass data were also collected. There was no BKGN diet × duration interaction ($P > 0.05$) for most of the production measures. As dietary CS content increased during BKGN, DMI and ADG decreased (quadratic, $P \leq 0.003$) and there was also a tendency ($P = 0.078$) for a decrease in G:F at the highest level of CS. However, the BKGN diet had no effect ($P > 0.05$) on DMI, ADG, and G:F during the FIN phase. Similarly, the BKGN diet had no effect ($P > 0.05$) on carcass traits including dressing percentage and quality grade. As expected, compared with SBKGN steers, LBKGN steers took longer (105 vs. 71 d; $P = 0.001$) to reach the end of BKGN target weight. As a result of their heavier weight at the beginning of FIN, LBKGN steers also had a higher DMI (11.6 vs. 11.0 kg/d; $P = 0.045$) and reached the FIN end point earlier (116 vs. 146 d; $P < 0.001$) than SBKGN steers. However, the duration of BKGN had no effect ($P > 0.05$) on carcass traits. In summary, inclusion of up to 90% CS in cattle diets fed over a short or long BKGN phase did not compromise production performance during FIN.

Key Words: backgrounding duration, corn silage, production performance

1442 In vitro starch and neutral detergent fiber degradability of corn silage hybrids.

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This study investigated in vitro starch and NDF rumen degradability of 5 corn silage hybrids: Hubner H5333RC3P, H6191RCSS, and H5222RC3P; Masters Choice MC 5250; and Healthy Herd Genetics 42HFC15. Three of these hybrids were rated as potentially high in starch degradability, whereas the other two, Hubner 5333 and Hubner 6191, were rated low to medium in starch degradability, respectively. Samples from a corn silage hybrid trial conducted in Centre County, PA, at The Pennsylvania State University's Russell Larson Research farm were ensiled (in triplicate) in sealed 2.5-kg-capacity plastic bags. Silages were moved to a −20°C freezer on d 0, 30, 60, 120, and 150 after ensiling and stored frozen for at least 30 d before analysis. Silage subsamples were dried at 65°C for 72 h, ground through a 4- (in vitro degradability) or 1-mm (NIR and chemical analyses) sieve, and analyzed for in vitro starch and NDF degradability in 2 commercial laboratories and one university laboratory. Seven-hour starch degradability was determined by in vitro incubation with ruminal inoculum (IVSD; 2 assays) and by NIR (2 assays). Silage samples were also analyzed for NDF degradability (NDFD) by 48-h in vitro incubation with ruminal inoculum (IVNDFD), for 30-h NDFD by NIR (NIRNDFD), and for total tract NDF digestibility by NIR (TTNDFD). IVSD varied from 65.1 to 68.3% and was not affected ($P \geq 0.50$) by hybrid. Starch degradability determined by NIR was higher than IVSD, 73 to 78%. IVSD clearly increased with increasing ensiling time ($P < 0.001$), from 58.3 and 66.0 (d 0) to 69.7 and 69.3% (d 150) for laboratories 1 and 2, respectively. The NIR analysis showed similar trends. Silage hybrids varied in NIRNDFD from 56.6 to 59.9% ($P = 0.001$), but there was no difference ($P = 0.15$) in IVNDFD due to hybrid. Hybrid also had no effect on TTNDFD. All procedures indicated decreased ($P \leq 0.002$) NDFD or TTNDFD with increasing ensiling time, particularly from d 0 (63.8%) to 30 (57.8%); for some hybrids, the decrease in NDFD reached 10 percentage units. In this study, IVSD was similar among corn hybrids and hybrid had no effect on IVNDFD. These data have to be confirmed in vivo. With all hybrids, IVSD clearly increased and NDFD decreased with ensiling time, particularly NDFD from d 0 to 30. The reason for the decrease in NDFD needs to be elucidated.

Key Words: corn silage, degradability, in vitro, neutral detergent fiber, starch

1443 Evaluation of use of heat-stable α-amylase for neutral detergent fiber contents by using cellulose standard in filter bags made from different textiles add starch in samples. T. N. P. Valente*[1], E. Detmann[2], and C. Batista Sampaio[3], *[1]IFGoiano, Posse, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil*.

The objective of this study was to evaluate the efficiency of using nylon textiles (50 μm), F57 (Ankom), and nonwoven textile (NWT; 100 g/m^2) on laboratory evaluation of NDF by using quantitative filter paper as purified cellulose standard (12.5 cm Ø; ashless with 0.0086% of ash and 96.53% of DM; code 050154; Vetec) by simulating composition of samples with additions of corn starch (Sigma S-5296; 91.62% DM). The quantitative filter paper was processed in a knife mill with a 1-mm screen sieve and the procedures for analyses of NDF contents were performed in a fiber analyzer (Ankom^{220}). The experiment was performed with additions of different ingredients into the filter paper: corn starch added at the levels of 15 or 50% of DM. The ratio 20 mg of DM/cm^2 of surface was followed. The treatment was based in the use or not of heat-stable α-amylase. The experiment was performed according to a completely random design using 3 textiles × 2 levels of starch × 2 using or not heat-stable α-amylase factorial arrangement. The recovery bias of NDF was NRF = (Mo − Me/Me) × 100, in which NRF = NDF recovery bias (%), Me = the expected mass of NDF or mass of cellulose standard (g), and Mo = the observed mass of NDF or the residue obtained after analysis (g). The bias estimates were obtained as described above based on assumption that the cellulose standard presents 100% of NDF. Statistical procedures were performed using by SAS. For type I error, 0.01 was adopted as the critical limit, using a Tukey–Kramer test. When heat-stable α-amylase was not used, the NDF contents were overestimated ($P < 0.01$) and presented similar biases for both starch levels. The biases varied from +3.89 to +9.88% observed for all types of filter bags. Such a pattern corroborates the interference of starch on laboratorial evaluation of NDF. The biases were generally lower for nylon than for F57 and NWT ($P < 0.01$) when 50% of starch was considered. The biases for both starch levels were not significant ($P > 0.01$) when α-amylase was used, which brings into evidence the removal of contaminant starch from insoluble residue. The use of F57 and NWT resulted in accurate estimates of NDF contents. For samples containing starch, use of heat-stable α-amylase is recommended in the evaluation of NDF contents. Thanks for financial support to IFGoiano, FAPEG, and CNPq.

Key Words: F57, nonwoven textile, nylon

1444 Production response of lactating cows to diets based on corn or forage sorghum silage harvested on two dates and supplemented with soybean meal or mechanically pressed cottonseed meal. J. K. Bernard*, S. Tao, and T. Smith, *University of Georgia, Tifton*.

A 6-wk randomized design trial with a 4 × 2 factorial arrangement of treatments was conducted to evaluate the production response of 48 lactating Holstein cows (140.9 ± 55.9 d in milk) to diets based on corn (CS) or forage sorghum silage (FS) harvested in the summer (S) or fall (F) and supplemented with either soybean meal (SBM) or mechanically pressed cottonseed meal (CSM). Corn was planted in April and harvested in July (CSS); a second crop was planted in August and harvested in November (CSF). Forage sorghum was planted in April, harvested in July (FSS), allowed to regrow, and harvested again in November (FSF). Ensiled forages provided 41.67% of the DM in the experimental diets. Approximately 19% of the total dietary N provided by SBM was replaced with CSM. Cows were fed a corn silage based diet for 2 wk before beginning the 4-wk experimental period. No differences ($P > 0.10$) were observed in DMI (23.6 ± 1.6 kg/d) or milk yield (35.0 ± 1.7 kg/d) among treatments. An interaction ($P = 0.03$) of forage source and protein supplement was observed for milk fat, which was lowest for CSF-CSM (3.09%) compared with the other treatments (3.64 ± 0.16%). Milk fat yield was greater ($P = 0.006$) for diets based on FS compared with diets based on CS (1.28 and 1.22 kg/d, respectively). No differences ($P > 0.10$) were observed in yield or concentration of milk protein, lactose, or SNF. An interaction ($P < 0.001$) was observed for efficiency of milk production, which was lowest for CSS-SBM (1.39) and CSF-CSM (1.39) compared with CSF-SBM, FSS-SBM, FSF-SBM, and FSF-CSM (1.54, 1.47, 1.48, and 1.58, respectively) but not different from CSS-CSM and FSS-CSM (1.44 and 1.44, respectively). Concentrations of milk urea N were lower for diets based on CS compared diets based on FS (8.50 and 11.50 mg/dL, respectively; $P < 0.001$) and for diets supplemented with CSM compared with diets supplemented with SBM (9.31 and 10.70 mg/dL, respectively; $P = 0.002$). Results of this trial indicate that diets based on CS or FS harvested in S or F can support similar performance and that CSM can be substituted for SBM without negatively affecting production.

Key Words: corn silage, forage sorghum, mechanically pressed cottonseed meal

1445 Commercial ground corn surface area is better related to rumen disappearance than geometric mean particle size. J. P. Goeser*[1,2], B. Beck[3], T. Koehler[4], D. Tanata[5], E. Reid[6], M. Kirk[7], and R. D. Shaver[8], *[1]University of Wisconsin, Madison, [2]Rock River Laboratory, Inc., Watertown, WI, [3]Witmers Feed and Grain, Columbiana, OH, [4]Landmark Cooperative, Cottage Grove, WI, [5]Medford Cooperative, Medford, WI, [6]Cooperative Feed Dealers, Conklin, NY, [7]Masters Choice, Anna, IL, [8]University of Wisconsin-Madison, Madison*.

Ground dry shelled corn is not uniform relative to animal performance. Geometric mean particle size (GMPS; μm) has been related to rumen digestion but research has evaluated only ground corns sized >700 μm GMPS. The industry has reduced GMPS to <400 μm in some cases. Furthermore, GMPS and standard deviation can be combined into a surface area measure (SA; cm^2). The objective of our work was to determine if GMPS or SA were related to rumen in situ starch disappearance (SD; % starch) for commercial dry ground shelled corns. Commercial dry, ground shelled corn ($n = 38$) samples were collected from feed mills in the Eastern and Midwestern United States. Samples were assessed for particle size by shaking eight sieves for 10 min, ranging from 2,000 μm to the pan, and determining percent weight retained on each. Geometric mean particle size and SA were determined using Kansas State University equations. Samples were assessed for starch (% DM) using the Hall 2008 AOAC procedure. Starch, GMPS, and SA mean and standard deviation were 70.6/3.2, 715/233, and 92.7/20.8, respectively. Three grams of corns were weighed into Ankom R510 bags (50-μm pores), soaked in warm water, and incubated for 0 or 7 h, in triplicate across three ruminally cannulated lactating dairy cows consuming a 60% forage, corn silage–based diet. After incubation, bags were rinsed in a commercial laundry machine, dried at 50°C for 24 h, and weighed to determine the DM disappearance. Residues were composited and starch was assessed. Corn SD at 0 (SD0) and 7 h (SD7) were determined as starch loss during incubation. The SD0 and SD7 (% starch) mean/standard deviation were 19.8/12.4 and 68.7/10.6, respectively, suggesting that a range in SD was achieved. Time point (class variable), starch, GMPS, and SA were related to SD using backward elimination and final model fit using Fit Model function within SAS JMP version 11.0. Geometric mean particle size and SA were not allowed within the same final model because GMPS is used within the SA calculation. The SA sum of squares was nearly 3 times that of GMPS (908 vs. 328), and hence only SA remained. Residual plots were assessed for normality. The final model exhibited $R^2 = 0.86$, SE = 10.3. Time, starch, and SA were ($P < 0.02$) related to SD, and time × starch showed a trend ($P < 0.06$). The parameter estimate for SA was 0.20 (SE 0.06). These observations suggest SA is better related to rumen starch disappearance than GMPS and should be considered by feed mills when evaluating ground corn and the top 15% SA here were >110 cm^2/g.

Key Words: corn, digestion, starch

1446 Effect of steam-flaked and ground corn with different particle size on dairy cow performance with high-concentrate diet. G. R. Ghorbani*, F. Ahmadi, and M. Haidary, *Isfahan University of Technology, Isfahan, the Islamic Republic of Iran*.

Eight midlactation Holstein cows were used to study the effect of steam-flaked and ground corn with different particle size on the performance of lactating cows with high concentrate. Cows were assigned to four treatments in a replicated 4 × 4 Latin square experiment. Cows were fed (ad libitum) a total mixed ration (36:64 forage:concentrate ratio, DM basis). The diets were different only in corn particle size. The treatments were ground corn with different particle size (mean particle size = 0.59, 0.68, and 0.82 mm, for treatments 1, 2, and 3, respectively) and steam-flaked corn for treatment 4 (density = 0.41 kg/L). Treatments had no effects on DMI, milk yield (MY), 3.5% fat-corrected milk (FCM 3.5%), milk protein, lactose, and SNF percentage. Milk fat percentage was significantly higher for cows receiving steam-flaked corn than for cows receiving treatment 1 and 2 diets (2.61, 2.48, and 2.70 vs. 2.75; $P = 0.003$). Rumen and urinary pH was greater for treatment 4 than for treatment 1, 2, and 3 (6.46 vs. 6.06, 5.92, and 6.05 [$P < 0.01$] and 8 vs. 7.93, 7.95, and 7.98, respectively). Feed efficiency (MY/DMI) was not affected by dietary treatments, whereas in treatment 4, 3.5% FCM/DMI was significantly ($P < 0.05$) higher than in treatment 1. Overall, these data indicate that ground corn with a mean particle size of 0.82 mm has effects similar to those of steam-flaked corn with 0.41 kg/L density.

Key Words: ground corn, Holstein dairy cows, particle size, performance, steam-flaked corn

1447 Effect of diastatic power and processing index on the feed value of barley grain for finishing feedlot cattle. G. O. Ribeiro Jr.*[1], M. L. Swift[2], and T. A. McAllister[1], *[1]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Hi-Pro Feeds, Okotoks, AB, Canada*.

The objective of this study was to assess the nutritional value of barley grain differing in diastatic power (DP; high vs. low, a malt trait) and processing index (PI; 75 vs. 85). One hundred sixty Angus × Hereford crossbred yearling steers (467 ± 38 kg; 144 intact; 16 rumen cannulated) were used in a complete randomized 2 × 2 factorial experiment. Steers were assigned to 16 pens, 8 of which were equipped with the GrowSafe system to measure individual feed intake. Cannulated steers (2 per pen) were randomly assigned to the 8 GrowSafe pens. Diets consisted of high- or low-DP barley grain (80.0% of diet DM) processed to an index of either 75 or 85% (PI). Ruminal pH in cannulated steers was measured over four 5-d periods using indwelling electrodes. Fecal samples were collected every 28 d from the rectum of each steer to assess digestibility using AIA as a marker. No differences ($P > 0.10$) in rumen pH were observed among cattle as measured by the indwelling pH meters. However, lower ($P < 0.05$) rumen pH was observed for steers fed low- as opposed to high-DP barley in rumen samples collected just before feeding and measured in the laboratory. Intake of DM and OM were not affected ($P \geq 0.24$) by DP but were lower ($P < 0.01$) with more severe processing (PI-75 vs. PI-85). Low-DP barley tended to exhibit higher ($P = 0.09$) total tract DM digestibility than high-DP barley. Steers fed PI-75 barley also had higher ($P = 0.06$) G:F and NE_g. Digestibility of DM, OM, CP, NDF, and starch was higher ($P < 0.05$) for PI-75 barley than for PI-85 barley. Low-DP barley increased ($P < 0.05$) carcass dressing percentage by 0.5% compared with high-DP barley, with a lower ($P = 0.06$) PI tending to increase rib eye area. Compared with high DP, steers fed low-DP diets had more ($P = 0.01$) total (41.7 vs. 19.4%) and severe liver abscesses (22.2 vs. 9.7%). Results suggest that although low-DP barley increased liver abscesses, differences in DP did not alter digestion or growth performance, but low-DP barley did improve dressing percentage. Barley with different DP responded similar to processing, with more intensive processing (PI-75) of barley improving starch digestion, feed efficiency, and NE_g without negatively affecting rumen pH.

Key Words: barley, beef cattle, malt traits, processing index

1448 Heating of ensiled high-moisture corn and aerobic loss of volatile organic compounds are delayed by inoculation with *Lactobacillus buchneri*. S. Qi, W. Rutherford, B. Smiley, B. Harman, and F. Owens*, *DuPont Pioneer, Johnston, IA*.

Volatile organic compounds (VOC) when combined with specific nitrous oxide air pollutants have been associated with smog. Volatile organic compounds are released from silage surfaces exposed for removal from storage and during feed mixing and delivery. Extent of loss of VOC depends on air exposure time and presumably is accelerated by silage heating. Inoculation of corn silage with *Lactobacillus buchneri* (LB) retards yeast growth and delays heating of corn silage exposed to air. This study was designed to measure effects of LB inoculation on heating and losses of VOC and DM from high-moisture corn (HMC). High-moisture corn from three different Pioneer hybrids was treated with 1×10^5 cfu LB/g wet material with a Pioneer brand LB inoculant or left untreated. Following treatment, samples were placed in triplicate PVC silos and allowed to ferment for 60 d. Following removal from storage, triplicate samples of each HMC were exposed to air in Honig adiabatic chambers with temperatures being continuously monitored. Wet silage samples were recovered after 24, 48, 72, 96, and 120 h of air exposure and a liquid extract was assayed for concentrations of specific VOC. Concentrations of ethanol, acetate, lactate, 2 propanediol (PD), and total VOC in fermented HMC were 0.5, 0.1, 0.8, 0.02, and 1.5% of DM for untreated HMC and 0.8, 0.5, 0.5, 0.04, and 2.0% of DM for LB-inoculated HMC, with LB silages being higher in total VOC and acetate ($P < 0.02$) but lower ($P < 0.02$) in lactate. Of the initial concentrations of total volatiles, ethanol, and lactate in fermented HMC, disappearance half-life during air exposure was shorter for control HMC (1.3, 1.4, and 1.1 d, respectively) than for LB-treated HMC (41, 11, and 300 d, respectively). Above and beyond this "hidden" loss of energy as volatiles, microbial metabolism during air exposure results in additional loss of DM. The DM lost during aerobic exposure was greater (4.92 vs. 0.3%; $P < 0.01$) for untreated HMC than for LB-treated HMC and time for silage temperature to increase by 1.7°C was shorter (55 vs. 150 h; $P < 0.01$) for control HMC than for LB-treated HMC. Results indicate that inoculation of HMC with LB postpones heating and retards release of VOC and DM from HMC. Through delaying the loss of VOC and increasing retention of DM during air exposure, inoculation of HMC with LB increased nutrient recovery from ensiled HMC.

Key Words: corn silage, *Lactobacillus buchneri*, volatile organic compounds recovery

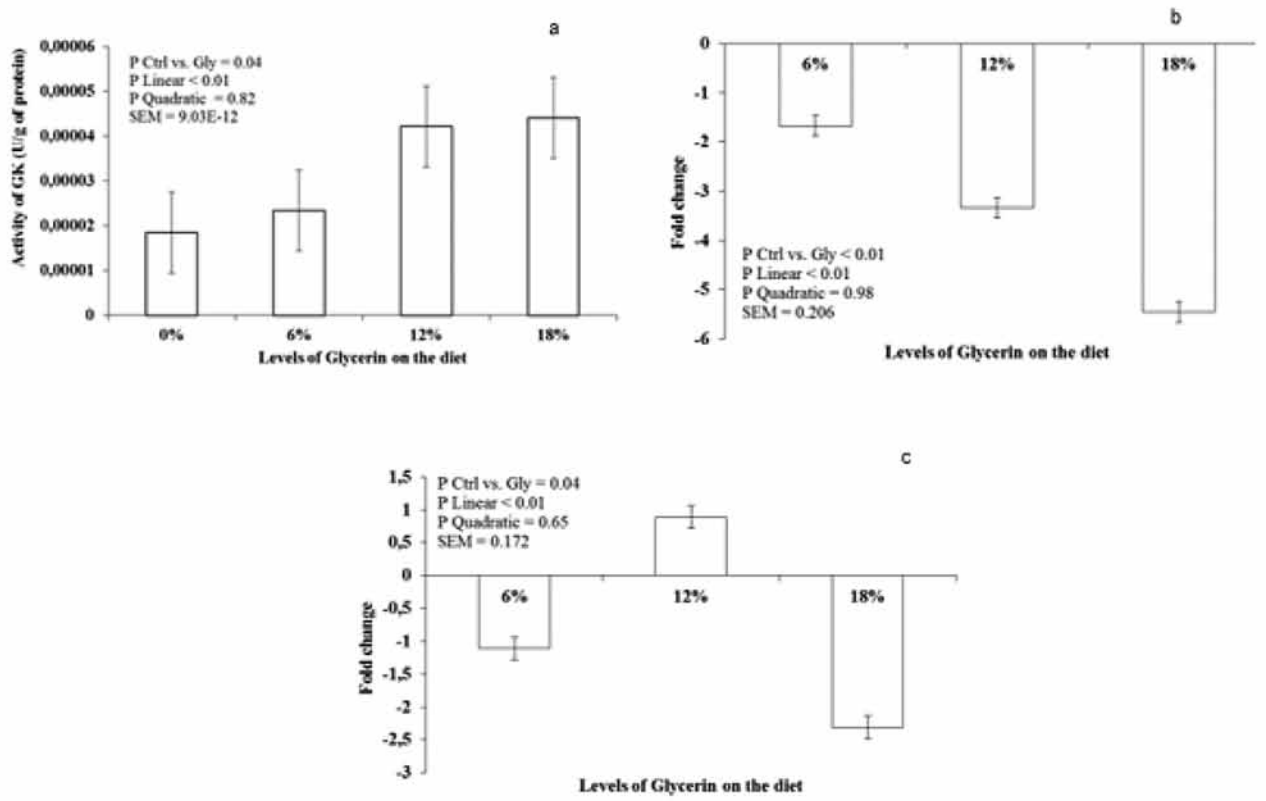

Figure 1449. Glycerol kinase activity (a), relative expression of *GK1* (b), and relative expression of *PCK1* (c) in the liver of young bulls fed with different crude glycerin concentrations.

1449 Liver gluconeogenesis in young bulls fed different levels of crude glycerin. M. M. Ladeira*[1], J. R. R. Carvalho[1], P. D. Teixeira[1], J. C. O. Dias[2], T. R. Gionbelli[1], A. C. Rodrigues[1], and D. M. Oliveira[3], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]IFNMG, Salinas, Brazil, [3]Universidade Estadual do Mato Grosso do Sul, Aquidauana, Brazil*.

This study aimed to evaluate gene expression of *glycerol kinase 1* (*GK1*) and *cytoplasmatic phosphoenolpyruvate carboxykinase* (*PCK1*) and glycerol kinase activity in the liver of young bulls fed different levels of crude glycerin. Forty-four crossbred young bulls (one-fourth Angus, one-fourth Nellore, one-fourth Senepol, and one-fourth Caracu), with initial BW of 368 ± 4 kg, were used in a completely randomized design, with four treatments (0, 6, 12, and 18% of crude glycerin in the diet, DM basis) and 11 replicates. Diets were formulated with corn silage as forage, and crude glycerin replaced ground corn. Corn gluten meal-21 was included in the diets with crude glycerin to provide similar levels of CP (13% CP). Immediately after slaughter of animals, liver samples were collected, frozen in liquid nitrogen, and stored in −80°C to analyze *GK1* and *PCK1* genes expression using RT-qPCR. In addition, same samples were used to measure glycerol kinase activity. Orthogonal contrasts were used to evaluate the linear and quadratic effects of glycerin and without-glycerin vs. glycerin diets. Liver glycerol kinase activity linearly increased ($P < 0.01$) following glycerin inclusion (Fig. 1a). On the other hand, the opposite results were detected on *GK1* and *PCK1* expressions (Fig. 1b and 1c, respectively). Expression of *GK1* in the liver was 1.61, 3.34, and 5.45 times lower when the animals were fed 6, 12, and 18% of crude glycerin, respectively, than in the liver of animals fed a diet without glycerin. Therefore, *GK1* expression was more affected by the diets than *PCK1*. In conclusion, the use of crude glycerin in feedlot diets downregulate the expression of *GK1* and *PCK1* and increases glycerol kinase activity in liver of young bulls.

Key Words: glycerol, glycerol kinase, *PCK1* gene

1450 Starch digestibility by lactating cows fed flint or dent corn silage stored two or six months before feeding. A. Laflotte[1], L. Aubry[2], B. Mahanna[3], and F. Owens*[3], *[1]U. Lorraine, Nancy, France, [2]DuPont Pioneer, Aussonne, France, [3]DuPont Pioneer, Johnston, IA*.

Starch availability from corn silage increases with duration of storage and is greater for grain from dent than from flint hybrids based on in situ or in vitro studies. This objective of this study was to determine the degree that starch digestibility by lactating cows changes during storage time from corn silages produced from one dent and one flint hybrid. Yields of DM for the dent and flint hybrid harvested and kernel processed from adjacent

1.1 ha plots in France on Oct 3 and Sep 26 at 41 and 37% DM were 16.1 and 15.1 t DM/ha, respectively; starch made up 32.5 and 27% of silage DM, respectively. Of ration DM, 53% was silage. Dietary energy levels were moderately low so that digestibility of starch from the silage could be accurately measured. Two groups of 10 lactating cows were fed each corn silage diet in a replicated crossover trial within periods that began 2 mo and again 6 mo after ensiling. Milk production and DMI were measured during 14-d periods of each segment. Fecal samples obtained from each cow on three nonconsecutive days during each segment were assayed for starch content. Milk yield, milk:intake ratio, and fecal starch concentrations all were greater ($P < 0.01$) 2 mo after ensiling, even though DMI was greater 6 mo after ensiling. Adjusted for differences in starch content of the diets, starch digestibility averaged 89 and 96% 2 mo after ensiling and 94 and 97% 6 mo after ensiling for the flint and the dent corn silages, respectively, increasing ($P < 0.05$) with silage storage time for the flint but not ($P = 0.66$) for the dent corn silage. After 6 mo of storage, starch digestibility was not different ($P = 0.17$) between the two corn silages. Averaged across periods, individual cows differed in starch digestibility being over 95.5% for 6 cows of the 20 cows but under 92% for 4 cows. Starch digestibility by individual cows was not correlated with parity, milk production, cow weight, or DM content of feces. In summary, when averaged across periods, total tract digestibility of starch was greater ($P < 0.02$) for this dent than this flint corn silage but tended to increase ($P < 0.07$) with duration of silage storage.

Key Words: corn silage, flint corn, starch digestion

1451 Ruminal in situ degradability and in vitro organic matter digestibility of peanut hulls under different incubation times with calcium oxide.

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Two experiments were conducted to evaluate the effects of calcium oxide (CaO) and different DM contents on ruminal in situ degradability and on in vitro OM digestibility (IVOMD) of peanut hulls (PH). In Exp. 1, PH were incubated in duplicate (2 consecutive years) in 20-L buckets following the treatments 1) as is, 2) 50% DM for 7 d, 3) 50% DM for 14 d, 4) 50% DM + 5% CaO for 7 d, and 5) 50% DM + 5% CaO for 14 d. After 7 or 14 d of incubation, bucket contents were dried and ground to pass a 4-mm screen. Ruminal in situ degradability of DM, OM, NDF, and ADF of PH, either treated or not with CaO, was determined by incubating nylon bags for 24, 48, and 72 h in duplicate, in 9 ruminally cannulated steers consuming bahiagrass hay. In Exp. 2, PH were incubated in 20-L buckets (2/treatment) following the treatments 1) 70% DM, 2) 70% DM + 5% CaO, 3) 50% DM, and 4) 50% DM + 5% CaO. Buckets were opened after 3, 6, 9, 12, and 15 d of incubation, when a representative sample was collected, dried, ground (2 mm), and incubated for 48 h to determine IVOMD. For Exp. 1, data were analyzed as a randomized complete block design, using bucket as the experimental unit. The model included the fixed effect of treatment and random effect of year. For Exp. 2, data were analyzed as a completely randomized design with repeated measures and the model included the fixed effects of DM content, CaO, incubation days, and their interactions. For Exp. 1, at all ruminal incubation time points, no differences ($P > 0.05$) were observed on in situ degradability of DM, OM, NDF, and ADF. For Exp. 2, no effect of DM content ($P = 0.64$), CaO ($P = 0.27$), or their interaction ($P = 0.33$) were observed; however, there was a CaO × day of incubation interaction ($P = 0.07$) where when CaO was added, IVOMD was greatest at 6 d of incubation, and up to 15 d of incubation, it decreased significantly. We conclude that treating PH with CaO was not effective at improving in situ ruminal degradability of nutrients. Moreover, regardless of moisture content, when PH was treated with CaO and incubated for more than 6 d, IVOMD was negatively affected.

Key Words: calcium oxide, digestibility, peanut hulls

1452 A comparison of Lacto-Whey to soybean meal in continuous cultures fed corn- or wheat-based diets.

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Lactate, a key intermediate in the fermentation of starch-based feeds, is either directly converted to propionate via acrylate by *Megasphaera elsdenii* or else is converted back to pyruvate and metabolized. In the latter process, more cellular carbon conversion into bacterial products should increase the assimilation of ammonia into bacterial nitrogen, primarily amino and nucleic acids. The effects of Lacto-Whey (LW), an ammonium lactate product, were investigated in dual-flow continuous culture systems ($n = 4$) using a 4 × 4 Latin square design. Lacto-Whey (+LW) was isonitrogenously dosed against soybean meal as a control (–LW) and factorialized with either a wheat- or a corn-based concentrate (formulated to have equal starch). Each individual continuous culture system was given 30 g of DM and their respective LW treatments in 2 equal feedings at 0800 and 2000 h (60 g/d). We hypothesized that the wheat +LW combination would increase propionate production while also increasing bacterial assimilation of ammonia. No differences ($P > 0.10$) were observed for total VFA or propionate production per day; however, the main effect of +LW tended ($P < 0.09$) to increase propionate at 1, 1.5, and 2 h after feeding. The main effect of corn increased

($P < 0.02$) the proportion of bacterial N derived from ammonia (as assessed using ^{15}N). No differences ($P > 0.10$) were observed in NDF or apparent OM digestibilities. Starch digestibility was moderately higher ($P = 0.09$) for corn than for wheat. To retain protozoa, the slower stirring speed probably sedimented grain and negated wheat starch from being more degradable than that from corn. An interaction between grain source and LW ($P < 0.05$) was explained by wheat without LW increasing lactate production but corn increasing lactate when combined with LW. Treatment × time interactions ($P < 0.05$) revealed higher lactate and total VFA concentrations in +LW treatments. Lactate in the LW dose disappeared by 1.5 h and was metabolized to propionate until 4 h. There were no treatment differences observed in the daily productions of methane and hydrogen, although the main effect of +LW numerically decreased methanogenesis. Under the conditions of this study, +LW supported microbial growth compared with soybean meal (–LW). Results are consistent with our expectation that Lacto-Whey should support lactate fermentation to propionate, thereby stabilizing ruminal fermentation.

Key Words: ammonium lactate, continuous cultures, starch source

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1453 Glucose precursor supplementation in Holstein and Jersey cows as a preventative treatment for ketosis in the transition period. K. E. Mitchell*, *UC Davis, Davis, CA*.

Glucogenic substances can help treat subclinical or clinical ketosis by lowering β-hydroxybutrate (BHBA) levels and raising glucose (Glu) levels. Subclinical ketosis is defined as BHBA ≥ 1.0 mmol/L and Glu < 60 mg/dL and clinical ketosis is defined as BHBA > 1.2 mmol/L and Glu < 60 mg/dL. The objectives of this study are to determine if supplementation with a glucose precursor powdered product (GP; Glucose Booster; Stuhr Enterprises, LLC) during transition would decrease subclinical or clinical ketosis and have an effect on health and milk production of multiparous Jersey and Holstein dairy cows. Holstein ($n = 106$) and Jersey ($n = 105$) cows at a commercial dairy were systematically enrolled into either a control (C; odd-numbered ear tags) or GP (even-numbered ear tags) treatments. Glucose precursor was top-dressed on the prepartum pen (PreP) TMR and postpartum pen (PPost) TMR at a rate of 300 g/cow per day and mixed in using a pushup tractor. Cows were then allowed access to the TMR. Daily feed samples were pooled weekly and sent to Analab (Agri-King, Fulton, IL) for nutrient analyses. Weekly blood samples were analyzed for Glu (mg/dL) and BHBA (mmol/L) using NovaMax (Nova Diabetes Care, Inc., Billerica, MA). Weekly milk samples were taken to approximately 21 DIM followed by monthly tests. Holstein ($n_{GP} = 52$ and $n_C = 54$) and Jersey ($n_{GP} = 53$ and $n_C = 52$) data was analyzed using the MIXED procedure of SAS (version 9.4; SAS Institute 2015) with repeated measures by cow, parity as a random effect and fixed effects treatment, previous lactation milk fat and protein yield, period of lactation, and DIM. Jersey cows did not show a response to treatment. Holstein cows supplemented with GP increased production by 4.05 kg/d milk yield ($P = 0.0011$), 0.22 kg/d fat yield ($P = 0.0002$), and 0.12 kg/d protein yield ($P = 0.0042$) while on treatment. After treatment, GP Holsteins' production was still greater than that of C Holsteins by 2.45 kg/d milk ($P = 0.0487$), 0.08 kg/d fat ($P = 0.17$), and 0.08 kg/d protein ($P = 0.055$) until 120 DIM. Total number of health events in the first 60 DIM for GP Holstein cows decreased ($N_{GP} = 32$ and $N_C = 44$) and incidence of clinical and subclinical ketosis decreased by 15%. Holsteins and Jerseys responded differently to treatment; therefore, different breeds face different issues during early lactation. Holsteins tend to have a difficult transition period and are more likely to benefit from GP. For Holsteins, supplementation with GP prevented ketosis, decreased health events, and increased milk yield and milk component production.

Key Words: ketosis, β-hydroxybutyrate, glucose

1454 Manipulation of lactating dairy cows diets using reduced-fat distillers' grains, corn oil, and calcium sulfate to reduce methane production measured by indirect calorimetry. J. V. Judy*[1], T. M. Brown-Brandl[2], S. C. Fernando[1], and P. J. Kononoff[1], *[1]University of Nebraska, Lincoln, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

A study using 16 multiparous (8 Holstein and 8 Jersey) (78 ± 15 DIM, mean ± SD) lactating dairy cows, was conducted to determine the effects of dietary manipulation on methane mitigation in dairy cattle. A replicated 4 × 4 Latin square design with 35-d periods (28 d of adaption and 7 d of collections) used to compare four different dietary treatments. Treatments were composed of a control (CON) diet, which did not contain reduced-fat distillers' grain plus solubles (RFDDGS), and treatment diets containing 20% (DM basis) RFDDGS (DDGS), 20% RFDDGS with 1.38% (DM basis) added corn oil (OIL), and 20% RFDDGS with 0.93% (DM basis) added calcium sulfate (CaS). Methane sampling was performed using indirect calorimeters (head boxes). Compared with CON, DMI was greater ($P = 0.030$) for DDGS but was not affected ($P > 0.05$) by either OIL or CaS. Milk production was lowest in CON ($P < 0.001$) compared with DDGS, OIL, and CaS (26.3 vs. 27.5, 28.3, and 27.6 ± 0.67 kg/d for CON vs. DDGS, OIL, and CaS, respectively). Compared with CON, fat-corrected milk was greater ($P = 0.007$) in RFDDGS and OIL (30.7 vs. 32.1, 32.4, and 31.2 ± 0.67 kg/d for the CON, DDGS, OIL, and CaS, respectively). The addition of DDGS did not affect ($P = 0.690$) total methane produced compared with the CON diet. However, the addition of CaS reduced ($P = 0.020$) methane production whereas the addition of OIL tended ($P = 0.177$) to reduce methane production compared with the CON diet (421.6, 429.5, 394.7, and 381.4 ± 14.41

L/d for CON, DDGS, OIL, and CaS, respectively). When expressed as methane per unit of fat-corrected milk, cows consuming OIL and CaS produced less methane ($P = 0.009$) compared with CON and DDGS (13.9, 13.6, 12.3, and 12.1 ± 0.49 L/kg per day for CON, DDGS, OIL, and CaS, respectively). Similarly, when expressing methane per unit of DMI, cows consuming OIL and CaS produced less methane ($P = 0.015$) compared with those consuming the CON diet (22.3, 21.4, 19.9, and 19.6 ± 0.75 L/kg per day for CON, DDGS, OIL, and CaS, respectively). Results of this study indicate that methane production may be reduced by feeding rations containing RFDDGS with added corn oil or calcium sulfate without adversely affecting milk production.

Key Words: dairy cows, dried distillers' grains and solubles, methane

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1455 Effect of particle size of a mash concentrate on behavior, rumen fermentation, and macroscopic and microscopic lesions of the digestive tract in Holstein bulls fed a high-concentrate diet.

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Twenty-four individually housed Holstein bulls (456 ± 6.9 kg of BW and 292 ± 1.4 d of age) were exposed to a 2 × 2 factorial design (ingredients ground with a hammer mill using a sieve size of 2 [HM2] or 3 mm [HM3] vs. the same sieve size for all ingredients exception for corn, which was ground using at 10 mm [HM210 or HM310]) to evaluate the effect of mash particle size in finishing diets. Concentrate (36% corn, 19% barley, 15% corn gluten feed, and 8.4% wheat; 14% CP and 3.28 Mcal/kg) consumption were recorded daily, straw consumption was recorded weekly, and animals were filmed weekly to register behavior. Bulls were slaughtered after 56 d of exposure to treatments. Digestive tract and liver lesions were recorded, and tissue samples were collected. Data were analyzed using an ANOVA. Mean meal particle size was 0.85 ± 0.01, 1.26 ± 0.06, 1.05 ± 0.08, 1.26 ± 0.05 mm and percentage of particles between 0.5 and 1 mm was 68 ± 2.9, 46 ± 1,7, 46 ± 5.0, and 39 ± 3.3% for HM2, HM210, HM3, and HM310, respectively. When ingredients were ground at 2 vs. 3 mm, bulls tended ($P = 0.07$) to perform less social behaviors (128 vs. 155 ± 10.1 min/d, respectively), whereas rumen papillae fusion and the percentage of rumens classified as dark decreased ($P < 0.05$) and the number of rumen papillae increased ($P < 0.05$). In addition, reducing sieve size from 3 to 2 mm tended ($P = 0.08$) to increase cecum total VFA concentrations. Moreover, when corn was sieved at 10 mm, time spent eating concentrate was lesser ($P < 0.05$) than when all ingredients were ground at 2 or 3 mm (81 vs. 63 ± 5.0 min/d, respectively). In the cecum, grinding corn at 10 mm tended ($P = 0.09$) to decrease crypt depth and to increase the acetate-to-propionate ratio. Straw intake was greatest with the HM210 treatment. Moreover, in the jejunum, papillae length and crypt depth, molar percentage of acetate, and pH, and in the cecum, molar percentage of butyrate and acetate were affected by a significant interaction ($P < 0.05$) between the main factors. In conclusion, the particle size of a mash in bulls fed high-concentrate diets modifies behavior and affects digestive tract macroscopic and microscopic morphology.

Key Words: behavior, bulls, digestive tract morphology, particle size of mash

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1456 Essential oils from three tropical *Citrus* species can reduce in vitro enteric methane production.

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The objective was to investigate the effects of essential oils from *Citrus sinensis* (SI), *Citrus limon* (LI), and *Citrus aurantifolia* (AU) on in vitro rumen fermentation, methane production, and digestibility of a total mixed ration (TMR). A TMR (0.5 g/sample) containing corn silage (28.5%), a ryegrass and triticale silage mixture (15.7%), and a corn–soybean–based grain mixture (55.8%) for dairy cows was treated with essential oils from SI, LI, or AU at doses of 0 (CON), 10 (Low), 20 (Med), and 30 mL/50 mL (High) of a rumen fluid–buffer inoculum (1:2 ratio) or with monensin (MON; 1.2 mg/g of TMR). Each treatment was incubated in triplicate in 120-mL gas-tight culture bottles at 39°C for 24 h. Each run was repeated thrice. Fermentation parameters, gas and methane production, and in vitro DM digestibility (IVDMD) were measured. Data for each essential oil were separately analyzed with the GLIMMIX procedure of SAS. Adding LI at Med and High doses increased IVDMD ($P < 0.05$) compared with MON (48.9 and 49.2 vs. 46.4% of DM, respectively) but had no effect compared with CON (48.9 and 49.2 vs. 48.1% of DM, respectively). All doses of SI and LI and Med and High doses of AU reduced ($P < 0.05$) methane production (mL/g of DMD). Compared with CON, gas volume (mL/g of DMD) was reduced ($P < 0.05$) by all doses of LI and by Med and High doses of AU. Ammonia N and total VFA concentrations and pH were unaffected by treatment. Compared with CON and MON, Med and High doses of LI and AU decreased ($P < 0.05$) molar proportion of acetate and increased ($P < 0.05$) that of propionate. Therefore, the acetate-to-propionate ratio was reduced ($P < 0.05$) by Med and High doses of LI (2.73 and 2.67 vs. 3.21 and 3.12, respectively) and AU (2.77 and 2.75 vs. 3.21 and 3.12, respectively) compared with CON and MON. Compared with CON, all doses of SI and LI as well as Med and High doses of AU reduced in vitro methane production

without reducing digestibility or total VFA concentration.

Key Words: citrus, essential oil, methane

1457 Enteric methane emissions from dairy cows fed a corn silage–based diet supplemented with increasing amounts of linseed oil.

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The objective of this study was to examine the effects of supplementing increasing amounts of linseed oil (LO) on intake, milk production, and enteric CH_4 emissions of dairy cows fed corn silage–based diets. Twelve lactating, multiparous Holstein cows (84 ± 28 d in milk and 42 ± 4.6 kg/d milk yield) were used in a replicated 4 × 4 Latin square design (35-d periods and 14 d of adaptation). Cows were fed ad libitum (5% orts, on an as-fed basis) a corn silage–based TMR (61:39 forage:concentrate ratio) not supplemented (control) or supplemented with 2, 3, or 4% LO (on a DM basis). Methane production was determined (3 consecutive days) using respiration chambers, and intake and milk yield were measured over 6 consecutive days. Data were analyzed using the MIXED procedure (SAS) and differences among treatments were declared significant at $P \leq 0.05$ using Dunnett's comparison test. Dry matter intake and energy-corrected milk (ECM) were not affected (23.5 and 33.1 kg/d, respectively) by supplementing LO at 2 and 3%, but they decreased (21.1 and 30.4 kg/d, respectively) when LO was added at 4%. Daily CH_4 emission averaged 515 g/d for cows fed the control diet and decreased by 8, 21, and 33% in cows fed 2, 3, and 4% LO, respectively. When adjusted for DMI, CH_4 emission averaged 21.7 g/kg for cows fed the control diet and declined in cows fed 2, 3, and 4% LO (19.7, 17.4, and 15.7 g/kg, respectively). When expressed per kilogram of ECM, CH_4 production was not affected by supplementing 2% LO (15.2 g/kg) but declined when LO was added at 3 and 4% (12.6 and 11.5 g/kg, respectively). Results of this study show that supplementing a corn silage–based diet with up to 3% of LO reduces enteric CH_4 production without adverse effects on DMI and milk production. However, a higher supplementation level (4%) impairs DMI and milk yield. These findings suggest that LO supplementation level should not exceed 3% (DM basis) in corn silage–based diets to mitigate enteric CH_4 without negatively affecting animal production.

Key Words: corn silage, linseed oil, methane

1458 Effect of different forages and concentrate levels on energy conversion, and enteric methane production of Holstein × Gyr heifers.

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The aim of this study was to evaluate the effect of diets containing corn silage (CS) or sugarcane (SC) with 30 or 50% of concentrate on energy conversion factors and methane production of Holstein × Gyr heifers. Sixteen Holstein × Gyr heifers with 12 ± 1.0 mo of age and average initial BW of 210 ± 20.2 kg were distributed in a completely randomized design using a 2 × 2 factorial scheme ($n = 4$), with two forages (CS or SC) and two levels of concentrate (30 or 50%) on a DM basis, during 112 d. For evaluation of energy losses, a digestibility assay was performed using the total collection of feces and urine over three consecutive days. The enteric CH_4 production was quantified by continuous analysis of regular samples of air excreted by the animals throughout the day, during six consecutive days. Greater ($P < 0.05$) CH_4 production as a function of DMI were observed for heifers fed SC-based diets. There was interaction ($P < 0.05$) between type of roughage and level of concentrate when CH_4 production was related to ADG and when expressed in relation to TDN, GE, and ME intakes. The increased level of concentrate in SC-based diets did not change ($P > 0.05$) CH_4 production in relation to TDN, GE, and ME intakes. Nevertheless, there was a reduction ($P < 0.05$) in CH_4 production related to ADG. The ratio between DE and TDN was influenced ($P < 0.05$) by type of roughage, and a greater ratio was observed for CS-based diets. The efficiency of the conversion from DE to ME was not influenced ($P > 0.05$) by variables analyzed in this study. However, the mean value observed in this study was above those proposed by the main systems of feed evaluation and nutrient requirements for ruminants. Therefore, we concluded that a greater inclusion of concentrate in SC-based diets can allow an improvement in CH_4 emissions per gain. The mean value suggested for the ME:DE ratio based on this study is 0.86.

Key Words: *Bos indicus*, calorimetry, methane

1459 Effects of duration of moderate increases in grain on bacterial diversity in the digestive tract of Holstein calves. S. Li[1], S. Moossavi[2], P. Azevedo[1], B. Schurmann[3], P. Gorka[4], G. B. Penner[5], J. C. Plaizier[1], and E. Khafipour*[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [2]Department of Medical Microbiology, University of Manitoba, Winnipeg, MB, Canada, [3]University of Saskatchewan,, Saskatoon, SK, Canada, [4]University of Agriculture, Krakow, Poland, [5]University of Saskatchewan, Saskatoon, SK, Canada*.

Feeding more grain to cattle alters the composition of digesta in the foregut and hindgut, including increasing its acidity, osmolality, and concentration of fermentable substrates. These changes may affect the composition and functionality of gut microbiota. In this study, effects of duration of grain feeding on the diversity of microbiota throughout the digestive tract were investigated in 25 Holstein steers (213 ± 23 kg; 5 to 7 mo of age). Animals received either a forage-based diet containing 92% hay and 8% of a mineral and vitamin pellet on a DM basis or a moderate-grain diet, obtained by replacing 41.5% percentage units of the hay in the forage-based diet with barley grain, for 7 or 21 d before slaughter. Immediately after slaughter, digesta samples were collected from the rumen, jejunum, ileum, cecum, colon, and rectum. Deoxyribonucleic acid was extracted from digesta samples and subjected to V4 sequencing of the 16S rRNA gene on an Illumina platform. Alpha-diversities of bacterial communities were calculated using various estimators. Differences in β-diversity of microbiota across treatments and time points were tested using permutational ANOVA. Across the digestive tract, the lowest α-diversity was observed in the ileum followed by the jejunum and rumen. The highest α-diversities were found in the cecum, colon, and rectum, with no differences among these three sites. Beta-diversity analyses showed that microbiota in the rumen, jejunum, and ileum were distinct ($P < 0.05$) and differed from those in the cecum, colon, and rectum ($P < 0.05$). Microbiota from the cecum, colon, and rectum were not distinct. Feeding the moderate-grain diet for 7 and 21 d reduced ($P < 0.05$) the richness of bacteria in rumen compared with feeding the forage-based diet during these periods. However, the moderate-grain diet did not affect these indices in the other sections of the digestive tract. Beta-diversity analysis indicated that the microbiota communities were altered in all sample sites on d 7 ($P < 0.05$) and did not change between d 7 and 21 of grain feeding. Overall, a moderate increase in the proportion of grain in the diet reduced bacteria diversity in the digestive tract of calves. The reduction occurred within 7 d after the increase in grain feeding and was maintained until 21 d after this change in diet.

Key Words: calf, grain, gut microbiome

1460 Muscle protein metabolism of growing Holstein × Gyr heifers. F. A. S. Silva*[1], S. C. Valadares Filho[2], L. N. Rennó[1], S. A. Santos[3], D. Zanetti[1], L. A. Godoi[1], M. V. C. Pacheco[1], H. M. Alhadas[1], P. P. Rotta[4], and L. F. Costa e Silva[4], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal da Bahia, Salvador, Brazil, [4]Colorado State University, Fort Collins*.

The aim of this study was to evaluate muscle protein metabolism of Holstein × Gyr heifers. Sixteen Holstein × Gyr heifers with an average age of 12 ± 1.0 mo and initial BW of 210 ± 20.2 kg were distributed in a completely randomized design using a 2 × 2 factorial scheme ($n = 4$), with two forages (corn silage or sugarcane) and two levels of concentrate (30 or 50%) on a DM basis, during 112 d. A total urine collection was performed from the 110th to the 112th day of the experimental period for quantification of 3-methylhistidine (3MH) excretion. Muscle protein metabolism was evaluated by the fractional synthesis rate (FSR), fractional degradation rate (FDR), and fractional accretion rate (FAR) of myofibril proteins. There was no interaction ($P > 0.05$) between type of forage and level of concentrate for any variable. Greater ($P < 0.05$) values for the daily excretion of 3MH, protein muscle gain, FSR, FDR, and FAR were observed for the animals fed 50% concentrate independent of forage type. Heifers fed sugarcane showed an increase in FSR and FDR with the increase in the concentrate level of approximately 54 and 53%, respectively. In the case of heifers fed corn silage–based diets, the increase in FSR and FDR was approximately 8 and 7%, respectively. This increase in concentrate level enabled animals consuming a sugarcane-based diet to reach protein turnover rates numerically similar to those animals consuming corn silage–based diets, even when it was associated with the inclusion of 50% concentrate. Therefore, the increase of 20% in concentrate levels using sugarcane-based diets is enough to raise the supply of nutrients and to provide a greater muscle growth in Holstein × Gyr heifers.

Key Words: dairy cattle, protein turnover, tissue deposition

1461 Effects of milk replacer feeding rate, egg yolk inclusion in milk replacer, and calf starter starch content on Holstein calf performance through four months of age. T. S. Dennis*, T. M. Hill, J. D. Quigley, F. X. Suarez-Mena, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH*.

The objectives of this research were to evaluate milk replacer (MR) feeding rates, alternative protein sources in MR, and calf starter starch concentration and their effects on calf performance to 4 mo of age. Male Holstein calves (42.6 ± 1.2 kg BW; $n = 192$) were assigned at 3 d of age to 1 of 6 treatments in a randomized complete block design with a 2 × 2 × 2 factorial arrangement of treatments. Factors tested from d 0 to 56 (nursery) were low- or high-MR feeding rates, 0 or 10% inclusion of spray-dried egg yolks in MR, and low- or high-starch calf starter. Low MR rate was 0.66 kg DM fed for 39 d followed by 0.33 kg DM for 3 d. High MR rate was 0.87 kg DM fed for 5 d, 1.08 kg DM for 37 d, and 0.43 kg DM for 7 d. The MR contained 27.5% CP and 19.6% fat (DM basis) and starters contained 21.2% CP; low starch was a complete pellet with 10.2% starch and high starch was textured with whole corn and oats with 43.3% starch. From d 56 to 112 (grower), calves were randomly assigned to pens (4 calves/pen) maintaining MR rate and starch content while stratifying yolk treatments within pen. Starter was blended with chopped hay (5% of the diet) during the grower phase. Data were analyzed as repeated measures with calf (nursery) or pen (grower) as the experimental unit. Calf ADG, hip width, and BCS change were greater ($P < 0.05$) for calves fed high vs. low MR, 0 vs. 10% yolk, and high vs. low starch in the nursery. Starter intake was less ($P < 0.05$) for calves fed high vs. low MR, 10 vs. 0% yolk, and low vs. high starch. In the grower phase, calves fed low MR and high starch had the greatest ADG and hip width change compared with calves fed low MR and low starch, with other treatments intermediate ($P < 0.05$). Overall, calves fed high MR had 9% greater ADG and 4% greater hip width change than calves fed low MR, yet nutrient efficiency was similar, despite 80% more MR intake than calves fed low MR. Additionally, calves fed high-starch starter achieved 18% greater ADG and 17% greater hip width than calves fed low-starch starter overall, an over 2-fold greater response than the effect of MR feeding rate.

Key Words: calf, feeding rate, starch

1462 Effects of mineral and vitamin supplementation to pasteurized whole milk diets on growth and health of preruminant Holstein bull calves. D. Wood*[1], L. A. Krueger[2,3], M. Dehghan Banadaky[4], J. R. Stabel[5], M. A. Engstrom[6], D. C. Beitz[7], and R. Blome[1], *[1]Animix, Juneau, WI, [2]Agri-King, Inc., Fulton, IL, [3]Dep. of Animal Science, Iowa State University, Ames, [4]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, the Islamic Republic of Iran, [5]Infectious Bacterial Diseases Research Unit, National Animal Disease Center, Agricultural Research Service, USDA, Ames, IA, [6]DSM Nutritional Products, LLC, Parsippany, NJ, [7]Iowa State University, Ames*.

Our objective was to determine whether supplementation of vitamins and trace minerals (VTM), formulated to meet or exceed NRC requirements when added to pasteurized whole milk (PWM), increases challenge resolution and prevents intestinal macromolecular permeability after injection with bacterial lipopolysaccharide (LPS). Neonatal Holstein bull calves ($n = 24$) were randomly assigned to 1 of 4 dietary treatments. Calves were individually fed PWM diets for 15 d at a low (LM; 3.8 L) or high level (HM; 7.6 L) of daily intake and were supplemented (+) or not supplemented (–) with a commercial VTM premix (Animix, Inc.). No starter grain was offered. At d 13 of age, calves were subcutaneously injected with LPS of *Escherichia coli* (3 μg/kg of BW) and orally administered d-mannitol and lactulose to measure intestinal paracellular transport of macromolecules. Vitamins and trace mineral supplementation increased vitamin E in serum at d 7 compared with VTM(–) calves (2.22 ± 0.26 and 1.37 ± 0.17 μg/mL, respectively; $P < 0.05$), but vitamin E was not different among groups at the time of challenge. VTM(+) calves also demonstrated increased plasma Fe at 48 h after challenge compared with VTM(–) calves (1.11 ± 0.18 and 0.58 ± 0.08 μg/mL, respectively; $P < 0.05$). Copper (0.87 ± 0.06 and 0.72 ± 0.05 μg/mL; $P < 0.05$), Mg (19.1 ± 0.37 and 17.98 ± 0.41 μg/mL; $P < 0.05$), and P (82.7 ± 2.6 and 75.8 ± 2.4 μg/mL; $P < 0.1$) were greater in HM calves than in LM calves, respectively, throughout the study. Inflammatory acute phase protein haptoglobin was greatest in HM(–) calves ($P < 0.05$) on both d 13 and 15 (1,040.7 ± 305.4 and 782.6 ± 204.1, respectively), whereas differences in serum amyloid A and intestinal permeability were not detected. Average daily gain from d 1 to 13 was greater in HM calves than in LM calves (0.57 ± 0.03 and 0.45 ± 0.04 kg/d, respectively; $P < 0.05$) with no VTM effect. From d 13 to 15 (during LPS challenge), total gain was greater in HM(+) calves than in HM(–) calves (0.48 ± 0.04 and 0.39 ± 0.04 kg, respectively; $P < 0.1$). We conclude that VTM supplementation to PWM improved performance during challenge and affected Fe and vitamin E, whereas increased milk intake increased Cu, Mg, and P in plasma. Increased haptoglobin in HM(–) calves indicates decreased challenge resolution

when fed PWM not supplemented with VTM according to NRC guidelines.

Key Words: calf, pasteurized whole milk, vitamin E

1463 Effect of Axcelera-C on calf performance, intake, digestive development, and immune function during the first three months of life. M. Terré[1], F. Fàbregas[2], and A. Bach*[3], [1]*IRTA, Caldes de Montbui, Spain,* [2]*Department of Ruminant Production, IRTA, Caldes de Montbui, Spain,* [3]*ICREA, Barcelona, Spain*.

Ax Celera-C is a pellet based on whey concentrate and soybean meal (20% CP and 12% fat). Forty newborn Holstein female calves (40 ± 0.97 kg BW) were distributed in two feeding programs: 20 calves were offered Axcelera-C (AX) alone during the first 15 d of age and later on in combination (150 g/d Axcelera-C) with a concentrate until weaning, and 20 calves (CT) were fed the same concentrate throughout the study. Calves were fed the same milk replacer at the rate of 5 L/d at 12.5% DM concentration until 49 d age, when it was reduced to 2 L/d until weaning (56 d age). Chopped oat hay was offered ad libitum in a separated bucket. Animals were weighed weekly, and feed intake was recorded daily from 11 to 90 d of age. Humoral immunity was evaluated as the antibody response to a double injection of 0.5 mg of hen egg white lysozyme (HEWL) at 49 and 63 d of age. At weaning, rumen liquid samples and epithelium biopsies were obtained to determine pH and VFA concentration and to assess gene expression of *acat1*, *errfi1*, *hmgcs2*, *bpifa1*, and *trim40* as indicators of rumen epithelial growth, innate immunity, and inflammation. Data were analyzed using a mixed-effects model. Average daily gain was greater from 14 to 21 d of age in AX calves than in CT calves (0.50 and 0.35 kg/d ± 0.040, respectively). From 11 to 15 d of age, AX calves tended ($P = 0.10$) to have a greater DMI than CT calves (103 vs. 70 g/d ± 14.4, respectively), and as a result, the G:F was improved ($P < 0.05$) in AX calves in this period. When Axcelera-C was mixed with the starter feed, differences in DMI and performance disappeared for the remainder of the study. Primary and secondary responses to HEWL were similar in both treatments. Rumen pH and epithelium gene expression did not differ between treatments, but AX calves had greater ($P < 0.05$) rumen molar proportions of acetate and lower of propionate than CT calves at 56 d of age (60.1 and 19.5 vs. 55.5 and 24.1% ± 1.76, respectively). In conclusion, the use of Axcelera-C as a prestarter in young calves seems promising because it stimulates starter feed intake during the first 2 wk of life, but further research is needed to optimize the transition to a regular starter feed.

Key Words: calves, concentrate, performance

1464 Colostrum supplement feeding with a medium-quality bovine colostrum: Passive immunity transfer, health, and performance of dairy calves. M. R. De Paula, N. B. Rocha, E. Miqueo, F. L. M. Silva, T. Manzoni, S. Baldassin, and C. M. M. Bittar*, *University of Sao Paulo, Piracicaba, Brazil*.

The aim of this study was to evaluate the transfer of passive immunity, performance, and health of Holstein calves fed colostrum supplement associated with a medium-quality colostrum. After birth, 44 newborn male calves were blocked according to birth weight (BW) and date of birth and distributed in the following treatments: 1) 15% BW of high-quality colostrum (70.6 mg immunoglobulin/mL; $n = 15$; BW = 39.2 kg), 2) 15% BW of medium-quality colostrum (42.7 mg immunoglobulin/mL; $n = 14$; BW = 38.0 kg), and 3) medium-quality colostrum (41.7 mg immunoglobulin/mL; $n = 15$; BW = 39.1 kg) + colostrum supplement (Feedtech Colostrum Supplement; DeLaval, São Paulo, Brazil). Colostrum was fed within the first 12 h of life in two meals. For calves receiving the colostrum supplement, the product was supplied with the two colostrum meals in a dose of 15 mL each. Blood samples were taken every 12 h up to 48 h of life. Calves were individually housed, with free access to water and concentrate, and fed 6 L of milk replacer daily (12.5% solids, 21% CP, and 15% fat and 0700 and 1800 h), up to the sixth week of life, when they began to receive 4 L/d until weaned with 8 wk. Colostrum feeding protocol affected the total serum protein concentration at the first 48 h of life ($P < 0.05$), whereas the concentrations of albumin, γ-glutamyl transferase, and alkaline phosphatase were not affected during the same period ($P > 0.05$). Colostrum feeding protocol did not affect the fecal score, the number of days with diarrhea, days with fever, and days of needed rehydration ($P > 0.05$); however, animals that received high-quality colostrum were treated for a shorter number of days ($P < 0.05$). The concentrate intake and total DMI were not affected by colostrum supplement ($P > 0.05$) and increased over the weeks ($P < 0.0001$). Body weight, weight gain, feed efficiency, and growth measures were not affected by supplement ($P > 0.05$), although there was an age effect ($P < 0.0001$). The total serum protein concentration during the liquid-feeding phase was higher for animals receiving high-quality colostrum when compared with animals receiving medium-quality colostrum ($P < 0.05$). However, concentrations of albumin, glucose, and β-hydroxybutyrate were not affected ($P > 0.05$). Feeding the colostrum supplement associated with the medium-quality maternal colostrum did not affect the transfer of passive immunity, performance, or metabolism of animals during the liquid-feeding phase.

Key Words: blood parameters, colostrum supply, diarrhea, immunity, immunoglobulin Y

1465 Thermoregulation, performance, and blood metabolites in calves fed different amounts of colostrum. F. L. M. Silva*, M. D. Silva, E. Miqueo, N. B. Rocha, T. Manzoni, M. G. Coelho, and C. M. M. Bittar, *University of Sao Paulo, Piracicaba, Brazil*.

Colostrum is an important immunity supply that protects calves against infectious diseases. Additionally, colostrum is an excellent energy source for thermogenesis for the newborn calf. However, the amount of colostrum required to promote heat is not well established. The objective of this study was to evaluate the newborn thermoregulation, performance, and blood metabolites in calves fed different amounts of colostrum. Thirty newborn Holstein male calves were blocked by birth weight (BW) in a randomized experimental design and fed high-quality colostrum in 3 different volumes: 10, 15, and 20% of BW. The colostrum intake occurred immediately after birth and 6 h after the first colostrum feed, totaling the treatment. At 24 h of life, each calf was placed in a temperature-controlled chamber at 10°C, for 150 min. Rectal temperature, skin surfaces temperatures, heart and respiratory frequency, and shivering were measured every 15 min, and blood samples were taken every 30 min. After challenge, calves were individually housed, with free access to water and starter concentrate (20% CP and 80% TDN), and received 6 L/d of milk replacer (Sucelac; Agroceres; 21.6:15.5 and 12.5% solids) until the eighth week of life, when weaned. Data were analyzed as repeated measures over time by using the MIXED procedure (SAS Inst. Inc.). Feeding colostrum to newborn at 15 or 20% of their BW tended to increase ($P = 0.06$) the rectal temperature during cold challenge (37.7, 38.1, and 38.0°C). However, there were no effects on skin surfaces temperatures ($P > 0.05$). During challenge, feeding higher volumes of colostrum did not affect blood metabolites but tended to decrease ($P = 0.07$) plasma lactate concentration (46.7, 45.0, and 34.6 mg/dL). There was no difference ($P > 0.05$) among colostrum volume for shivering behavior. Concerning performance, there were no effects on growth ($P > 0.05$), but feeding colostrum at 15 or 20% of their BW increased ($P \leq 0.05$) heart girth (84.1, 86.9, and 86.6 cm). There were no effects ($P > 0.05$) on DMI and blood metabolites. As animals were growing, all parameters were significantly affected by age ($P \leq 0.05$); however, there were no treatment and age interaction effect ($P > 0.05$). Feeding newborn calves colostrum at 15 or 20% of their BW can increase thermoregulatory responses in newborns and improve some growing features during the liquid-feeding period. Supported by FAPESP.

Key Words: blood parameters, cold challenge, weight gain

1466 The effects of supplementing a ruminally protected B-vitamin complex on preweaning growth and performance of Holstein heifer calves. K. M. Wood*[1], E. Evans[2], C. L. Girard[3], H. Leclerc[4], L. Doepel[5], and G. B. Penner[6], *[1]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada, [2]Technical Advisory Services, Bowmanville, ON, Canada, [3]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [4]Jefo Nutrition, St. Hyacinthe, QC, Canada, [5]University of Calgary, Calgary, AB, Canada, [6]University of Saskatchewan, Saskatoon, SK, Canada*.

For preweaned dairy calves, incomplete rumen development may limit microbial B vitamin synthesis, resulting in a mild B-vitamin deficiency. Seventy Holstein heifer calves were used to evaluate the effect of providing a B-vitamin supplement in the starter on DMI, growth, and blood parameters. Calves were individually housed and fed in 1 of 3 rooms (block) until weaning at 9 wk of age. Dietary treatments were 13 g/d commercially available palmitic acid (CON; $n = 35$) or ruminally protected B vitamins (ProB; $n = 35$), in which 5 g of a B-vitamin supplement was blended with 8 g of palmitic acid. Treatments began at 1 wk of age. The 13 g of supplement was mixed with 50 g of calf starter and fed once per day. Once the calves consumed the supplement, they were offered calf starter ad libitum. Heifers were also fed 600 g of milk replacer (150 g/L water) divided into 2 feedings. After 7 wk, milk replacer was reduced to 300 g/d and calves were weaned at the end of wk 9. Calf BW and hip and rump height were measured on a weekly basis. Blood samples were collected on d 2 and 63 and analyzed for total protein concentration and platelet, white blood cell (WBC), and red blood cell (RBC) counts. Data were analyzed as a completely randomized block design with the mixed model using fixed effects of block, treatment, time, and their interaction. Regression was used to calculate growth traits. Calf ADG was 0.71 kg/d for both treatments (SEM = 0.017, $P = 0.84$). Hip and wither heights and ADG did not differ ($P \geq 0.77$) between treatments. There were no treatment differences ($P = 0.94$) for supplement intake or total DMI (CON = 933.8 kg/d and ProB = 967.2 kg/d; SEM = 40.5, $P = 0.56$). Final blood platelet count was 484.3×10^9/L for CON and 551.5×10^9/L for ProB (SEM = 22.5) and was greater in ProB than in CON ($P = 0.035$); however, final WBC and RBC did not differ ($P \geq 0.23$). These data indicate that supplemental ruminally protected B vitamins do not affect preweaning calf growth. However, supplementation may have implications on immune function, which may have implications for overall calf health.

Key Words: B vitamins, calf, preweaning

1467 RNaseq-based whole transcriptome analysis in the jejunum of preweaned calves under different milk feeding regimes. H. M. Hammon[1], D. Frieten[2], C. Gerbert[3], C. Koch[3], G. Dusel[2], R. Weikard[1], and C. Kühn*[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]University of Applied Sciences, Bingen, Germany, [3]Educational and Research Centre for Animal Husbandry, Hofgut Neumuehle, Muenchweiler, Germany*.

An early dietary nutrition plan in calves is crucial for later appropriate heifer and cow performance. However, there is controversy about the appropriate milk supply during the first weeks of life. Currently, there is only limited knowledge about the genomewide expression pattern for the juvenile intestine. Therefore, we performed a next-generation-sequencing–based holistic whole transcriptome analysis of the jejunum in male German Holstein calves fed two different diets. Calves received colostrum for 3 d and then milk replacer (MR; 125 g powder/L). For one group of calves, MR was restricted to a volume of 6 L MR ($n = 6$), whereas the alternative group was fed on an ad libitum protocol for 8 wk ($n = 6$). Subsequently, MR intake for all calves was reduced to 2 L/d from wk 8 to 10 and maintained at this level until the end of the trial. During the entire experiment, both groups were provided hay and concentrate ad libitum. Eighty-one days after birth, the calves were euthanized, and epithelial sections of the jejunum were collected, snap frozen in liquid nitrogen, and stored at −80°C until further analyses. Total RNA was isolated with specific attention to avoid genomic DNA contamination. For each sample, an indexed, stranded sequencing library was prepared including a polyA bead-based selection step. Libraries were sequenced in a 2 × 80 bp paired-end protocol on an Illumina HiSeq2500. After demultiplexing, reads were trimmed for quality and adaptor sequences. The reads passing quality control were aligned to the bovine genome, and transcripts were assembled with an annotation-guided approach enabling discovery of yet-unannotated genes and transcripts. Differential expression between calf groups was analyzed based on expression normalized on total number of reads and length of the respective genes. On average, 56.8 million paired-end reads were obtained per sample, and the average percentage of reads mapping to the bovine genome was 88%. Between 18,395 and 20,904 genes per sample could be identified after applying a threshold of 10 read counts per gene. The number of novel transcripts amounted to 16,378. Applying a threshold of $q < 0.1$, which accounted for multiple testing, 99 genes showed a differential expression between groups. Among those, 22 were without previous annotation in the bovine genome. Our analyses provide the first comprehensive catalog of RNaseq-based whole transcriptome for the calf jejunum. Furthermore, our data prove persistent effects of differential milk diets on the jejunal gene expression pattern.

Key Words: calves, milk feeding, trancriptome

1468 Comparison of two calf-rearing programs on the performance and cost–benefit ratio. L. M. Gomez*, J. A. Henao, A. K. Amorocho, M. R. Valenzuela, C. Mesa, and P. Aguirre, *Nutri-Solla Group, Research and Development Unit, Solla S.A., Medellin, Colombia*.

There is a deep interest in assessing different kinds of calf rearing programs based on greater rates of liquid feeding to increase ADG and to decrease age at first calving. In a complete randomized design with repeated measures, two milk feeding plans (treatments) were evaluated in 57 Holstein female dairy calves (37.3 ± 3.7 kg BW and 3 d old) during 10 wk. Treatment 1 (T1) consisted of feeding 12% of weight at 3 d in whole milk and treatment 2 (T2) a consisted of a step-down program of 20 (from 0 d to 2 wk), 15 (3–4 wk), and 10% (5–10 wk) of weight at 3 d in whole milk. Calves were fed colostrum (IgG; 100 mg/mL) at 30 min of life and after that, they were left with the cow suckling ad libitum until 3 d of life without access to solid feed. Calves were housed in individual hutches with ad libitum access to T1 ($n = 28$) and T2 ($n = 29$). From the third day, calves were offered pelleted starter feed (173.1 g CP, 460.1 g NSC, and 201 g NDF per kilogram DM) in the morning at 0700 h. Water was offered ad libitum. The calves were weaned when the intake of the starter feed was over 1.000 g/d during three consecutive days, from Day 1 to 4 after weaning half of the milk amount was given and since 5 d without milk. Body weight, DMI, ADG, days to weaning (DW), feed:gain ratio, total protein and energy intake, chest girth (CG), height at withers (HW), height at sacrum (HS), and total cost of production were measured. No differences were found ($P > 0.05$) on BW, CG, and HW and HS changes during the 10 wk among treatments. At the end of the trial, no differences were detected ($P > 0.05$) in BW, ADG, DW, concentrate DMI and feed:gain ratio, CG, and HW and HS. Calves fed T2 tended ($P = 0.11$) to have greater total DMI and protein DMI (79.6 and 19 kg) than calves fed T1 (73.7 kg and 17.6 kg). Calves fed T2 had greater ($P < 0.05$) milk DMI, ME of DMI, and cost of production (33.3 kg, 341.5 Mcal, and 105.4 USD) than calves fed T1 (28.7 kg, 312.2 Mcal, and 93 USD). Feeding with a step-down program having more milk does not support improvements of performance and increases the average cost of production.

Key Words: calves, cost–benefit ratio, performance, weaning

Table 1469.

Table 1. Growth performance, ruminal fermentation, and digestibility of weaned calves feeding different forage combination

Items	AH	OH	WS	Items	AH	OH	WS
Growth performance				Ruminal fermentation			
DMI, kg/d	2.78	2.75	2.91	Acetate acid, %	64.95	64.99	65.69
Body weight, kg	112.51^{a}	114.61^{a}	109.65^{b}	Propionate acid, %	20.45^{b}	19.55^{c}	21.76^{a}
ADG, kg/d	0.93^{a}	1.00^{a}	0.89^{b}	Butyric acid, %	6.92^{b}	7.38^{a}	4.97^{c}
G/F, %	33.45	36.36	30.58	Acetate/propionate	3.18^{b}	3.33^{a}	3.02^{c}
Heart girth, cm	11.73^{b}	12.83^{a}	11.80^{b}	TVFA, mmol/L	60.97^{b}	64.95^{a}	48.39^{c}
Digestibility				Protozoal protein, mg/Ml	2.35^{a}	2.54^{a}	2.03^{b}
CP digestibility, %	71.29^{b}	73.00^{a}	69.95^{c}	Bacterial protein, mg/Ml	2.00^{ab}	2.08^{a}	1.92^{b}
P digestibility, %	69.56^{ab}	70.95^{a}	66.98^{b}	Microprotein, mg/mL	4.35^{a}	4.62^{a}	3.96^{b}
Diarrhea frequency, %	25.90	12.76	20.57				
Diarrhea rate, %	45.33	21.33	33.33				
Feces index	1.89	1.45	1.63				

AH – 100% alfalfa hay, OH – 66.7% alfalfa hay + 33.3% oat hay, WS – 66.7% alfalfa hay + 33.3% whole corn silage.

a, b – different superscript letters with the same row represent a significant difference between treatments (P<0.05).

1469 Effects of different forage combination on growth performance, ruminal fermentation, and digestibility of weaned calves. Y. Zou*, X. Zou, Z. J. Cao, Y. Wang, and S. L. Li, *State Key Laboratory of Animal Nutrition, Beijing Engineering Technology Research Center of Raw Milk Quality and Safety Control, College of Animal Science and Technology, China Agricultural University, Beijing, P. R. China*.

The effects of feeding different forage combinations on growth performance, ruminal fermentation, and digestibility were investigated in weaned calves for 35 d. Forty-five female calves weaned at 60 d with similar weight were randomly arranged into three treatments 1 wk after weaning with same pellet feed (60% of the diet); forage combinations were 1) 100% alfalfa hay (AH), 2) 66.7% alfalfa hay + 33.3% oat hay (OH), and 3) 66.7% alfalfa hay + 33.3% whole corn silage (WS). There was no significant difference (P > 0.05) among the three treatments with weaned calves in DMI. However, the BW and ADG of calves fed AH and OH were significantly higher (P < 0.05) than WS calves, with higher heart girth in OH calves (P < 0.05). Proportion of butyric acid, ratio of acetate to propionate, total VFA concentration, protozoal protein, bacterial protein, and microprotein in rumen were highest in OH (P < 0.05), AH was intermediate, and WS was lowest. Oat hay feeding increased CP and P digestibility (P < 0.05) and decreased diarrhea frequency, diarrhea rate, and feces index at the mean time. In conclusion, a forage combination of alfalfa hay and oat hay had certain advantages to promote the ruminal development of calves and reduce feed cost and diarrhea incidence. Based on this study, a feeding pattern of "26.67% alfalfa hay + 12.33% oat hay + 60% starter feed" is more suitable for 3-mo weaned calves.

Key Words: oat hay, ruminal fermentation, weaned calves

1470 Use of the Brix refractometer to evaluate milk replacer solutions for calves. H. K. Floren*[1], W. M. Sischo[1], C. Crudo[1], and D. A. Moore[2], *[1]Washington State University, Pullman, [2]Department of Veterinary Clinical Sciences, Washington State University, Pullman, WA*.

The Brix refractometer is used on dairy farms and calf ranches for several reasons including evaluation of colostrum quality (estimation of IgG concentration), estimation of serum IgG concentration in neonatal calves, and nonsalable milk evaluation of total solids for calf nutrition. Another potential use is to estimate the total solids concentrations of milk replacer mixes as an aid in monitoring feeding consistency. The purpose of this study was to evaluate the use of Brix refractometers to estimate total solids in milk replacer solutions. Five different milk replacer powders were mixed to achieve total solids concentrations from approximately 5.5 to 18%, for a total of 90 different solutions. Both digital and optical Brix refractometers were used to compare with total solids. The two types of refractometers' readings correlated well with one another (R^2 = 0.997). The Brix readings were highly correlated with the total solids percentage (R^2 = 0.94). A value of approximately 1.08 to 1.47 would need to be added to the Brix reading to estimate the total solids in the milk replacer mixes. Osmolality was correlated to the Brix reading but the relationship was different depending on the type of milk replacer. The Brix refractometer can be successfully used to estimate total solids concentration in milk replacer mixes to help monitor milk replacer feeding consistency.

Key Words: calf, milk replacer, refractometer

1471 Effect of corn wet distillers' grains inclusion in growing diets on backgrounded cattle performance. M. Arcieri*[1], P. Davies[2], D. Méndez[2], J. Elizalde[3], and I. Ceconi[2], *[1]Universidad Nacional de Córdoba, Córdoba, Argentina, [2]Instituto Nacional de Tecnología Agropecuaria, General Villegas, Argentina, [3]Private consultant, Rosario, Argentina*.

Distillers' grains (DG) can be used as energy as well as protein dietary sources. An experiment was conducted to evaluate the effect of partially replacing dry-rolled corn (DRC) and sunflower meal (SFM) with corn wet DG (WDG) in growing diets on cattle performance. One hundred ninety-two Angus calves (199 ± 3 kg initial BW) were assigned by weight to 1 of 3 blocks and group housed in 1 of 24 pens. Pens were randomly assigned to 1 of 4 diets containing (DM basis) 0% WDG, 19.4% DRC, and 20.4% SFM (CON); 10.0% WDG, 13.9% DRC, and 15.9% SFM (10-DG); 20.0% WDG, 8.0% DRC, and 11.8% SFM (20-DG); or 35.0% WDG, 0% DRC, and 4.8% SFM (35-DG). All diets contained 58.2% sorghum-sudangrass silage and 2.0% dry supplement. Diets were formulated to generate a RDP balance equal to zero and to meet or exceed MP requirements at expected ad libitum DMI and ADG. Dietary CP and lipid concentrations and IVDMD measured 12.0, 2.97, and 66.3%; 13.5, 4.00, and 66.8%; 15.1, 5.04, and 67.3%; and 17.3, 6.61, and 68.2% for CON, 10-DG, 20-DG, and 35-DG, respectively. Calves were fed once daily for 85 d and held off feed for 16 h to record initial and final individual BW. Data were analyzed as a generalized randomized complete block design. Cattle ADG was greater ($P < 0.01$) for calves fed the 20-DG diet (913 ± 20 g) compared with those fed the CON (682 ± 20 g) or 10-DG (829 ± 20 g) diets, although it was similar ($P = 0.93$) to those fed the 35-DG (915 ± 20 g) diet. Conversely, DMI was similar ($P > 0.65$) between cattle fed the CON (6.01 ± 0.27 kg/d), 10-DG (5.97 ± 0.27 kg/d), and 20-DG (5.93 kg/d) diets and smaller ($P < 0.01$) compared with cattle fed the 35-DG (5.41 ± 0.27 kg/d) diet. Consequently, G:F improved ($P < 0.01$) with increasing WDG dietary inclusion (114.4, 139.5, 154.2, and 169.6 ± 6.7 for CON, 10-DG, 20-DG, and 35-DG, respectively). Greatest lipid concentration in the 35-DG diet may have decreased fiber digestibility, which, in turn, could relate to reduced DMI. Additionally, ADG quadratic response ($P < 0.01$) may have resulted from greater NEg concentration and from DMI quadratic response ($P < 0.01$) with increasing WDG dietary inclusion. Including 35% WDG in a silage-based diet resulted in greatest G:F and growing-according ADG.

Key Words: backgrounding, cattle performance, distillers' grains

1472 Effects of *Saccharomyces cerevisiae* fermentation products on intestinal villi integrity in neonatal calves naturally infected with *Cryptosporidium* spp. S. Vázquez Flores[1], M. de Jesús Guerrero Carrillo[2], M. F. Scott[3], J. Hamann*[3], S. Barrera Almanza[1], C. Guizar Bravo[1], A. Patricia Baños Quintana[1], and P. Jazmin Aranda Vargasb[2], *[1]ESIABA-Tecnológico de Monterrey-Campus Querétaro, Querétaro, Mexico, [2]Facultad de Ciencias Naturales, Universidad Autónoma de Querétaro, Querétaro, Mexico, [3]Diamond V, Cedar Rapids, IA*.

The objective of this study was to characterize the integrity of intestinal villi in neonatal bull calves naturally infected with *Cryptosporidium* spp. This study took place on a commercial dairy near Querétaro, México (1,100 cows in production). At birth, all calves received a colostrum substitute and were randomly allocated to one of three treatments: maltodextrin (placebo control [C]), SmartCare + Original XPC (T1), or Biomos (T2). All calves showed satisfactory levels of serum IgG as determined by a commercial serum radio-diffusion kit (C = 1,367.5 ± 292.1, T1 = 1,492.3 ± 48.2, and T2 = 1,572.8 ± 106.5). Calves were then given UV-purified whole milk and calf starter until d 28. On d 28, all calves were humanely sacrificed within the university premises for postmortem analysis and intestinal sample collection (duodenum, jejunum, and ileum). All samples were formalin fixed, and the histopathological smears were stained with hematoxylin–eosin. Villi scores (length and width) were measured twice by 2 different trained analysts using 10 fields per smear with an optic microscope (40x). Oocyst concentration was made using a modified concentration technique (Arrowood, 1987), with Sheather's solution at 1.12 specific gravity, in fecal samples collected on d 0, 7, 10, 14, and 28. Villi integrity was characterized as normal, fragmented, atrophied, or blunt. Statistical analysis was performed using parametric (Hsu's MCB) and nonparametric (Wilcoxon) analyses in JMP 11.1.0. In general, the number of intestinal villi per field varied from 10.1 to 12.5. There were no differences in duodenal villi scores between treatments. Villi were less ($P < 0.05$) fragmented and atrophied for T1 compared with C and T2 in the jejunum and ileum. Compared with C, T1 and T2 had larger ($P < 0.001$) crypts present in the ileum. *Cryptosporidium* spp. was present in 100% of the bull calves and ranged in concentration from 8×10^4 to 4×10^9 oocysts/mL. The use of *Saccharomyces cerevisiae* fermentation products shows promising results in maintaining intestinal villi integrity in spite of the protozoan infection

Key Words: intestinal villi integrity, neonatal calves, *Saccharomyces cerevisiae* fermentation product

1473 Evaluation of Brix refractometer to assess immunoglobulin G concentration of first and second colostrum from Jersey cows. D. Rolle, S. Rodríguez, A. Valldecabres, and N. Silva-del-Rio*, *Veterinary Medicine Teaching and Research Center, University of California Davis, Tulare*.

The objective of this study was to evaluate if concentration of IgG in first and second colostrum from Jersey cows may be estimated using Brix refractometry on farm. Colostrum samples and total weight of first (n = 136) and second (n = 70) milking after calving were collected from multiparous Jersey cows on a 3,500-cow California herd. The first colostrum was collected at 9.4 ± 3.8 h after calving and the second colostrum at 21.0 ± 3.7 h after calving. Fresh colostrum samples were evaluated for Brix percentage by using a handheld electronic refractometer (Reichert Inc., Depew, NY). Colostrum samples were aliquoted in 2-mL vials and frozen before IgG analysis by radial immunodiffusion (RID). The association between Brix percentage and IgG concentration was evaluated with the CORR procedure of SAS. The GLM procedure of SAS was used to describe the regression equation between Brix percentage and IgG concentration. Observations above the maximum Brix reading (>32%) were removed. Concentration of IgG was higher (P < 0.001) for first colostrum, averaging 83.8 g/L (range: 23.7 to 172.9 g/L), than for second colostrum at 46.9 g/L (6.2 to 100 g/L). Similarly, Brix percentage was higher (P < 0.001) for first colostrum, with an average of 25.4% (range: 16.2 to 37.1%), than for second colostrum with an average of 18.4% (range: 13.1 to 29.1%). Readings of Brix percentage were highly correlated with concentration of IgG in first (r = 0.81) and second (r = 0.77) colostrum. Harvested colostrum weighed 3.9 ± 2.6 kg at first milking and 4.2 ± 2.1 kg at second milking. Based on the regression equation, the most adequate Brix percentage cut points to define colostrum quality (50 g of IgG/L) were 19.1 and 18.7% for first and second colostrum, respectively. For first colostrum, sensitivity of Brix refractometer was 96.1%, specificity was 60.0%, and positive and negative predictive values were 96.8 and 54.5%, respectively. For second colostrum, sensitivity of Brix refractometer was 78.6%, specificity was 79.5%, and positive and negative predictive values were 73.3 and 83.7%, respectively. Our results indicate that Brix measurements can be used to rapidly estimate IgG concentration on first and second milking colostrum from Jersey cows. To identify colostrum samples with >50 IgG g/L, the most adequate cut point was slightly inferior to the 21% Brix reading that previous studies suggested.

Key Words: Brix refractometer, colostrum immunoglobulin G, Jersey cow

1474 Effects of lactose inclusion in calf starters on starter intake, growth performance, and digestive organ development. K. Inouchi*[1], A. Saegusa[2], Y. Inabu[3], T. Sugino[3], and M. Oba[4], *[1]ZEN-RAKU-REN, Nishi-shirakawa, Japan, [2]ZEN-RAKU-REN, Fukushima, Japan, [3]Hiroshima University, Higashi-hiroshima, Japan, [4]University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to evaluate the effects of lactose inclusion in calf starters on starter intake, growth performance, and digestive organ development. Sixty Holstein bull calves were raised on an intensified nursing program using milk replacer containing 28% CP and 15% fat and fed the texturized calf starter containing lactose at 0 (Control), 5.0 (LAC5), or 10.0% on a DM basis (LAC10; n = 20 for each treatment). All calf starters were formulated for 23.1% CP. As the pellet portion contained lactose and all adjusted ingredients, treatment calf starters differed only in the pellet. Ethanol soluble carbohydrate concentrations of Control, LAC5, and LAC10 were 7.3, 12.3, and 16.8% (DM), respectively. Starch concentrations of Control, LAC5, and LAC10 were 29.7, 27.0, and 21.4% (DM), respectively. All calves were fed treatment calf starters ad libitum, and their hay intake was limited to 150 g/d. Body weight, hip height, withers height, body length, hip width, and heart girth were measured weekly. Fifteen calves were killed at the age of 62 d, and 45 calves were killed at the age of 80 d. Digestive organs were harvested, emptied, rinsed and weighed. Starter DMI intake was 267 ± 45 (Control; mean ± SE), 216 ± 20 (LAC5), and 283 ± 31 g/d (LAC10) before weaning (d 7–56); 1,516 ± 156 (Control), 1,344 ± 105 (LAC5), and 1,622 ± 127 g/d (LAC10) during weaning transition (d 49–63); and 2,778 ± 164 (Control), 2,636 ± 109 (LAC5), and 2,812 ± 164 g/d (LAC10) after weaning (d 56–80). Average daily gain was 0.64 ± 0.03 (Control), 0.64 ± 0.03 (LAC5), and 0.71 ± 0.34 kg/d (LAC10) before weaning (d 7–56); 1.02 ± 0.76 (Control), 1.03 ± 0.08 (LAC5), and 1.17 ± 0.08 kg/d (LAC10) during weaning transition (d 49–63); and 1.41 ± 0.06 (Control), 1.40 ± 0.06 (LAC5), and 1.34 ± 0.06 kg/d (LAC10) after weaning (d 56–80). Wet mass of the reticulorumen was 1.37 ± 0.14 (Control), 1.49 ± 0.04 (LAC5), and 1.60 ± 0.09% BW (LAC10) at d 62 and 2.21 ± 0.08 (Control), 2.03 ± 0.07 (LAC5), and 1.97 ± 0.16% BW (LAC10) at d 80. None of the response variables above were significantly different (P > 0.05). In addition, treatments did not affect (P > 0.05) the other primary response variables including body height, body length, heart girth, and wet mass of the other digestive organs. These results indicate that inclusion of lactose in calf starters up to 10% of DM may not affect starter intake, growth performance, and digestive organ development.

Key Words: calf, lactose, starter

1475 Bioavailability of different sources of zinc using stable isotopes in male Holstein calves.

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Trace minerals are an important component of ruminant nutrition. Furthermore, understanding the bioavailability of various trace mineral sources is essential for accurate dietary formulation. The objective of this trial was to determine bioavailability of Zn when provided in either an inorganic or an organic form. Sixteen weaned male Holstein calves (BW = 60 ± 2 kg [mean ± SE]) were used in a randomized compete block design. Calves were individually fed a common texturized starter formulated to meet NRC nutrient requirements. Calves were orally administered 4 or 8 mg of Zn from 2 sources: ^{67}Zn oxide and ^{70}Zn-methionine hydroxy analog chelate (^{70}Zn-MHAC). Blood was collected via catheters before isotope administration and 0.25, 0.5, 0.75, 1, 2, 4, 6, 8, 10, 12, 16, 20, 24, 36, 48, and 72 h after isotope administration for determination of isotope enrichment. Calves were euthanized 72 h after isotope administration, and target tissues were weighed and sampled for determination of isotope enrichment. Plasma area under the curve (AUC) for isotope enrichment was significantly ($P < 0.01$) greater with ^{70}Zn-MHAC (2.02 ± 0.12 ppm) compared with ^{67}Zn oxide (1.20 ± 0.12 ppm). When dose was considered, plasma AUC for isotope enrichment was significantly ($P < 0.01$) greater with 8 mg of labeled Zn (2.34 ± 0.12 ppm) compared with 4 mg (0.87 ± 0.12 ppm). Isotope enrichment was significantly ($P < 0.01$) greater with ^{70}Zn-MHAC compared with ^{67}Zn oxide for all tissues with the exception of omasal tissue, which tended ($P = 0.07$) to be greater. When dose was considered, isotope enrichment was significantly ($P < 0.01$) greater with 8 mg of labeled Zn compared with 4 mg for all tissues except muscle ($P = 0.17$) and tibia ($P = 0.42$). The slope for ^{70}Zn-MHAC was significantly ($P \leq 0.01$) higher compared with that of ^{67}Zn oxide for abomasal tissue (0.036 vs. 0.011; $r^2 = 0.88$), duodenal tissue (0.070 vs. 0.043; $r^2 = 0.90$), ileal tissue (0.069 vs. 0.028; $r^2 = 0.95$), jejunal tissue (0.072 vs. 0.024; $r^2 = 0.93$), liver (0.096 vs. 0.012; $r^2 = 0.83$), muscle (0.016 vs. −0.031; $r^2 = 0.89$), pancreas (0.076 vs. 0.003; $r^2 = 0.82$), thymus (0.023 vs. −0.003; $r^2 = 0.85$), and tibia (0.007 vs. −0.003; $r^2 = 0.86$). Together these data demonstrates using stable isotopes as a valid technique to measure bioavailability and greater bioavailability was observed from Zn-MHAC when compared with zinc oxide.

Key Words: bioavailability, stable isotopes, zinc

1476 Endocannabinoid concentrations in plasma associated with feed efficiency and carcass composition on crossbreed steers.

V. M. Artegoitia*[1], A. P. Foote[2], R. M. Lewis[3], D. A. King[2], S. D. Shackelford[2], T. L. Wheeler[2], and H. C. Freetly[2], *[1]University of Nebraska, Lincoln, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [3]University of Nebraska-Lincoln, Lincoln*.

Endocannabinoids, including anandamide (AEA) and 2-arachidonoylglycerol (2-AG), are a class of endogenous lipid mediators that activate cannabinoids receptors and may be involved in the control of feed intake and energy metabolism. The objective of this study was to quantify AEA and 2-AG in plasma and identify possible associations with production traits and carcass composition in finishing beef steers. Individual DMI and BW gain was measured on 140 crossbred steers for 105 d on a finishing ration. Blood samples were collected on d 84 of the experiment, which was 40 d before slaughter. Variables were analyzed using Pearson CORR procedure of SAS. Mean endocannabinoid concentrations in plasma were 4.48 ± 1.82 and 0.43 ± 0.24 ng/mL for AEA and 2-AG, respectively. The AEA concentration was positively correlated with G:F ($r = 0.20$, $P = 0.02$), indicating that more efficient animals were correlated with higher AEA plasma concentration. Nevertheless, AEA concentration was negatively correlated with metabolic BW at the midpoint of the experiment ($r = −15$, $P = 0.07$) and initial BW ($r = −0.19$, $P = 0.03$). In addition, AEA concentration was negatively correlated with the 12th rib fat thickness ($r = 0.17$, $P = 0.07$), but no correlation was found with USDA-calculated yield grade ($r = −0.14$, $P = 0.11$) or marbling score ($r = 0.05$, $P = 0.54$). The concentration of 2-AG was positively correlated with AEA ($r = 0.21$, $P = 0.01$); however, 2-AG concentration was not correlated with parameters of feed efficiency or carcass composition. In summary, the present study is the first to report plasma concentration of endocannabinoids in steers. These results provide evidence that plasma concentration of a key endocannabinoid, AEA, was favorably correlated with feed efficiency and fat thickness on crossbred steers at finishing. The USDA is an equal opportunity provider and employer.

Key Words: anandamide, 2-arachidonoylglycerol, ultra-performance liquid chromatography tandem mass spectrometry

1477 The phenotypic relationship between residual feed intake and ultrasound carcass traits in Santa Gertrudis steers. C. R. Branton*, *Stephen F. Austin State University, Nacogdoches, TX*.

Numerous studies have been conducted characterizing phenotypic and genetic variation in RFI in beef cattle, but limited studies have examined effects of diet and/or stage of maturity on phenotypic reranking of cattle for feed efficiency traits. For this study, 2 trials were conducted with Santa Gertrudis steers (N = 233). Steers were fed a roughage-based diet (2.1 Mcal ME/kg DM) during the growing phase and a high-grain diet (3.0 Mcal ME/kg DM) during the finishing phase. Steers were weighed at 14-d intervals and DMI was measured (Calan gate or GrowSafe) for 70 d during both the growing and finishing phases, with ultrasound measurements obtained on Day 70 of each feeding phase. RFIp was calculated as the difference between actual DMI and expected DMI based on regression of DMI on ADG and mid-test $BW^{0.75}$. Stepwise regression revealed that final back fat depth (BF) accounted for additional variation in RFI in both the growing (R^2 = 0.43 vs. 0.46) and finishing (R^2 = 0.54 vs. 0.56) phases. Therefore, RFIc was computed for both phases based on regression of DMI on ADG, mid-test $BW^{0.75}$, and final BF depth. During the growing phase, RFI_p was positively correlated ($P < 0.01$) with DMI (0.75), feed:gain ratio (0.49), and final BF depth (0.13) but not with ADG or BW. Feed:gain ratio was negatively correlated ($P < 0.01$) with ADG (−0.70) but was not correlated with DMI. During the finishing phase, RFI_p was positively correlated ($P < 0.01$) with DMI (0.65), feed:gain ratio (0.51), and final BF depth (0.17) but not with ADG or BW. Feed:gain ratio was negatively correlated ($P < 0.01$) with ADG (−0.69) but was not correlated with DMI. Correlations between RFIp and RFIc were 0.91 and 0.92 during the growing and finishing phases, respectively. Spearman rank correlations revealed that ADG and feed:gain ratio measured during the growing phase were weakly associated with ADG (0.21) and feed:gain ratio (0.12) measured during the finishing phase, whereas rank correlations were moderate for DMI (0.47), RFIp (0.45), and RFIc (0.28) measured during the growing and finishing phases. Although these results indicate that a moderately positive rank correlation exists between RFI measured when steers are fed high-roughage vs. high-grain diets, these two feed efficiency traits may not be biologically similar. It is unclear as to whether the lack of a strong correlation between RFI measured during growing vs. finishing phases was due to influences of diet and/or stage of maturity.

Key Words: carcass composition, residual feed intake, Santa Gertrudis steer

1478 Using indigestible rare earth markers and internal markers to predict dry matter intake and residual feed intake. K. A. Weld* and L. E. Armentano, *University of Wisconsin – Madison, Madison*.

Residual feed intake (RFI) is a feed efficiency measure that requires multiple animal individual intakes. The objective of this trial was to determine the plausibility of using a known daily dose of a rare earth marker combined with an inherent, internal total mixed ration (TMR) indigestible component and spot fecal sampling to predict DMI and RFI of lactating dairy cattle. Fifteen lactating Holstein cows (107 ± 20 d in milk) were maintained on a single diet for 5 wk in tie stalls. Milk production and DMI were recorded daily, and milk samples and BW were taken weekly. Indigestible rare earth markers were administered orally by 3 methods: once daily by bolus (ytterbium), once daily by top-dressing TMR (samarium), or twice daily by bolus (lanthanum). Cows received all external rare earth markers the last 10 d of the trial with the final 3 d being used to collect 10 fecal samples. Fecal samples were composited and analyzed for concentrations of rare earths by inductively coupled plasma mass spectrometry (CV mean ± SD: 3.8 ± 1.7) and indigestible NDF (CV: 3.6 ± 4.3) and indigestible DM (CV: 5.4 ± 4.6) using a 288-h in situ incubation. Combining one of the three rare earth external markers with one of the two diet internal markers allows prediction of DMI and RFI as a 3 × 2 factorial. There was a significant correlation between measured DMI in the final week and DMI predicted using 1x bolusing ($r > 0.60$, $P < 0.02$) but not using top-dressing ($r > 0.42$, $P > 0.08$) or 2x bolusing ($r = 0.33$, $P = 0.22$). Phenotypic RFI was calculated as the difference between individual cow DMI and regression estimated DMI where the regression included $BW^{0.75}$, BW change (deltaBW; BW in kg), and milk energy (Mcal). Individual regressions were calculated for measured DMI and the 6 marker predicted DMI. The solutions from these regressions differed: (coefficient [±SE]; 5 wk of intakes: DMI = 0.50 (±0.10) × milk energy + 0.57 (±0.04) × $BW^{0.75}$ − 0.28 (±0.45) × deltaBW − 1.51 (±7.56); 1 wk intakes: DMI = 0.39 (±0.09) × milk energy + 0.11 (±0.03) × $BW^{0.75}$ − 0.37 (±0.39) × deltaBW − 11.47 (±6.51); and predicted DMI 1x/iNDF: DMI = 0.53 (±0.12) × milk energy − 0.07 (±0.05) − $BW^{0.75}$ + 1.48 (±0.55) × deltaBW + 23.57 (±9.27)).There was a correlation between the RFI calculated from the actual DMI in the last week and the RFI calculated from 5 wk of data ($r = 0.61$, $P < 0.05$).The actual RFI, from observed DMI of 5 wk or 7 d, were not correlated with the RFI calculated using the marker predicted DMI.

Key Words: digestibility marker, intake prediction, residual feed intake

Table 1479.

Item	Equation	R^2	P
DMVI	4.6733 (STIR) + 4.7374	.7011	<.0001
DMD	6.6871 (STIR) + 401.52	.1292	= .003
DDMI	2.6198 (STIR) - 0.7004	.5301	<.0001

1479 Short-term intake technique to predict dry matter intake and digestibility in forages.
F. M. Ingentron[1,2], B. C. Lentz[1], N. P. Stritzler[1], C. N. Rabotnikof[1], M. Menghini[3,4], and H. M. Arelovich*[3,4,5], *[1]Fac. Agronomia, Universidad Nacional de La Pampa, Santa Rosa, Argentina, [2]CONICET, Santa Rosa, Argentina, [3]CIC, Bahia Blanca, Argentina, [4]Dto. Agronomia, Universidad Nacional del Sur, Bahia Blanca, Argentina, [5]CERZOS, Bahia Blanca, Argentina*.

The objective of this study was to evaluate short-term intake rate (STIR) to predict DM voluntary intake (DMVI) and digestibility (DMD) in rams when offered different grass species usually grazed in semiarid Argentina. The evaluated forages were 3 warm-season grasses—fingergrass (F; *Digitaria eriantha eriantha* cv. Irene), kleingrass (K; *Panicum coloratum* cv. Verde), and switchgrass (S; *Panicum virgatum* cv. Alamo)—at vegetative (ve) and deferred (d) stages plus 4 small grains—wheat (W; *Triticum aestivum*) oats (O; *Avena sativa*), rye (R; *Secale cereale*), and triticale (T)—and alfalfa hay (AH; control forage for STIR). In separate experiments, 6 Pampinta rams (56 kg mean BW) were individually fed indoors ad libitum each forage in 2 daily meals (1000 and 1600 h) for 7 d of adaptation plus 7 d of DMVI observations and total fecal collection in bags. Simultaneously, a different group of 6 rams of similar BW were used to measure STIR. This group was fed once daily at maintenance level with AH. After 4 h of fasting, the animals were allowed active consumption of each forage for a 4-min period, controlled by an independent observer standing by each ram. Both DMVI and STIR were determined by subtracting refused from offered DM. Dry matter digestibility was calculated from DMVI and feces output, and digestible DMI (DDMI) was computed as well. The range of variable means and SE across grass species were 21.2 ± 2.3 (Sd) to 127.7 ± 7.2 (O), 34.3 ± 5.8 (Sd) to 69.1 ± 2.4 (AH), and 7.7 ± 1.5 (Sd) to 63.5 ± 3.3 (AH) for DMVI (g/kg $W^{0.75}$ per day), DMD (%), and DDMI (g/kg $W^{0.75}$ per day), respectively. The association between STIR and the variables DMVI, DMD, and DDMI (n = 6 for each forage) was studied by regression against the mean STIR value. Linear regression equations describing these relationships are shown in the table. There is strong positive association between STIR and DMVI; however, when a quality factor, such as DMD alone or linked to DMVI, is included, the STIR prediction potential seems to become weaker. Other factors such as palatability and leaf:stem ratio may have an influence not determined by this study.

Key Words: intake prediction, forages, sheep

1480 Effects of a blend of essential oils on milk yield and feed efficiency of lactating cows.
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The objective of this study was to assess the effect on milk yield and feed efficiency of a combination of essential oils for lactating dairy cows. A 56-d experiment was conducted involving 40 Holstein cows (688 ± 87 kg BW, yield 29.1 ± 73.0, and 220 ± 5.2 DIM) and 2 treatments. The study followed a randomized complete block design and lasted 8 wk. Treatments were either no supplementation (Control) or a supplementation of 1 g/d of Agolin Ruminant (Agolin, Switzerland) (AGR). Agolin Ruminant is combination of microencapsulated essential oil compounds (containing coriander oil, geranylacetate, and eugenol). All cows were fed a common TMR containing 15.3% CP, 34.6% NDF, and 1.53 Mcal of ENl/kg that was delivered twice daily. Treatments were applied in the milking parlor using a precision feeding system. The control cows received 300 g of soybean meal at each milking, and AGL cows received 300 g of soybean meal containing 1.66 g/kg of Agolin Ruminant at each milking (twice daily). Individual milk production, milk composition, and feed intake were recorded daily, and feed efficiency was then calculated (as kg of milk/kg of DMI). Treatment was individually applied, and cow was the experimental unit (n = 20). Data were analyzed with a mixed-effects model with repeated measures. Cows on AGL produced more (P < 0.05) milk (31.1 ± 1.02 kg/d) between 25 and 56 d of study than Control cows (29.7 ± 1.02 kg/d), but overall, there were no differences between treatments in milk yield. Milk fat (3.90 ± 0.08%) and milk protein (3.94 ± 0.08%) were not affected by treatment. There were, overall, no differences in DMI (24.8 ± 0.67 kg/d) between treatments, but AGL cows tended (P = 0.06) to consume less feed (24.2 ± 0.94 kg/d) than Control cows (24.8 ± 0.94 kg/d) in several days during the last 23 d of study. As a result, feed efficiency was greater (P < 0.01) in AGL cows (1.33 ± 0.05) for most days after 33 d of study than in Control cows (1.25 ± 0.05). It is concluded that Agolin Ruminant increases milk production after about 3 wk of treatment, and because feed intake does not change or even tends to decrease, feed efficiency increases.

Key Words: essential oil, milk efficiency, yield

1481 Repeatability of feed efficiency in beef cattle offered grass silage and zero-grazed grass.
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The objective of the study was to examine the within-animal repeatability of intake, growth, and feed efficiency between two consecutive feeding periods in beef cattle fed grass silage followed by zero-grazed grass. One hundred eighty-three steers comprising 94 Charolais (CH) and 89 Holstein-Friesian (HF) were used. Individual DMI and growth were measured over two consecutive 70-d feeding phases. Each feeding phase was preceded by a dietary adaptation period. For phase 1, steers were offered first-harvest grass silage (DM 290 g/kg and DM digestibility 700 g/kg) ad libitum, and for phase 2, they were offered zero-grazed grass (DM 196 g/kg) ad libitum. The grass herbage was harvested (without chopping) twice daily from *Lolium perenne* dominant swards using a "zero-grazer." The residuals of the regression of DMI on ADG and mid-test metabolic BW, within each breed, were used to compute individual residual feed intake (RFI) coefficients for each feeding phase. Repeatability between the two feeding phases for ADG, DMI, G:F, and RFI was estimated using Pearson correlation coefficients. Mean BW (SD) and age (SD) at the start of phase 1 were 485 kg (38.0) and 373 d (18.0) and 401 kg (43.3) and 399 d (7.6) for CH and HF, respectively. Corresponding BW at the start of phase 2 were 519 (38.3) and 441 (39.2) kg. During phase 1, overall ADG, DMI, G:F, and RFI (SD) for CH were 0.40 kg (0.17), 6.5 kg/d (0.57), 0.06 kg BW gain/kg DM (0.03), and −0.01 kg DM/d (0.35). Corresponding values for HF were 0.46 (0.17), 7.1 (0.60), 0.07 (0.02), and −0.02 (0.48). For phase 2, respective values were 1.31 (0.19), 9.1 (0.55), 0.14 (0.02), and −0.03 (0.34) and 1.25 (0.22), 9.5 (0.56), 0.13 (0.02), and −0.02 (0.43). For CH, correlations between the two feeding phases for ADG, DMI, G:F, and RFI were $r = 0.13$ ($P > 0.05$), $r = 0.70$ ($P < 0.001$), $r = 0.07$ ($P > 0.05$), and $r = 0.40$ ($P < 0.001$), respectively. Corresponding values for HF were −0.03 ($P > 0.05$), 0.51 ($P < 0.001$), 0.04 ($P > 0.05$), and 0.30 ($P < 0.01$). We conclude that DMI and, to a lesser extent, RFI are repeatable traits when cattle are offered grass silage and zero-grazed grass.

Key Words: beef cattle, feed efficiency, repeatability

1482 Repeatability of feed efficiency in steers offered a high-concentrate diet.
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The objective of the study was to examine the within-animal repeatability of intake, growth, and feed efficiency between the growing and finishing stages for beef cattle fed the same diet. One hundred sixty-seven steers comprising 90 Charolais (CH) and 77 Holstein-Friesian (HF) were used. Following a dietary adaptation period, individual DMI and growth were measured over two 71-d feeding phases 300 d apart. Mean BW (SD) and age (SD) at the start of phase 1 were 395 kg (37.8) and 283 d (18.3) and 294 kg (42.3) and 306 d (7.7) for CH and HF, respectively. Corresponding BW at the start of phase 2 were 675 (49.8) and 611 (49.3) kg. During both feeding phases, steers were individually offered the same concentrates (860 g/kg rolled barley, 60 g/kg soya bean meal, 60 g/kg molasses, and 20 g/kg minerals and vitamins) ad libitum plus a restricted allowance of grass silage daily. Throughout the interim period, they were all offered either grass silage or fresh grass herbage. The residuals of the regression of DMI on ADG and mid-test metabolic BW, within each breed, were used to compute individual residual feed intake (RFI) coefficients for each feeding phase. Repeatability between the two feeding phases for ADG, DMI, G:F, and RFI was estimated using Pearson correlation coefficients. During phase 1, overall ADG, DMI, G:F, and RFI (SD) for CH were 1.26 kg (0.26), 8.4 kg/d (0.82), 0.15 kg BW gain/kg DM (0.03), and −0.02 kg DM/d (0.51). Corresponding values for HF were 1.40 (0.22), 8.8 (0.84), 0.16 (0.02), and −0.05 (0.50). For phase 2, respective values were 1.39 (0.26), 11.5 (1.11), 0.12 (0.02), and −0.01 (0.69) and 1.31 (0.37), 12.5 (1.30), 0.11 (0.03), and −0.08 (0.95). For CH, correlations between the two feeding phases for ADG, DMI, G:F, and RFI were $r = 0.21$ ($P > 0.05$), $r = 0.63$ ($P < 0.001$), $r = 0.07$ ($P > 0.05$), and $r = 0.35$ ($P < 0.001$), respectively. Corresponding values for HF were 0.22 ($P = 0.06$), 0.56 ($P < 0.001$), 0.08 ($P > 0.05$), and 0.29 ($P < 0.05$). We conclude that DMI and, to a lesser extent, RFI are repeatable traits when cattle are offered a high-concentrate diet.

Key Words: beef cattle, feed efficiency, repeatability

1483 NADH dehydrogenase (ubiquinone) Fe-S protein-1 (NDUFS1), a core subunit of mitochondrial complex I, is not differentially expressed in peripheral blood mononuclear cells of beef steers with divergent residual feed intakes.
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Mitochondrial complex I (NADH:ubiquinone oxidoreductase) plays a crucial role in energy production and is intrinsically linked to animal bioenergetics. Several studies suggest mitochondrial protein complex subunits are differentially expressed in tissues and cells of chickens and cattle with divergent residual feed intake (RFI). The objective was to evaluate differences in mitochondrial complex I in peripheral blood mononuclear cells (PBMC) as a marker to identify different

RFI phenotypes. Crossbred steers fed corn- or roughage-based diets were RFI tested during the growing phase at the University of Missouri and shipped to Iowa State University where they were fed corn- or byproduct-based diets until harvest. Blood samples were collected on d 59 of the finishing phase from 37 steers that represented low and high extremes in growing phase RFI (n = 8 and 11 and mean RFI = −1.25 and 1.20 kg for corn-based diet and n = 10 and 8 and mean RFI = −1.67 and 1.25 kg for roughage-based diet, respectively). The PBMC were isolated and lysate proteins (50 μg total protein/lane) were separated by PAGE and blotted onto nitrocellulose membranes. A polyclonal antibody against NADH dehydrogenase (ubiquinone) Fe-S protein-1 (NDUFS1), a marker of complex I, was used to determine relative abundance of the protein in PBMC. Primary antibody binding specificity was confirmed with a commercially available bovine heart mitochondria lysate, which was also the positive control. Antibody binding was determined by chemiluminescence after blots were incubated with a horseradish peroxidase conjugated secondary antibody. The NDUFS1 band signal intensities were adjusted relative to the signal intensity of the positive control for each gel and normalized to total protein in the lane. There were no effects of diet (P = 0.50) or RFI phenotype (P = 0.45) on relative abundance of NDUFS1 protein in PBMC of steers. Examination of data from only steers with low RFI suggested a tendency, a slight positive relationship (r = 0.36, P = 0.14), between NDUFS1 protein abundance and low RFI, regardless of diet. A similar response was not evident in steers with high RFI (P = 0.79). Relative expression of the protein NDUFS1 is not clearly related to RFI of steers fed corn- or roughage-based diets and cannot be used as a marker for selection of efficient animals. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30214 from the USDA National Institute of Food and Agriculture.

Key Words: NDUFS1 protein, residual feed intake, steer

1484 Dry matter intake prediction of heifers under tropical conditions. M. I. Marcondes*[1] and A. L. Silva[2], [1]*Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Brazil,* [2]*Universidade Federal de Vicosa, Vicosa, Brazil*.

The objective was to develop a model able to predict DMI of heifers raised under tropical conditions as well as to test the effect of breed (Holstein purebred vs. Holstein × Gyr crossbreed) on DMI. A database composed of 389 individual animal observations, from 14 experiments, was used to develop the model for DMI. Only experiments that had concurrent information about DMI, average BW, ADG, and breed were used. Animals that had ≥87.5% Holstein crosses were considered pure breeds and the others were considered crossbreeds. The data were analyzed following a meta-analysis procedure, where each experiment was considered a random sample for large populations. The model used to fit the DMI was $DMI = \beta_0 + \beta_1 \times BW + \beta_2 \times BW^2 + \beta_3 \times ADG + \beta_4 \times ADG^2$, in which DMI = dry matter intake (kg/d); BW = average body weight (kg); ADG = average daily gain (kg/d); and β_0, β_1, β_2, β_3, and β_4 are equation parameters. To test the random effects of independent variables on the intercept and slope, the variance components (VC), heterogeneous first-order autoregressive (ARH (1)), and unstructured (UN) matrices of (co)variance were tested. All statistical procedures were performed using the MIXED procedure of SAS and Akaike's information criteria was used to indicate the best (co)variance matrix. Breed effect was tested every equation parameter. Observations with Studentized residuals > |2.5| were considered outliers. For all statistical procedures, a significance level of 5% was adopted for fixed effects and a level of 20% was adopted for the random (study) effect. Heifer DMI values were linearly affected by BW and ADG and quadratically affected by ADG. Genetic group affected the BW and ADG coefficients, demonstrating that this is an important source of variation and that different models should be used to estimate the DMI of Holstein purebred and crossbred heifers. The fitted models were $DMI_{Holstein} = -0.2092 + 0.0169 \times BW + 2.5833 \times ADG - 0.5126 \times ADG^2$ and $DMI_{Crossbred} = -0.2092 + 0.0179 \times BW + 2.3048 \times ADG - 0.5126 \times ADG^2$, in which $DMI_{Holstein}$ = DMI of Holstein heifers (kg/d), $DMI_{Crossbred}$ = DMI of crossbred heifers (kg/d), BW = average body weight (kg), and ADG = average daily gain (kg/d). It can be concluded that DMI in heifers is affected by BW and ADG and different equations should be used to estimate DMI in Holstein purebreds and Holstein × Gyr crossbred dairy heifers raised under tropical conditions.

Key Words: dairy heifers, growing animals, Holstein × Gyr

1485 An improved model for predicting dry matter intake in prepartum dairy cows. F. A. Paiva*[1], F. Peñagaricano[1], J. K. Drackley[2], and J. E. P. Santos[1], [1]*University of Florida, Gainesville,* [2]*University of Illinois, Urbana*.

The objective was to develop a mathematical model to predict DMI in prepartum Holstein cows. Data on daily DMI, parity, BW, body condition (BCS), and chemical composition of diets fed ad libitum to 1,451 Holsteins during the final 21 d of gestation in 31 experiments were compiled. Cows were grouped according to parity prepartum as nulliparous (n = 290), primiparous (n = 510), or multiparous (n = 660) and BCS as thin (BCS < 3.00), moderate (3.00–3.50), or fat (BCS > 3.50). Body weight was used as percentage of the mean BW within parity for nulliparous (620 kg), primiparous (690 kg), and multiparous (760 kg) and day relative to calving (DRC) was used as a categorical variable. Dietary factors included NE for lactation, CP, ruminal degradable and undegradable protein, ash, fat, NDF, ADF, nonfibrous carbohydrates, percent dietary forage, forage NDF, Ca, P, Mg, and

Table 1485.

Table 1. Comparison of prediction models for DMI of prepartum dairy cows

Variables	Hayirli et al. (2003)[1]	NRC (2001)	Cross-validation	Final[2]
Observed mean (Y)	11.58	11.58	11.58	11.58
Predicted mean ($\hat{Y}$)	12.69	12.31	11.54	11.55
Bias (Y-$\hat{Y}$)	-1.11	-0.73	0.04	0.03
R^2	0.11	0.11	0.20	0.22
MSPE	13.31	12.57	9.86	9.53
Root MSPE (kg/d)	3.65	3.55	3.14	3.09
Root MSPE (% Y)	31.49	30.61	27.11	26.62
Mean bias, % MSPE	9.22	4.13	0.02	0.02
Slope bias, % MSPE	9.13	9.15	0.66	0.19
Dispersion error, % MSPE	81.65	86.71	99.32	99.80
Concordance correlation coefficient	0.28	0.29	0.36	0.38

[1] Hayirli et al. (2003): J. Dairy Sci. 86:1771-1779.

[2] DMI, kg/d = 6.8591 + (BW% x 3.8748) + (NDF% x -0.1146) + (DCAD mEq/Kg x 0.006618) + Null (0) / Prim (2.5684) / Mult (2.2892) + Thin (0.4825) / Mod (0.3655) / Fat (0) + DRC (estimates)

dietary cation–anion difference (DCAD). Models were built with parameters entered in sequence using the MIXED procedures of SAS and R. Initial model included the random effects of study and cow nested within parity and study and the fixed effect of DRC. Each cow-level or diet-level factor was individually analyzed and fixed effects with $P < 0.05$ were used to build multivariable models. Multicollinearity among diet-level factors was assessed and parameters with high collinearity were individually evaluated in separate models. The final model was built using only significant variables and best fit assessed according to lowest Akaike's (AIC) and Bayesian (BIC) information criteria. The final model was DMI (kg/d) = intercept + [BW (% mean parity BW) × estimate] + [NDF (% of DM) × estimate] + [DCAD (mEq/kg) × estimate] + parity estimates + BCS category estimates + DRC estimates. The model was rerun 31 times excluding 1 of the 31 experiments each time, which was used to evaluate predictive ability using cross-validation (cross-validation model). Therefore, 31 different models were generated and the excluded experiment was used to evaluate the prediction of DMI. The final model was contrasted with other prediction models for DMI (Table 1). Of the total variance in DMI, the random effects accounted for 46.1%, the fixed effects accounted for 21.2%, and the residual accounted for 32.7%. The final model reduced the root of mean square of the predicted error by 0.46 to 0.56 kg/d, therefore more accurately predicting DMI of prepartum cows compared with currently used models.

Key Words: dry matter intake, model, prepartum

1486 The use of artificial neural network to estimate feed intake in lactating cows through milk mid-infrared spectra of individual cow milk samples.

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Feed intake is one of the most important components of feed efficiency in dairy systems. It is, however, a difficult trait to measure in the field. The use of milk spectrum from mid-infrared (MIR) spectroscopy previously has been used to estimate milk traits and could be an alternative to direct measurement of DMI. The objective of this study was to develop a Fourier transform MIR-based milk analysis method coupled with artificial neural networks (ANN) to estimate DMI in lactating Holstein cows. Five hundred ninety-nine milk samples from 189 lactating cows housed at either the Emmons Blaine Dairy Cattle Research Center (Arlington, WI; $n = 129$ cows) or the Dairy Forage Research Center (USDA, Prairie Du Sac, WI; $n = 60$ cows) were analyzed for MIR spectra. Individual DMI was periodically recorded from cows housed in a free-stall barn equipped with 32 Insentec electronic feeding gates (Arlington) or directly measured on tie-stall barn (USDA). The spectra absorbance values were used as input variables to develop and optimize the ANN configuration. Wavelengths with less than 10% of CV among samples were not used. The ability of the resulting one-hidden-layer ANN model was compared with a linear predictive model developed through partial least squares (PLS) regression. Four ANN models were developed considering 5, 10, 15, and 20 neurons. A 7-fold cross-validation method was used to assess the predictive ability of the models. The r^2 of cross-validation increased as the number of neurons increased from 5 to 20 ($r^2 = 0.31$, 0.43, 0.45, and 0.48, respectively). The root mean square error (RMSE) decreased as the number of neurons increased up to 15 (RMSE = 4.13, 3.61, 3.30, and 3.38 kg/d, respectively). In contrast, the PLS model (7 factors) resulted in lower $r^2 = 0.14$ and greater RMSE = 4.41 kg/d. Compared with established statistical method (PLS), the proposed ANN model demonstrates the potential to provide improved prediction of DMI. Future research should be conducted to investigate alternative ANN architectures and to assess its performance using test validation in an independent data set.

Key Words: artificial neural network, intake, mid infrared

1487 Effects of supplementing lactating dairy cow ration with sodium sesquicarbonate on reticulorumen pH, rumination, and dry matter intake.

1488 Toxicity of antibiotics on rumen protozoan *Entodinium caudatum* and its associated microbes.
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Rumen ciliate protozoa play important roles in rumen function. However, knowledge on the metabolism and physiology of rumen protozoa is limited, mostly because of lack of axenic cultures of rumen ciliate protozoa needed to generate direct evidence. Antibiotics alone and in combination with physical separation have been successfully used in generating axenic cultures of free-living aerobic ciliate protozoa, such as species of *Tetrahymena* and *Paramecium*. However, no effort has been successful in developing axenic cultures of rumen protozoa. Rumen protozoa have lived together with a high density of rumen bacteria and other groups of microbes for many millions of years, and killing of the associated bacteria and/or archaea resulted in loss of viability of rumen protozoa. The objective of this experiment was to evaluate the toxicity of different antibiotics to *Entodinium caudatum*, a major species of *Entodinium*, which, as a genus, accounts for more than 90% of the total rumen protozoa in cattle and sheep fed high-concentrate diets. Based on the mode of action, eight antibiotics were selected that each has a broad spectrum to kill or to inhibit bacteria. *Entodinium caudatum* cells grown in a culture were filtrated and washed to remove most of the free-living bacteria and methanogens. The washed *E. caudatum* cells were then fed a protozoal feed containing ground wheat, alfalfa, and grass and incubated for 72 h with 4 different concentrations and three replicates per antibiotic treatment. After incubation, *E. caudatum* cell counts, optical density, and electron microscopy (both scanning and transmission) were used to determine *E. caudatum* viability, growth of contaminating bacteria, and changes of intracellular structure of *E. caudatum* cells. Except ampicillin, all the tested antibiotics decreased *E. caudatum* growth in a concentration-dependent manner. Chloramphenicol appeared to be the most toxic to the viability of *E. caudatum*. Scanning electron microscopy and transmission electron microscopy revealed few ecto- or endosymbiotic microbes of the *E. caudatum* cells irrespective of the antibiotic treatments. Damages to the intracellular structures were detected by scanning electron microscopy, especially among the *E. caudatum* cells treated with chloramphenicol. Transmission electron microscopy is underway to further examine cellular damages, and several antibiotics cocktails are being evaluated for their usefulness to kill the associated microbes and generate an axenic *E. caudatum* culture.

Key Words: axenic culture, electron microscopy, *Entodinium caudatum*

1489 Effect of diets containing different levels of crude glycerol on nutrient intake in lambs.
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Crude glycerin is a byproduct of biodiesel production that represents a potential ingredient for use in animal nutrition. The objective of this study was to evaluate the effect of diets containing different levels of crude glycerin on nutrient intake in male lambs. The experiment was conducted in the animal metabolism laboratory of Universidade Estadual de Londrina. Four castrated male lambs (25 ± 2.6 kg) were used in a 4 × 4 Latin square design. Animals were identified and individually allocated to metabolic cages containing a feeder and a water trough. The experiment was divided in 4 periods of 13 d, with the first 7 d for diet adaptation and 6 d of sample collection. A basal diet (50:50 forage to concentrate) consisting of chopped *Brachiaria dictyoneura* hay, ground corn, soybean meal, urea, and a mineral and vitamin premix was provided throughout the experiment. Crude glycerin was added to the basal diet at either 0, 5, 10 or 15% of diet DM. Diets were made isocaloric and isonitrogenous by the addition of ground corn and urea, respectively. Daily intake was measured based on individual orts. Samples of offered diets and orts were analyzed for DM, OM, CP, NDF, ADF, ether extract (EE) and total carbohydrates (TC). Data was submitted to ANOVA and regression with a 5% significance level. The inclusion of crude glycerin influenced the intake of nutrients ($P < 0.01$) when expressed as grams per day, percent BW, and grams per kilogram$^{0.75}$, with a quadratic response for all parameters evaluated. Overall, the highest theoretical nutrient intake in kilograms per day was between 3.81 and 5.14% glycerol inclusion. Only CP and EE, when expressed as percent BW and grams per day, resulted in higher theoretical intake for diets containing glycerin at 10.88 and 7.91% inclusion, respectively. Nutrient intake for all treatments was sufficient to meet the nutritional requirements and to keep the BCS within the desired to maintain the physiological status of the animals during the experimental period. Crude glycerin, when fed to lambs in a 50:50 forage-to-concentrate diet, can be included up to 5.14% of diet DM without negatively affect the intake of nutrients in grams per day and grams per kilogram$^{0.75}$.

Key Words: byproduct, energy, small ruminants

1490 Effects of corn particle size and neutral detergent fiber:starch ratio on in vitro neutral detergent fiber degradability.
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Reducing particle size is the most common technique to increase starch digestibility, especially for corn, and both the

amount and the size of starch source may affect the rumen environment. The objective of our study was to verify the effects of specific ranges of corn particle size and NDF:starch ratios on starch and NDF degradability (NDFd). The same batch of corn was milled using a Wiley mill with either a 1- or a 2-mm screen. The corn was sieved and separated using the following sizes: <250, 250 to 500, 500 to 1,180, and 1,180 to 2,000 μm. All sizes were analyzed for starch, CP, EE, and NDF. Oat hay and alfalfa were used separately to evaluate the effects of particle size on NDFd using the NDF:starch ratios of 1:1 and 1:1.25. Ratios were adjusted for each size class based on actual starch and NDF contents of both corn and forages. Higher ratios were excluded because the buffering capacity of the medium avoided changes in pH and NDF digestibility. Residual starch and NDF of the fermented samples were obtained at 3, 6, 9, 12, 24, and 48 h. Rates of digestion (kdStarch and kdNDF) were calculated using a first-order decay model and estimated indigestible starch and NDF using the 48 and 240 h fermentation residuals, respectively. Indigestible starch was numerically different across sizes. Data were analyzed according to a randomized complete block design with a factorial arrangement of treatments. The main tested effects were size, ratio, forage, and their interactions. Fermentation run was considered a random effect. With increasing particle size, starch decreased from 79 to 55%, NDF increased from 3.4 to 33.1%, EE increased from 2.17 to 3.78%, and CP increased from 6.40 to 8.21%. Both forage type and NDF:starch ratio did not have any effect ($P > 0.45$) on ivSD and kdStarch. As expected, kdStarch linearly increased ($P < 0.01$) with smaller particle size with no interaction with either forage or NDF:starch ratio, from 0.14 to 0.47 h^{-1}. Interaction was present ($P < 0.01$) between forage and particle size for ivSD and kdStarch, with more starch degraded for the two smallest sizes and alfalfa. Particle size, and not amount, affected NDF digestibility for both forages ($P < 0.01$), with consistently higher NDFd and kdNDF for the largest size. Particle size affected NDF fermentation more than amount for corn, even if the medium might have decreased the effect of larger amount of starch.

Key Words: in vitro, neutral detergent fiber, particle size, starch

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1491 Associations between residual feed intake and metabolite profiles and feeding behavior traits in feedlot cattle. M. D. Miller*[1], G. E. Carstens[1], J. M. Thomson[2], J. G. Berardinelli[2], M. R. Herrygers[2], J. White[2], L. O. Tedeschi[1], and P. K. Riggs[1], *[1]Texas A&M University, College Station, [2]Montana State University, Bozeman*.

Objectives of this study were to evaluate the effects of residual feed intake (RFI) classification on performance and feed efficiency in steers fed a high-grain diet and to examine associations between RFI and blood metabolite profiles and feeding behavior traits to identify RFI biomarkers. Performance, DMI, and feeding behavior traits were measured for 70 d in Angus crossbred steers ($N = 168$) using a GrowSafe system. Steers were classified into low- ($n = 52$), medium- ($n = 64$), and high- ($n = 52$) RFI groups based on ±0.5 SD from the mean RFI of 0.00 (SD = 0.82). Low-RFI steers consumed 17% less ($P < 0.0001$) DMI (9.05 vs. 10.89 ± 0.14 kg/d), had 18% lesser ($P < 0.0001$) feed:gain ratio (5.05 vs. 6.11 ± 0.10), and generated $95 per head more ($P < 0.001$) profit compared with high-RFI steers, even though ADG and carcass value were not affected by RFI classification. Blood samples were collected from steers with lowest RFI ($n = 25$) and highest RFI ($n = 24$) on Day 70 of the trial, and serum metabolite concentrations were analyzed using ^{1}H-NMR spectroscopy. Partial least squares (PLS; MetaboAnalyst) were used to examine associations between RFI and metabolites and feeding behavior traits. Of the 12 feeding behavior traits evaluated, 4 traits had variable of importance in projection (VIP) scores > 1.0, which included head-down (HD) duration, bunk visit (BV) duration, nonfeeding interval (NFI) duration, and head-down–to–meal duration ratio (HD:MD). The first 2 components of PLS accounted for 54% of between-animal variance in RFI. Steers with low RFI had longer ($P < 0.001$) NFI duration (less time at the bunk), 45% lower HD duration, 35% lower BV duration, and 32% lower HD:MD than high-RFI steers. Of the 44 metabolites detected by ^{1}H-NMR, 5 metabolites had VIP scores > 2, which included glycine, betaine, tyrosine, valine, and leucine. The first 2 components of PLS accounted for 34% of between-animal variance in RFI. Steers with low RFI had higher ($P < 0.001$) concentrations of glycine and lower ($P < 0.06$) concentrations of betaine, tyrosine, valine, and leucine than high-RFI steers. These preliminary results reveal that metabolomic profiling and feeding behavior traits may provide opportunities to identify biomarkers that are predictive of RFI in beef cattle.

Key Words: feedlot cattle, metabolites, residual feed intake

1492 Effects of acidity and silage type on lysine retention among two lipid-coated ruminally protected lysine products. J. N. Reiners* and D. W. Brake, *South Dakota State University, Brookings*.

Milk protein secretion among cattle consuming corn-based diets can be limited by metabolizable Lys. Therefore, ruminally protected AA (RPAA) are commonly included in cattle diets to increase metabolizable Lys intake. Previous data suggest that Lys associated with lipid-coated RPAA is reduced by greater diet moisture content. Effects of silage type and acidity on Lys associated with lipid-coated RPAA products (EB and EC) were evaluated over time. Crystalline Lys and Lys mixed with lipid in amounts equal to either EB or EC served as negative controls. Controls and each lipid-coated RPAA (4 g) were placed in mesh bags (10 by 20 cm; pore size = 50 mm) and mixed with

Table 1493. Effect of DIM on fecal composition and nutrient digestibility.

	Low DIM, AM	Low DIM, PM	High DIM, AM	High DIM, PM	SED	*P* values		
						Group	Time	Group × Time
Fecal nutrient								
Dry matter	11.96^{B}	11.61^{B}	13.43^{A}	13.30^{A}	0.46	0.01	0.46	0.74
Crude protein	17.85^{A}	16.49^{B}	17.57^{A,B}	17.01^{A,B}	0.60	0.73	0.03	0.36
ADF	29.82^{B}	32.62^{A}	31.57^{A,B}	32.22^{A,B}	0.67	0.40	0.001	0.01
NDF	46.19^{B}	49.59^{A}	47.55^{A,B}	48.06^{A,B}	0.94	0.91	0.01	0.03
Starch	8.63^{A}	6.93^{A,B}	6.66^{B}	7.31^{A,B}	0.84	0.26	0.36	0.06
Ash	10.11^{B}	11.04^{A,B}	11.06^{A,B}	11.45^{A}	0.37	0.14	0.01	0.26
Apparent digestibility								
pdNDF	67.85	68.25	68.83	70.13	2.69	0.57	0.62	0.79
NDF	51.50	52.28	52.22	53.74	2.60	0.67	0.47	0.81
Protein	65.19	67.99	66.84	66.99	1.66	0.70	0.29	0.33
Starch	89.13^{B}	91.43^{A}	91.97^{A}	90.87^{A,B}	1.06	0.25	0.42	0.03

either alfalfa silage or corn silage at 2 different levels of acidity (pH = 4.6 or pH = 6.6) for 0, 6, 12, or 24 h. Silage pH was modified by mixing with 10% (wt/wt) NaOH. After removal, mesh bags were rinsed with cold water and contents of each bag were lyophilized. Lipid-associated Lys was subsequently determined by analyzing total free Lys content after removal of triacylglycerols and free fatty acids with hexane:methanol. Dissociation kinetics were calculated using the nonlinear procedure of SAS, and data were analyzed as a completely randomized design. As expected, the proportion of Lys that dissociated after initial contact (ID) from the negative controls was complete (100 ± 2.5%) and indicated that Lys analyses reflected measures of lipid-associated Lys. The ID from RPAA was less ($P = 0.02$) for EB (20.4 ± 2.8%) than for EC (31.3 ± 2.8%). Additionally, ID increased as acidity increased when RPAA was mixed with corn silage; however, ID was not affected by acidity when mixed with alfalfa silage (silage × pH ≤ 0.01). Amounts of Lys that slowly dissociated (SD) from RPAA during silage incubation were greater ($P = 0.01$) for EB (59.6 ± 4.8%) than for EC (38.4 ± 4.8%). Furthermore, SD increased with greater acidity in corn silage but did not differ among alfalfa silage with either greater or lesser acidity (silage × pH = 0.01). Rate of Lys dissociation was not different among either RPAA ($P = 0.40$; 10.9 ± 1.9%/h) and was not affected by acidity ($P = 0.73$) or silage type ($P = 0.62$). Lipid-associated Lys remaining at 24 h for EB (20.1 ± 5.7%) was not different ($P = 0.24$) compared with that for EC (30.3 ± 5.7%).

Key Words: amino acid, cattle, lysine

1493 Relationship of days in milk to nutrient digestibility in lactating multiparous cows.

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The objective was to determine if differences in days in milk (DIM) affect apparent nutrient digestibility in lactating multiparous cows fed the same ration. Of 136 cows in a multiparous, high-producing pen on a 1,000-cow commercial dairy, 24 were selected for sampling based on differences in DIM and milk yield (Low DIM: $n = 12$, milk = 64 ± 6 kg, and DIM = 85 ± 6; High DIM: $n = 12$, milk = 55 ± 4 kg, and DIM = 158 ± 15). Milk, fecal, and TMR samples were collected once daily for 10 consecutive days. Samples were collected in the morning on 6 d and the afternoon on 4 d. Individual cow milk and fecal samples were composited into one daily milk or fecal sample per DIM group and analyzed for nutrient composition. In addition, daily fecal composite and TMR samples were analyzed for apparent digestibility of potentially digestible NDF (PdNDFd), NDF (NDFd), protein (Protd), and starch (Starchd). Fecal nutrient composition and apparent digestibility data were analyzed using the Glimmix procedure of SAS. The model included fixed effects of group, sampling time, and their interaction. Day was included as a repeated measure. The CORR and REG procedures were used for comparing daily variations in digestibility with milk yield and composition. For fecal nutrient composition, DIM × sampling time was significant for ADF and NDF, due to sampling time differences in the low-DIM group (Table 1). There was a group effect on fecal DM in which DM was lower in low-DIM cows. Time effects were also observed, with CP being higher before noon and ADF, NDF, and ash being higher after noon. There was no effect of DIM on PdNDFd, NDFd, Protd, or Starchd. There was an effect of DIM × sampling time on Starchd ($P = 0.03$) due to higher Starchd at the before-noon sampling for high-DIM cows ($P = 0.03$). There were no significant correlations of digestibility measures with milk yield. A 1% increase in PdNDFd ($P = 0.02$) and NDFd ($P = 0.006$) was associated with a 0.04 and 0.05% increase, respectively, in milk fat percentage. A 1% increase in Starchd ($P = 0.003$) was associated with a 0.03% increase in milk protein percentage. Because DIM had minimal effects on digestibility measures, it is likely not necessary to consider DIM when selecting cows for estimation of nutrient digestibility within a high-producing pen.

Key Words: days in milk, fecal composition, nutrient digestibility

1494 Effects of animal and diet characteristics on digestibilities of dry matter, fiber, and starch in lactating cows. R. A. De Souza*[1], R. J. Tempelman[1], M. S. Allen[1], J. K. Bernard[2], B. Weiss[3], and M. J. VandeHaar[1], *[1]Michigan State University, East Lansing, [2]University of Georgia, Tifton, [3]The Ohio State University, Wooster*.

Our objective was to determine the effects of DMI, BW, and diet characteristics on total tract digestibilities of DM, NDF, and starch (DMD, NDFD, and StarchD, respectively) in high-producing cows. The database was constructed with individual observations of digestibilities, ingredients, and chemical composition of diets; BW and DMI; experimental design; and treatment arrangement. The data set contained 1,942 observations on 635 cows from 56 studies with >6 observations per treatment in Michigan, Ohio, and Georgia. Forage sources included corn, alfalfa, wheat straw, and orchardgrass. Nutrient digestibility means were 66 ± 6, 42 ± 11, and 93 ± 5% for DMD, NDFD, and StarchD, respectively. Diet nutrient contents (% DM) were 31 ± 5% NDF, 27 ± 6% starch, 2.6 ± 1.2% FA, and 17 ± 1.4% CP. Dry matter intake and BW were 23 ± 5 and 669 ± 79 kg, respectively. Data was analyzed using a mixed model with HPMIXED procedure of SAS. The full model included linear and quadratic effects of diets, $BW^{0.75}$, DMI, and all possible 2-way interactions between diet variables and DMI as fixed effects. Cow, block, period, and study were used as random effects. Best fitting reduced models were generated using backward and stepwise regression procedures. Interactions were not significant. A simplest model was generated using only DMI and the random effects. The backward, stepwise, and simplest models were cross-validated using five folds, and the resulting correlations coefficients across studies (CORR) were compared by *t* test. The model that resulted in the highest CORR and lowest number of variables was accepted as the best fitting model for each nutrient digestibility. The best fitting prediction equations were DMD = 69 − 0.20 × DMI (MSE = 8.5, r^2 = 0.68, CORR = 0.20); NDFD = 32 + 0.26 × grass + 0.46 × starch + 3.4 × FA + 0.83 × DMI − 0.020 × $starch^2$ − 0.34 × FA^2 − 0.030 × DMI^2 (MSE = 26, r^2 = 0.80, CORR = 0.41); and StarchD = 97 − 0.30 × DMI (MSE = 3.1, r^2 = 0.84, CORR = 0.22); grass, starch, and FA are expressed as percentage of DM and DMI is expressed as percentage of $BW^{0.75}$. Our results confirm that digestibility was reduced as DMI increased but at a lower rate than the previous equation used by NRC (2001). Digestibility of DM and StarchD can be predicted based on only DMI; however, NDFD required diet characteristics in addition to DMI. Starch levels > 25% and FA > 5% dramatically reduced NDFD.

Key Words: digestibility, intake, model, neutral detergent fiber, starch

1495 Effects of silage type and inclusion level on ruminal characteristics and feeding behavior of feedlot steers. P. R. B. Campanili*[1], J. O. Sarturi[1], S. J. Trojan[1], M. A. Ballou[1], L. A. Pellarin[1], J. D. Sugg[2], L. A. Ovinge[1], A. Alrumaih[1], and A. A. Hoffman[1], *[1]Texas Tech University, Lubbock, [2]Angelo State University, San Angelo, TX*.

Silage type and level of inclusion on beef cattle finishing diets ruminal fermentation and degradability, digestibility, and feeding behavior were evaluated. In Study 1, beef steers (*n* = 6; BW = 363 ± 23 kg) fitted with ruminal cannula were used (6 × 4 unbalanced Latin square design). Treatments (*n* = 4) consisted of silage type (corn = BH8895 and sorghum = AF7401) and silage inclusion (10 or 20%, DM basis). Each period consisted of 14 d for adaptation and 7 d for collections. Steers were individually fed ad libitum once daily. Silage degradability was studied by in situ technique. In Study 2, the same technique was used to study the degradability of intact ensiled sorghum grain (*n* = 10; 18.9-L units; 112 d of storage; 2 sites). Beef steers (*n* = 3; BW = 547 ± 56 kg) fed a growing diet were used. Data were analyzed using Glimmix procedure of SAS (day as repeated measure). Steers fed 20% sorghum silage had greater DMI (P = 0.03) and total VFA (P = 0.01) but tended (P = 0.07) to the least propionate molar proportion compared with other treatments. Steers fed 10% corn silage had the greatest (P = 0.04) ruminal butyrate and the least (P < 0.01) ruminal pH average compared with other treatments, which reached nadir at 5.62 (P < 0.01) 12 h after feeding. Additionally, the 10% corn silage treatment tended (P = 0.09) to have the least in vitro methane production. Starch digestibility tended (P = 0.08) to peak for steers fed 10 and 20% corn silage (98%) and bottom for steers fed 20% sorghum silage (92%). Steers fed corn silage had greater ($P \leq 0.01$) total tract apparent digestibility (11% DM and 32% NDF), lower (P < 0.01) acetate/propionate, and 34% greater (P < 0.01) silage ruminal degradation and tended (P = 0.07) to chew 1.1 h/d less compared with steers fed sorghum silage diets. Steers fed 20% silage chewed and ruminated more ($P \leq 0.04$), degraded more (P < 0.01) NDF, and had greater (P < 0.01) acetate/propionate but less DM digestibility than 10% silage-fed steers. Sorghum grain ruminal degradability reached 52% at 96 h. Replacement of corn silage with sorghum silage in beef finishing diets requires adjustments to balance dietary energy. Sorghum material induced a desirable roughage effect in feeding behavior but also offered potential to be improved regarding fiber digestibility and intact grain ruminal degradability.

Key Words: corn, silage, sorghum

1496 Identification of biological pathways involved in residual feed intake in Hereford cattle through gene set enrichment analysis. J. L. Mutch*[1], M. Neupane[1], C. M. Seabury[2], H. L. Neibergs[1], P. C. Tizioto[3], D. J. Garrick[4], M. S. Kerley[3], D. W. Shike[5], J. E. Beever[5], J. F. Taylor[3], U. S. Feed Efficiency Consortium[3], and K. A. Johnson[1], *[1]Department of Animal Sciences, Washington State University, Pullman, [2]College of Veterinary Medicine, Texas A&M University, College Station, [3]University of Missouri, Columbia, [4]Department of Animal Science, Iowa State University, Ames, [5]University of Illinois, Urbana*.

Understanding the biological differences between animals with different feed efficiency phenotypes enhances our understanding of the trait. The objective was to use gene set enrichment analysis-SNP (GSEA-SNP) to identify gene sets (GS) associated with the residual feed intake (RFI) phenotype in Hereford cattle. Feed intake and BW gain were measured on 847 steers and heifers at Olsen Ranches in Harrisburg, NE. Animals were genotyped using the Illumina BovineSNP50 (n = 358) or BovineHD BeadChips (n = 459). BovineSNP50 genotypes were imputed with Beagle 4.1 to the density of the Illumina BovineHD BeadChip using the BovineHD genotyped Herefords as a reference. Genomewide association analysis (GWAA) was performed using GRAMMAR mixed model software, and the most significant SNP for each of 19,723 genes from the UMD-3.1 reference assembly were selected as a proxy for that gene. Gene proxies were considered only for SNP that were located within 8.5 kb of a gene, as this is representative of the average haplotype block size in Herefords (determined by a haplotype block analysis). Following GWAA, GSEA-SNP was conducted with 4,389 GS from Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), Reactome, Biocarta, and Panther. Significance was calculated using the null distribution estimated from 10,000 permutations for each GS using GenABEL in R. An enrichment score was calculated for each GS using a modified Kolmogorov–Smirnov statistic and normalized (NES) based on the size of each GS. The GS associated (NES > 3.0) with RFI were centrosome (37 leading edge genes [LEG]) and cytoskeleton (97 LEG) from GO and peroxisome from KEGG (30 LEG). The centrosome GS is involved in mitosis and cell cycle regulation and the peroxisome GS is involved in lipid homeostasis. The cytoskeleton organization GS contained four differentially expressed LEG: *Type I keratin 19* (*KRT19*), *α 1 actin I* (*ACTA1*), *α 1 actinin* (*ACTN1*), and *cysteine and glycine-rich protein 3* (*CSRP3*). These genes were previously found by this consortium to be differentially expressed between the high- and low-RFI groups of Herefords. In the low-RFI group, expression of *KRT19* in the liver was greater than in the high-RFI cattle. Low-RFI Herefords also had reduced expression of *ACTA1* in the liver and pituitary, *ACTN1* in the hypothalamus, and *CSRP3* in the liver. Alterations in lipid metabolism and cell cycle regulation are associated with the RFI phenotype. This project was supported by AFRI Competitive Grant no. 2011-68004-30214 from the USDA National Institute of Food and Agriculture.

Key Words: cattle, gene set enrichment analysis, residual feed intake

1497 Updating equations to estimate dry matter intake of Nellore and beef crossbred cattle. L. F. Costa e Silva*[1], S. C. Valadares Filho[2], P. P. Rotta[3], J. A. G. Azevedo[4], F. F. Silva[1], A. C. B. Menezes[1], and B. C. Silva[3], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [4]Universidade Estadual de Santa Cruz, Ilheus, Bahia, Brazil*.

Dry matter intake is the most important variable that affects animal performance, mainly in beef cattle due to economic impact and its complex gastrointestinal system with peculiar metabolic functions. A database with 1,459 animals, being 1,188 Nellore and 271 beef crossbred cattle, was developed to generate equations estimating DMI for animals raised on feedlot. Variables such as DMI, BW, metabolic BW (mBW), ADG, and level of concentrate (LC) were collected. First of all, a PROC CORR was used to evaluate which variables are significantly correlated with DMI. The variables mBW, LC, and ADG presented the highest correlation with DMI, and those were chosen to be part of the equations generated. The range of DMI in this database was from 2.96 to 12.3 kg/d whereas LC was from 0 to 100% and ADG was from −0.36 to 2.26. After all, statistical models were fitted by the cross-validation procedure. Also, differences between genetic group (Nellore and beef crossbred cattle) were evaluated, which allowed us to develop two different equations. Then, the following equations were developed to estimate DMI of Nellore and beef crossbred cattle, respectively: for Nelore cattle, DMI $= -2.406 + 0.064 \times LC - 0.00065 \times LC^2 + 0.070 \times BW^{0.75} + 4.384 \times ADG - 1.255 \times ADG^2$ ($R^2 = 0.797$), and for beef crossbred cattle, DMI $= -4.355 + 0.0598 \times LC - 0.00049 \times LC^2 + 0.128 \times BW^{0.75} + 3.974 \times ADG - 1.128 \times ADG^2$ ($R^2 = 0.717$). From this, if we derive these equations in function of level of concentrate, we can know at which amount of concentrate each genetic group is able to reach the maximum DMI. Therefore, Nellore cattle reach maximum DMI when 49.2% of concentrate is provided in diet whereas beef crossbred cattle reach this amount for 61.0% of concentrate. This statement proves that Nellore cattle are more sensible to high amounts of concentrate than beef crossbred cattle. Moreover, if we derive these equations in function of ADG, we are able to know at which ADG the animals reach maximum DMI. For Nellore and beef crossbred cattle, the maximum DMI is reached when

ADG is 1.75 and 1.76 kg/d, respectively. Therefore, Nellore cattle are more sensible when level of concentrate is increased in diet when compared with beef crossbred cattle.

Key Words: beef crossbred cattle, cross-validation, level of concentrate, Nellore

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1498 Rumen bacterial species associate with residual feed intake in beef cattle.

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Residual feed intake (RFI) describes an animal's feed conversion efficiency independent of phenotypic performance. The objective of this study was to quantify differences in ruminal bacteria between the most efficient animals and the most inefficient animals and any interaction with rumen sample fraction. One-hundred fifty Red Angus cattle were allocated to three groups according to sex and herd origin. Animals were fed in confinement for at least 78 d to determine the RFI category for each. Within each contemporary group, the two most efficient (n = 6) and least efficient animals (n = 6) were selected. Rumen solids and fluid were collected immediately after slaughter. Bacterial DNA extraction from the solid fraction included mechanical homogenization followed by enzymatic and bead beating lysis for all samples. Real-time quantitative PCR was used to examine the relative abundance of specific ruminal bacteria compared with the geometric mean of two universal 16S rRNA primers. Data were analyzed using the MIXED procedure of SAS 9.3. Fixed effects in the model included RFI category, rumen fraction, RFI × fraction, and sex. Individual animal was the experimental unit and incorporated into the statistical model as a random effect nested within group. Of the nine species evaluated, *Succinivibrio dextrinosolvens* was the most abundant, averaging 1.8% of 16S rRNA copy number. Results indicated most efficient cattle had a 6-fold decrease (P = 0.04) in relative abundance of *S. dextrinosolvens* and also had a 4-fold reduction (P = 0.02) in *Anaerovibrio lipolytica*. Although most efficient cattle tended (P = 0.09) to have greater relative abundance of *Eubacterium ruminantium*, a tendency (P = 0.10) for an RFI × fraction effect indicated the greatest differences were between the solid fraction of most efficient and least efficient cattle. Fraction effects were observed for *Butyrivibrio proteoclasticus* (P < 0.001) and *Selenomonas ruminantium* (P < 0.001) as each were increased within the solid fraction compared with the liquid. An RFI × fraction effect (P = 0.01) also was observed for *Fibrobacter succinogenes*, with a greater relative abundance in the liquid compared with the solid fraction for least efficient cattle. No effect of RFI or fraction was observed for *Megasphaera elsdenii* or *Prevotella bryantii*. These findings indicate large differences in RFI phenotypes in beef cattle are associated with bacterial species in the rumen, and they may have a role in conferring feed efficiency.

Key Words: bacteria, residual feed efficiency, rumen

1499 The association between body condition score, residual feed intake, and hyperketonemia.

F. M. Tiberio*[1], R. S. Pralle[1], C. A. Getschel[1], R. C. Oliveira[1], S. J. Bertics[1], K. A. Weigel[1], R. D. Shaver[1], L. E. Armentano[2], and H. M. White[1], *[1]Department of Dairy Science, University of Wisconsin, Madison, [2]University of Wisconsin – Madison, Madison*.

The transition period in dairy cows is associated with the onset of negative energy balance and body fat mobilization. Mobilized lipids can lead to excessive ketone production. The objective of this trial was to characterize the relationship between hyperketonemia (HYK) and milk production, BCS, and residual feed intake (RFI). Blood and milk samples were collected twice weekly from cows 5 to 18 d in milk (DIM) for a total of 4 samples. Hyperketonemia was diagnosed using the Precision Xtra Meter and defined as blood β-hydroxybutyrate (BHBA) ≥ 1.2 mmol/L. Cows were treated on diagnosis. Dry period (−28 DBCS), calving, and final blood sampling BCS was recorded. Previous midlactation production and DMI were used to calculate RFI by subtracting predicted energy intake from the observed energy intake. Effect of milk composition, milk yield, lactation number, BCS, and previous RFI on the observed maximum BHBA concentration (MAXBHBA) was determined using PROC MIXED of SAS 9.4. Least squares means ± SE are reported. Of the 570 cows sampled, 19.7% were diagnosed with HYK. Mean DIM at the first positive HYK test was 9 ± 0.9 d and the average BHBA concentration at the first positive HYK test was 1.53 ± 0.14 mmol/L. MAXBHBA was greater ($P \leq 0.05$) for multiparous cows compared with primiparous cows. Milk fat content was increased (4.33 vs. 4.69 ± 0.05%; $P < 0.0001$), milk protein content was decreased (3.60 vs. 3.40 ± 0.02%; $P < 0.0001$), somatic cell count was decreased, and milk yield was increased (44.02 vs. 47.47 ± 1.46 kg/d; $P < 0.0001$) in the first 30 DIM for cows positive for HYK compared with negative cows. Cows with a DBCS ≥ 4.0 had greater MAXBHBA (0.88 vs. 1.28 ± 0.08 mmol/L; $P \leq 0.05$) than cows with lower BCS. Cows that lost >0.75 BCS units after calving had greater ($P \leq 0.05$) MAXBHBA than cows that lost ≤0.75 BCS units. MAXBHBA was not significantly correlated to RFI. Prompt diagnosis and treatment of HYK appears to prevent HYK-associated decreases in milk production. Avoiding overconditioning of dry cows and excessive fat mobilization during the transition period may decrease HYK incidence; however, previous lactation RFI does not appear to be correlated to developing HYK.

Key Words: body condition score, hyperketonemia, residual feed intake

1500 Effects of arginine infusion through jugular vein on the milk performance and casein synthesis in midlactation cows. M. Z. Wang*, *Yangzhou University, Yangzhou, P. R. China*.

Previous studies show that milk protein yield increases with arginine infusion (Doepel and Lapierre, 2011). Our previous in vitro work by Chen et al. (2013) demonstrates that arginine increases casein protein synthesis in bovine mammary epithelial cells and that arginine plays an important role in the transcriptional regulation of casein genes and mTOR-related genes in bovine mammary epithelial cells (Wang et al., 2014). Subsequently, our Wistar rats feeding trail found that a 2x Arg group had significant effects on the mammary gland development and its casein protein synthesis (Hu et al., 2015). But whether arginine promotes the growth of the cow mammary tissue and casein expression is unknown. Therefore, this study was performed to investigate the responses of milk yield and milk composition for arginine infusion by midlactating Holstein cows. Six healthy lactating cows at similar lactation stages with similar weights, parities, milk yields, and body conditions were divided into 3 groups (2 for each group), casein model group (control group), arginine infusion group (37.66 g arginine contenting 12.10 g N/d), and alanine isonitrogen group (77.24 g alanine containing N 12.13 g N/d), respectively, in a 3 × 3 Latin square trail with a 7-d infusion plus a 15-d interval per period. The milk performance, casein content, and casein gene expression were detected. The results showed that at Day 5, the arginine infusion group was higher than the casein model group in the contents of milk protein and nonfat milk solids ($P < 0.05$), whereas at Day 6, the arginine infusion group was higher in milk fat content compared with the alanine isonitrogen group ($P < 0.05$). As for the milk casein contents, α-casein in the casein model group was lower than these in the other 2 groups ($P < 0.05$), β-casein had no difference between groups ($P > 0.05$), and κ-casein of the arginine infusion group was the highest among the groups ($P < 0.05$). In addition, arginine the infusion group had significantly higher expression in genes CSN1S1 and CSN1S2 ($P < 0.05$), and numerically higher expression in gene CSN3 compared with the other 2 groups. We therefore concluded that for the first time, arginine infusion increases the contents of α-casein and κ-casein in milk as well as their gene expressions in mammary tissue from dairy cows, which is contributed to the improvements of milk protein content and milk quality.

Key Words: arginine, casein, jugular infusion, milk performance

1501 Diet starch content and fermentability affects feed intake and milk yield of cows in the postpartum period. R. I. Albornoz*, *Michigan State University, East Lansing*.

The objective of this study was to evaluate the effects of diet starch content and fermentability fed during the postpartum (PP) period on DMI, yields of milk (MY) and milk components, and body reserves. Fifty-two multiparous Holstein cows were used in a randomized block design with a 2 × 2 factorial arrangement of treatments. Diets were formulated to 22 (LS) or 28% (HS) starch with dry ground corn (DGC) or high-moisture corn (HMC) as the primary starch source. Treatments were fed from 1 to 23 d PP and then switched to a common diet until 72 d PP to measure carryover (CO) effects. Treatment period (TP) diets were formulated for 22% forage NDF and 17% CP, and starch concentration was adjusted by substitution of corn grain for soyhulls. The diet for the CO period was formulated to 20% forage NDF, 17% CP, and 30% starch. Throughout the experiment, both DMI and MY were measured daily, and milk components, BCS, and back fat thickness (BFT) were measured weekly. During TP, DGC increased DMI by 2.2 kg/d compared with HMC ($P < 0.01$) but tended to increase DMI more with HS (3.4 kg/d) than LS (1 kg/d; interaction, $P = 0.12$). Treatments also interacted over time; DGC increased DMI throughout the TP for HS but only after the first week for LS compared with the HMC treatments ($P < 0.01$). There was no main effect of starch content on DMI. The effect of corn source diminished over time during the CO period ($P = 0.03$), with no main effects of treatment on DMI. Dry ground corn increased yields of milk by 2.6 kg/d ($P = 0.12$), 3.5% fat-corrected milk (FCM) by 4.3 kg/d ($P = 0.02$), fat by 165 g/d ($P = 0.03$), and protein by 165 g/d ($P = 0.01$) compared with HMC, with no effect of starch content throughout the TP. Starch source and content interacted ($P < 0.05$) to affect yields of fat and FCM during the CO period, which were greater for DGC-HS and HMC-LS (1.78 and 52.1 kg/d, respectively) than for DGC-LS and HMC-HS (1.62 and 48.6 kg/d, respectively). Dry ground corn tended to decrease BCS loss until the third week of TP ($P < 0.15$) compared with HMC but had no effect overall. No effects of treatment were detected for BFT during TP but HMC increased BFT 0.1 mm ($P = 0.04$) during the CO period. Ruminal fermentability of starch is an important consideration for diets of cows in the PP period.

Key Words: dry corn, fresh cows, high-moisture corn

Table 1503.

Item	LMP55	LHMP55	HMP43	SE
wk -6 to calving				
DMI, kg/d	14.6^{by}	14.6^{by}	16.4^{ax}	0.3
Plasma total protein, g/dL	7.5	7.4	7.7	0.1
Plasma urea nitrogen, mg/dL	11.0^{cz}	13.4^{by}	14.8^{ax}	0.4
wk 1 to 12				
DMI, kg/d	25.7	24.7	24.9	0.5
Milk, kg/d	51.3^{x}	47.5^{y}	47.8^{xy}	1.2
Solids-corrected milk, kg/d	50.9	47.9	49.3	1.1
Fat, %	4.08	4.14	4.34	0.10
True protein, %	3.08	3.17	3.19	0.04
wk 1 to 2				
Plasma total protein, g/dL	7.1	7.1	7.3	0.1
Plasma albumin, g/dL	3.5	3.4	3.4	0.1
Plasma nonesterified fatty acid, uEq/L	547	502	584	33
Blood β-hydroxybutyrate, mmol/L	0.65	0.67	0.74	-

^{abc} $P \leq 0.05$
^{xyz} $P \leq 0.10$

1502 Effects of feeding a histidine-deficient diet on lactational performance of dairy cows.

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A 10-wk randomized complete block design study with 24 Holstein cows (87 ± 22 days in milk and 630 ± 56 kg BW) was conducted to determine the effects of feeding a His-deficient diet on lactational performance of dairy cows. Following a 2-wk covariate period, cows were blocked by days in milk, milk yield, and parity and randomly assigned to one of the following 2 treatments: His-adequate diet (HAD; digestible His [dHis] supply of 75 g/d, or 2.8% of MP requirements) and His-deficient diet (HDD; dHis supply of 50 g/d, or 2.0% of MP requirements). Both HAD and HDD were supplemented with rumen-protected (RP) Met (Mepron; Evonik Nutrition & Care GmbH) and RP Lys (AjiPro-L; Ajinomoto Co., Inc.) supplying dMet and dLys at 2.5 and 2.4% and 7.5 and 7.2%, respectively, of MP requirements. At the end of the study, HDD was supplemented with RP His (an experimental product supplying 9.3 g/d of dHis; total dHis supply of 62 g/d, or 2.5% of MP requirements) for 9 d. The diets consisted of (DM basis) 45% corn and 20% alfalfa silages and 35% concentrates. Diets contained 16.3 and 16.2% CP, respectively, and supplied MP and NE_L in excess of cow requirements. Dry matter intake and yields of milk, energy-corrected milk, and milk protein were decreased ($P \leq 0.02$) by HDD (25.4, 37.6, 34.4, and 1.07 kg/d, respectively) compared with HAD (27.1, 40.5, 37.4, and 1.18 kg/d, respectively). Milk urea nitrogen was decreased ($P < 0.01$) by HDD vs. HAD. Feed and energy-corrected milk feed efficiencies, milk nitrogen efficiency, milk fat and protein concentrations, milk fat yield, and BW change of the cows were not affected by treatments ($P \geq 0.12$). Blood hemoglobin concentration was 5.4% lower ($P < 0.01$) in cows fed HDD compared with cows fed HAD, suggesting a provision of about 24 g of His from this endogenous depot during the 8-wk experimental period. Plasma His concentration was decreased ($P < 0.01$) by HDD vs. HAD. Supplementation of RP His increased DMI (26.6 vs. 25.1 kg/d; $P < 0.01$) but did not affect milk yield (36.0 vs. 34.8 kg/d; $P = 0.28$) compared with HDD during the last 9 d of the study. Overall, feeding a diet deficient in His but supplying adequate MP, Met, and Lys had negative effects on DMI and lactational performance of dairy cows. The effect on DMI was reversed when RP His was supplemented.

Key Words: dairy cow, dry matter intake, histidine

1503 The effect of metabolizable protein supply for dry Holstein dairy cows on periparturient feed intake, metabolism, and lactation performance.

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Some nutritionists increase MP supply for dry cows to improve subsequent lactation performance and health based on field observations. This study determined the effect of MP supply during the dry period on DMI, metabolism, and early lactation performance. Eighty Holstein cows that had completed ≥1 lactation were randomly assigned to treatments: 1) a 55-d dry period with approximately 84 g MP/kg DMI in the far-off (13.1% CP, 9.4% starch, and 51.7% NDF) and close-up (12.9% CP, 14.9% starch, and 47.0% NDF) diets (LMP55), 2) a 55-d dry period with approximately 84 g MP/kg DMI in the far-off diet (13.1% CP, 9.4% starch, and 51.7% NDF) and approximately 108 g MP/kg DMI in the close-up diet (14.5% CP, 15.1% starch, and 43.0% NDF; LHMP55), and 3) a 43-d dry period with approximately 108 g MP/kg DMI in a 1-group

diet (14.5% CP, 15.1% starch, and 43.0% NDF; HMP43). Close-up diets were fed for 3 wk before expected calving. Dry diets supplied ≥29 g Met/d and ≥91 g Lys/d. A fresh diet (15.6% CP, 21.7% starch, and 33.5% NDF) was fed for 2 wk and then a high diet (15.2% CP, 26.1% starch, and 30.2% NDF) was fed for 10 wk. Diets were modeled with CNCPS version 6.5. Cows were individually fed 1x/d, group housed, and milked 3x/d. Milk was sampled weekly. Coccygeal blood was collected −3 to 2 wk relative to calving. Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS with model effects of treatment, time, and treatment × time. Metabolism and lactation performance were not improved by providing additional MP during the dry period compared with a lower MP diet that met the Met and Lys requirements.

Key Words: dry period, metabolizable protein, transition cow

1504 Meta-analysis to predict amino acids limiting dairy cattle performance. I. J. Lean*[1], M. B. De Ondarza[2], C. J. Sniffen[3], and K. E. Griswold[4], *[1]Scibus, Camden, Australia, [2]Paradox Nutrition, West Chazy, NY, [3]Fencrest, LLC, Holderness, NH, [4]Kemin Industries, Inc., Des Moines, IA*.

Meta-analytic methods were used to provide statistical relationships between estimated MP (EMP) AA supply (g or g/ME) and milk protein content, milk protein percentage, and milk yield in lactating dairy cows. Sixty-three research publications (258 individual observations) were identified through a search of published literature using 3 search engines and met the criteria for inclusion in the meta-analysis. An advanced nutrition model (CNCPS 6.5 with NDS platform; RUM&N Sas, Italy) was used to determine dietary nutrient parameters including EMP AA. Two approaches were used to analyze the data: 1) a mixed models weighted analysis with a random effect of study to determine whether the explanatory variables predicted cow responses and 2) a classical effect size meta-analytical evaluation of responses to treatment. Regardless of the analytical approach or method of expression (g or g/ME), EMP Met increased milk protein yield, milk protein percentage, or milk yield, confirming that it can be first limiting in lactating dairy cow diets. With a difference of 0.07 units EMP His (g/ME) (1.13 vs. 1.20 for control and treatment, respectively), effect size analysis determined that each additional unit of EMP His (g/ME) increased milk protein yield by 1.72 kg, identifying His as a possible limiting AA. Milk yield increased by 3.28 kg/unit of EMP Trp (g/ME) (0.60 vs. 0.616 for control vs. treatment, respectively). Milk true protein yield was improved by EMP Leu (g). Estimated MP Lys (g or g/ME) did not increase responses in production outcomes. However, mean EMP Lys supply was lower than typically recommended and the change with treatment was minimal (157 vs. 162 g; 6.36 vs. 6.38% MP). This meta-analysis supports other research indicating the positive impact of Met and His as limiting AA for protein synthesis and suggests Leu, Trp, and Lys be given greater consideration in future research.

Key Words: amino acids, meta-analysis, milk protein

1505 Influence of essential amino acid balancing postpartum on lactation performance by dairy cows through a meta-analysis. L. F. Ferraretto*[1], C. S. Ballard[1], C. J. Sniffen[2], and I. Shinzato[3], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Fencrest, LLC, Holderness, NH, [3]Ajinomoto Heartland Inc., Chicago, IL*.

A meta-analysis was performed to evaluate the impact of dietary individual essential AA concentration (g of AA/Mcal of ME) on lactation performance by dairy cows during the initial 4 wk of lactation. The data set comprised 20 unpublished feeding trials evaluating the effect of lysine or lysine/methionine supplementation. Diets were formulated with CPM/CNCPS, which provided a complete dietary AA profile. Data were analyzed using Proc Mixed of SAS with treatments as fixed effects and trial as a random effect. Positive relationships between methionine and milk and milk protein yields were observed ($P < 0.10$ and $P < 0.07$, respectively) during wk 1 to 4. Actual and energy-corrected milk (ECM) yields increased ($P < 0.04$ and $P < 0.08$, respectively) along with lysine concentration on wk 1, 2, and 4 whereas milk protein yield increased ($P < 0.03$) during the 4 initial weeks of lactation. Arginine and threonine were negatively related to milk fat content and yield ($P < 0.07$ and $P < 0.10$, respectively) on wk 3 and 4. Quadratic relationships between milk or milk protein yields and dietary concentrations of leucine and phenylalanine ($P < 0.06$ and $P < 0.09$, respectively) were observed during wk 1 to 4. Isoleucine concentration was negatively related to ECM and milk protein yields ($P < 0.09$ and $P < 0.07$, respectively) during wk 3 and 4 and to milk and milk fat yields ($P < 0.09$ and $P < 0.05$, respectively) on wk 3. Dietary valine was positively related to ECM ($P < 0.10$) and negatively related to milk protein concentration ($P < 0.08$) on wk 2 and 3. On wk 3 and 4, a positive relationship between milk yield and valine was observed ($P < 0.08$). Dietary histidine was positively related to milk yield ($P < 0.07$) but negatively related to milk protein content ($P < 0.06$) on wk 2 to 4. Concentration of tryptophan was negatively related to ECM ($P < 0.07$), milk fat content ($P < 0.03$), and yield ($P < 0.02$). Overall, benefits on lactation performance were observed with increased concentrations of methionine, lysine, valine, and histidine. In contrast, isoleucine and tryptophan were negatively related to lactation performance whereas arginine and threonine depressed milk fat. These results underscore the importance of AA balancing beyond lysine:methionine ratio when formulating diets for early lactation dairy cows.

Key Words: amino acids, lactation performance, postpartum

1506 Canola meal in dairy cow diets during early lactation increases production compared with soybean meal. S. A. E. Moore*[1] and K. F. Kalscheur[2], *[1]University of Wisconsin-Madison, Madison, [2]USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI*.

Replacement of traditional protein sources such as soybean meal (SBM) with canola meal (CM) has resulted in increased milk yield for dairy cows in mid to late lactation. The objective was to determine performance of early lactation dairy cows fed diets formulated with CM or SBM as the main protein source at either a high (HI; 17.6%) or low (LO; 15.4%) CP concentration. Seventy-nine multiparous Holstein cows (mean ± SD, 2.76 ± 0.87 parity) received the treatment diet beginning at calving. Cows were blocked by calving date and maintained the same treatment assignment until the experiment ended at wk 16 of lactation. Diets were formulated to contain 39.6% corn silage, 15.4% alfalfa silage, and 45% concentrate mix on a DM basis. Canola meal was included at 19.4 and 11.9% DM, whereas SBM was included at 14.5 and 8.9% DM. Data were analyzed using the MIXED procedure of SAS. Body condition score and BW at calving and previous lactation mature equivalent 305 were used as covariates. Cows fed CM diets were has milk yield compared with cows fed SBM (mean ± SEM, 55.7 vs. 51.2 ± 0.97 kg/d; $P < 0.01$). Dry matter intake tended to be greater for cows fed CM diets (25.8 vs. 25.0 ± 0.34 kg/d; $P = 0.09$). The source of CP did not affect milk fat, protein, lactose, or total solids percentage. Decreasing dietary CP concentration increased milk fat (4.09 vs. 3.90 ± 0.07%; $P < 0.05$) and total solids (12.8 vs. 12.5 ± 0.95%; $P = 0.07$). Cows fed HI diets produced greater milk urea N (MUN) than cows fed LO diets (12.6 vs. 9.82 ± 0.22 mg/dL; $P < 0.01$). Milk urea N tended to be lower for cows fed CM compared with cows fed SBM (10.9 vs. 11.4 ± 0.22 mg/dL; $P = 0.10$). Milk fat, protein, lactose, and total solids were greater for cows fed CM in agreement with increased milk production. Dry matter intake, milk yield, milk protein percentage, and lactose percentage did not differ with varying CP concentration. Energy-corrected milk (ECM) was greater for cows fed CM compared with cows fed SBM (57.6 vs. 53.6 ± 0.95 kg/d; $P < 0.01$). Cows fed CM exhibited a trend in feed efficiency (ECM/DMI) compared with cows fed SBM (2.27 vs. 2.16 ± 0.38; $P = 0.06$). These data suggest milk yield and feed efficiency can be improved in early lactation with the inclusion of CM.

Key Words: canola meal, early lactation, transition period

1507 The effects of heat stress on protein metabolism in lactating Holstein cows. S. Gao[1], J. Guo[1], S. Quan[2], X. Nan[1], L. H. Baumgard[3], and D. Bu*[1,4,5], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, [2]The Animal Physiology and Biochemistry Laboratory of the Ministry of Agriculture in Nanjing Agriculture University, Nanjing, P. R. China, [3]Iowa State University, Ames, [4]Hunan Co-Innovation Center of Animal Production Safety, CICAPS, Changsha, P. R. China, [5]CAAS-ICRAF Joint Laboratory of Agroforestry and Sustainable Animal Husbandry, World Agroforestry Centre, East and Central Asia, Beijing, P. R. China*.

Independent of decreased feed intake, heat stress (HS) decreases the synthesis of milk protein, but the mechanisms responsible for the decrease are not clear. To research the direct (not mediated by feed intake) effect of HS on the synthesis of milk protein, four multiparous, lactating Holstein cows (101 ± 10 DIM, 574 ± 36 kg BW, and 38 ± 2.4 kg milk/d) were randomly assigned to four environmental chambers and divided into two groups, for two experimental periods of 18 d (a 9-d control period and a 9-d trail period). A crossover design was used and period 1 and 2 were separated by 30 d. Cows in the control period of both period 1 and 2 were exposed to constant thermal neutral (TN) conditions (20°C, 55% humidity, temperature–humidity index [THI] = 65.5, and 12 h light and dark cycles) and allowed to eat ad libitum for 9 d. The trial period of both period 1 and 2 included a HS ($n = 2$) group and a pair-fed TN (PFTN; $n = 2$) group and two groups exposed to HS (36°C from 0600 to 1800 h, 32°C from 1800 to 0600 h, 40% humidity, THI = 84.5, and 12-h light and dark cycles) and TN, respectively. The pattern and magnitude of reduced feed intake in the PFTN cows mirrored that of the HS cows. Compared with PFTN, HS decreased milk protein yield (17.7%) and content (4.1%) ($P < 0.05$). Heat stress increased before-feeding rumen liquid NH_3–N concentration compared with PFTN. Microbial CP, estimated by urinary excretion of purine derivatives, absorbed by intestine was not different between HS and PFTN cows. Heat stress decreased plasma AA (total AA and 5 specific of free AA) ($P < 0.05$) and plasma glucose ($P < 0.1$) and tended to increase BUN and increased urea nitrogen in urine and decreased NEFA. The decrease in plasma AA could have resulted from an increase in nonmammary AA oxidation or an increase in AA utilization for the synthesis of ligands involved with an acute phase protein response. Regardless, it appears blood AA utilization is reprioritized away from milk protein synthesis during HS.

Key Words: heat stress, milk protein, milk protein precursor, protein metabolism, restricted intake

1508 The effect of fructose infusion on dry matter intake in dairy cattle. R. Yair* and M. S. Allen, *Michigan State University, East Lansing*.

Loading of fructose or its analogs in mammals resulted in the accumulation of fructose 1-phosphate in the liver, sequestering organic phosphate (Pi), preventing ATP production, and most likely, as a consequence, increasing feed intake. The objectives of this work were to determine the effects of fructose and Pi infusions on feeding behavior of dairy cows to link hepatic ATP synthesis and feeding behavior and better understand the mechanisms controlling feed intake. Eight Holstein cows from 4 to 8 d postpartum (PP) were used in a duplicated 4 × 4 Latin square design experiment with one block each of multiparous and primiparous cows. Periods were 24 h, including a 2-h infusion and a 22-h recovery period. Treatments were arranged in a 2 × 2 factorial with fructose and Pi infusions as main effects. Cows were infused through a jugular catheter with 0.6 mol/h of fructose or glucose and 0.3 mol/h of NaCl or NaH_2PO_4. Effects of treatment on DMI were analyzed by ANOVA with repeated measures. Both fructose and Pi had hyperphagic effects; fructose increased DMI by 23.11% in the first 0.5 h of infusion compared with glucose (4.16 vs. 3.38 kg; $P < 0.01$) but the effect diminished over time with no effect detected by 1 h following the start of infusion. An interaction was detected between Pi and block ($P = 0.06$); NaH_2PO_4 increased DMI over the 2-h infusion period by 36.9% compared with NaCl for multiparous cows (8.41 vs. 6.14 kg; $P < 0.001$) but did not affect DMI for primiparous cows. Although effects of fructose on DMI hints at a connection between ATP synthesis and intake, Pi infusion was expected to reduce the effect of fructose by providing Pi for ATP synthesis rather than increasing intake. It is possible that the infused phosphate did not enter the liver and, therefore, did not have the expected effect. Reducing dietary P is essential to limit P excretion. Previous works showed that feeding P levels similar to this work (0.37% of DM) does not reduce DMI; however, such level might be insufficient specifically for cows in the PP period. Accordingly, further research to understand the hyperphagic effect of Pi might have implications for diet formulation for cows in the PP period. Better understanding the effects of Pi and fructose on hepatic ATP synthesis should provide insights on the connection between ATP synthesis and feeding behavior in dairy cows.

Key Words: dry matter intake, fructose, phosphate

1509 Effects of maternal nutrient restriction and melatonin supplementation on vascularity in ovine maternal and fetal jejunum. G. Jia*, *North Dakota State University, Fargo*.

Mounting evidence from previous studies suggests that melatonin, a neurohormone secreted by the pineal gland, likely plays a role in regulating nutrient delivery by regulating blood flow and improving vascular development. Therefore, this study was conducted to investigate the effect of maternal nutrient restriction and melatonin supplementation on vascular development of maternal and fetal small intestine in sheep. Thirty-one primiparous ewes were randomly assigned to receive 5 mg of melatonin/d (MEL) or no melatonin (CON) and 100 (adequate fed [ADQ]) or 60% (restricted [RES]) of nutrient recommendations from d 50 to 130 of gestation. At d 130 of gestation, ewes were euthanized and small intestinal (jejunal) tissues were collected from the dam and fetus. Intestinal capillaries were stained using Anti-CD31 (Abcam) followed by fluorescently labeled goat anti-rabbit secondary antibody (Alexa Fluor 633; Abcam). A DAPI stain was used to counterstain cell nuclei. Z-stacks of 15-μm-deep optical sections of jejunal tissues including intact villi were obtained using a confocal laser-scanning microscope (Zeiss AxioObserver Z1 with LSM700). Rendered 3D images were analyzed for capillary volume, which was expressed as a percentage of the total villous volume by using Imaris 7 software (Bitplane, South Windsor, CT). Data were analyzed as a completely randomized design, with a 2 × 2 factorial arrangement of treatments. In the maternal jejunum, there was no effect of maternal melatonin treatment or nutritional level on capillary volume density ($P > 0.59$); however, due to the large decrease in jejunal mass (RES only 0.69 of ADQ; $P < 0.001$), total jejunal vascularity was decreased ($P = 0.02$) in RES ewes vs. ADQ ewes. For the fetal intestine, neither capillary volume density nor total intestinal vascularity was affected by MEL supplementation or nutritional level, and a melatonin × nutrition interaction was not observed. Our data suggest that nutritional level affects maternal jejunal mass and total vascularity. However, neither melatonin supplementation nor nutritional level affected capillary volume density of maternal jejunum or capillary volume density or total vascularity of fetal intestine. Future research is needed to investigate whether maternal melatonin supplementation or nutritional level, or both, postnatally affect vascularity of the intestine.

Key Words: intestine, maternal melatonin treatment, vascularity

1510 Production level of dairy cows affects the extent of diet-induced milk fat depression. Y. Sun*, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing*.

The interaction between diet and milk production level on the risk of diet-induced milk fat depression (MFD) was evaluated in a crossover design experiment with a covariate period. Thirty-two mid- and late-lactation multiparous Holstein cows (14 rumen cannulated and 18 noncannulated), with a wide range and uniform distribution of milk yield (25 to 60 kg/d), were randomly assigned to treatment sequence within level of milk yield. Treatment diets and composition (% DM) were 1) control diet (CON), containing 24% starch, 33% NDF, 22% forage NDF, and 3% fatty acids, and 2) MFD-inducing diet (MFDI), containing 30% starch, 28% NDF, 17% forage NDF, and 4% fatty acids. Treatment periods were 28 d with the last 7 d for data and sample collection. The statistical model included the random effect of cow and fixed effects of period, treatment, cannulation block, and the interactions of cannulation block and treatment and of treatment and period. Linear and quadratic effects for the interaction between covariate milk yield and treatment were added to evaluate responses to treatment by level of milk yield. The MFDI decreased milk fat concentration (3.31 vs. 3.69%; $P < 0.01$) and tended to decrease milk fat yield (1.21 vs. 1.28 kg; $P < 0.10$) and 3.5% fat-corrected milk (35.6 vs. 37.0 kg; $P < 0.10$) compared with the CON. There was no main effect of treatment on DMI but treatments interacted with covariate milk yield ($P < 0.01$); MFDI decreased DMI for higher producing cows but increased DMI for lower producing cows. Linear interactions ($P < 0.10$) were detected between treatment and covariate milk yield for milk fat content and yields of milk fat and 3.5% fat-corrected milk; compared with CON, MFDI decreased content and yield of milk fat and 3.5% fat-corrected milk to a greater extent in higher producing cows than lower producing cows. The MFDI treatment decreased mean ruminal pH compared with CON (6.00 vs. 6.13; $P < 0.01$), and treatments interacted with covariate milk yield ($P < 0.10$), with less difference between CON and MFDI in higher producing cows than lower producing cows. Compared with CON, MFDI increased BCS change (0.18 vs. 0.11; $P < 0.01$) but response was not related to covariate milk yield. In conclusion, higher producing cows were at higher risk for milk fat depression induced by a high-starch, low-forage NDF diet containing supplemental fat.

Key Words: milk fat depression, production level, rumen pH

1511 Effect of production level and parity on responses of milk fat to supplementation with 2-hydroxy-4-(methylthio)butanoate. M. Baldin*[1], H. A. Tucker[2], and K. J. Harvatine[1], *[1]Penn State University, University Park, PA, [2]Novus International Inc., St. Charles, MO*.

We previously reported that high-producing cows are at higher risk of biohydrogenation-induced milk fat depression (MFD) and that 2-hydroxy-4-(methylthio)butanoate (HMTBa) reduced MFD in high-risk situations. The objective was to determine the relationship between production level and parity and responses of milk fat to supplementation with HMTBa (ALIMET; Novus International, Inc., St. Charles, MO). Twelve primiparous and 24 multiparous Holstein cows were used in a crossover design preceded by a 14-d pretrial period. The 35-d treatment periods included 28 d of a low-risk diet (31% NDF, 27% starch, and 4.2% EE) followed by 7 d of a moderate-risk diet (29% NDF, 30% starch, and 1% soybean oil). Treatments were control (corn carrier) and HMTBa (0.1% of diet DM). At the end of pretrial period, cows averaged 127 ± 33 DIM (mean ± SD) and 41 ± 9 kg milk/d (minimum 27 kg/d and maximum 61 kg/d). Milk yield and DMI were measured daily, and milk was sampled every 7 d and analyzed for fat and protein concentration. Data were analyzed using PROC MIXED with repeated measures, with cow by treatment as the subject, and the effect of treatment was tested at each time point. During the low-risk phase, no overall effect of treatment or treatment × time interactions were observed for DMI, milk yield, and milk fat and protein yield and concentration ($P > 0.2$ for all). Additionally, no treatment × parity or treatment × parity × time interactions were observed for milk fat concentration ($P = 0.2$) and yield ($P = 0.9$). During the moderate-risk phase, no overall effect of treatment or treatment × time interactions were observed for DMI, milk yield, and milk protein concentration and yield ($P > 0.4$ for all). 2-Hydroxy-4-(methylthio)butanoate supplementation maintained higher milk fat concentration (3.67 vs. 3.86; $P < 0.001$) and yield (1.37 vs. 1.47; $P < 0.001$) at the end of the moderate-risk phase. No treatment × parity or treatment × parity × time interactions were observed for milk fat variables ($P > 0.4$ for both). On d 35, responses (HMTBa; control) of milk fat concentration and yield correlated positively with pretrial milk yield (0.35 [$P = 0.03$] and 0.38 [$P = 0.02$], respectively). In conclusion, HMTBa maintained milk fat yield when cows were fed a diet with moderate risk of biohydrogenation-induced MFD and milk fat response to treatment was correlated with production level but not affected by parity.

Key Words: HMTBa, milk fat

1512 The timing of feed availability entrains the circadian rhythm of milk synthesis in dairy cattle. I. J. Salfer*, J. Y. Ying, and K. J. Harvatine, *Penn State University, State College, PA*.

Dairy cows have well-recognized natural daily rhythms of feed intake and milk synthesis. However, little is known about the regulation of these circadian rhythms. Variation in feed intake throughout the day results in a daily pattern of nutrient absorption, which may entrain the rhythm of milk synthesis. The objective of this study was to investigate the effect of the timing of feed availability on the daily rhythm of milk synthesis. Sixteen cows were randomly assigned to one of two treatment sequences in a crossover design. All cows were fed the same total mixed ration ad libitum for 16 h/d either during the day (DF) or the night (NF). Cows on the DF treatment had feed available from 0700 to 2300 h, whereas NF cows were offered feed from 1900 to 1100 h. Treatment periods were 17 d, and cows were milked every 6 h the last 7 d of each period. Milk samples were collected at each milking on the final 2 d of each period and analyzed for fat, protein, and milk urea nitrogen (MUN). Blood samples were collected on the final 3 d of each period to represent every 4 h over the day. Body temperature was monitored using vaginal temperature loggers. Data was analyzed as a crossover design in Proc Mixed and by cosine analysis to determine the phase (time at peak) and amplitude (peak to mean) of daily rhythms. Milk yield; fat and protein yield; and fat, protein, and MUN concentration displayed 24-h rhythms. Treatment modified the rhythm of milk yield, protein yield, and MUN, fat, and protein concentration ($P < 0.05$). Briefly, milk yield and lactose concentration were phase delayed by approximately 4 h in NF cows ($P < 0.05$). The daily rhythms of fat, protein, and MUN concentration of NF cows were phase advanced by 2, 10, and 3 h, respectively ($P < 0.05$). The rhythms of fat, protein, and MUN concentration exhibited a greater amplitude in NF compared with DF. Blood glucose followed a daily rhythm that was not affected by the timing of feed availability ($P > 0.10$). There was a daily rhythm of body temperature that was phase advanced 4 h by NF ($P < 0.05$). The timing of feed availability modified the rhythm of milk synthesis and body temperature in dairy cattle but did not modify the daily pattern of plasma glucose.

Key Words: circadian rhythm, food entrainment, milk synthesis

1513 Characterization of peripartum liver and skeletal muscle ceramide concentrations in lean and overweight Holstein dairy cows. S. Saed Samii*, J. E. Rico, and J. W. McFadden, *West Virginia University, Morgantown*.

Circulating sphingolipid ceramide is associated with the development of insulin resistance in overweight monogastrics. An increase in NEFA delivery to the liver can increase lipoprotein ceramide packaging and secretion. In turn, lipoprotein ceramide can antagonize insulin action in skeletal muscle. We recently discovered that ceramide concomitantly increases with hyperlipidemia in overweight cows transitioning from gestation to lactation. Considering evidence in monogastrics, our objective was to characterize the relationship between adiposity and liver and skeletal muscle ceramide concentrations. Multiparous Holstein cows were grouped by adiposity at d −28 prepartum as either lean (2.9 ± 0.1 BCS; $n = 7$; LEAN) or overweight (4.0 ± 0.2 BCS; $n = 7$; OVER). Diets were formulated to meet or exceed requirements. Blood samples were routinely collected from d −21 to 21, relative to calving, and liver and skeletal muscle biopsies were performed at d −21, −7, and 4. Liquid chromatography tandem mass spectrometry was used to quantify ceramide, monohexosylceramide (GlcCer), and lactosylceramide (LacCer). Data were analyzed as repeated measures using a mixed model with fixed effects of adiposity and time. Pearson's correlations were analyzed. Relative to LEAN, OVER experienced increased BCS loss, plasma NEFA, hepatic total lipid accumulation, and circulating ceramide (e.g., C24:0-ceramide) during the transition from gestation to lactation ($P < 0.05$). Comparable to plasma, C24:0-ceramide was the most abundant ceramide in the liver and muscle. To support a relationship between liver and plasma ceramides, plasma total ceramide and liver total ceramide were positively correlated during transition ($r = 0.39$, $P < 0.05$). Similarly, plasma C24:0-ceramide and liver C24:0-ceramide were positively correlated ($r = 0.41$, $P < 0.05$). Coinciding with an increase in circulating NEFA, hepatic total ceramide and C24:0-ceramide increased postpartum in OVER ($P < 0.05$). Liver total ceramide and C24:0-ceramide were positively correlated with plasma NEFA ($r = 0.44$ and 0.49, respectively; $P < 0.05$). Additionally, we observed an increase in postpartum hepatic C22:0-ceramide in OVER ($P < 0.05$). Hepatic total GlcCer tended to be increased postpartum for all cows ($P = 0.10$); however, hepatic total LacCer increased only in LEAN ($P < 0.05$). Muscle total ceramide and C24:0-ceramide levels were lower prepartum in OVER ($P < 0.05$). In contrast, postpartum muscle C16:0- and C24:0-ceramide were higher in OVER ($P < 0.05$). We conclude that enhanced lipolysis in overweight dairy cows increases hepatic ceramide synthesis to support ceramide accumulation in circulation. The ability of hepatic-derived ceramide to antagonize insulin action in extrahepatic tissues

during early lactation requires further investigation.

Key Words: ceramide, insulin resistance, peripartal dairy cow

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1514 Variation in rumen epithelial fatty acid metabolism and cholesterol homeostasis contributes to different responses to the high-grain diet adaptation in beef cattle. K. Zhao*[1,2], Y. Chen[1], G. B. Penner[3], M. Oba[1], and L. L. Guan[1], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]College of Medicine, Xi'an Jiaotong University, Xi'an, P. R. China, [3]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada*.

Ruminal digestive disorders are common during high-grain diet transition. However, little is known about the mechanism regulating this process, especially at the transcriptional level. In this study, we conducted a genomewide transcriptome comparison of ruminal epithelia when cattle were exposed to a rapid high-grain transition. Transcriptome analysis of ruminal papillae, collected from 15 beef heifers when fed 3 different dietary steps during the transition (3, 75, and 92% grain), were performed using RNA-seq. Expression of 11,044, 11,322 and 11,282 genes were detected (with reads per million [RPM] > 1 in 15 heifers of each diet) under the 3, 75, and 92% grain diets, respectively. Principle component analysis showed that the transcriptome profile of rumen epithelia between the low-grain diet (LGD; 3%) and high-grain diets (HGD; 75 and 92%) were different. During the transition from 75 to 92% grain, the ruminal pH showed varied change patterns: decreased (DG; $n = 5$) or increased (UG; $n = 5$). When the ruminal tissue transcriptomes were compared between 75 and 92% grain diets (92 vs. 75%) in each group, the expression of some ketone body and cholesterol synthesis–related genes tended to be decreased in UG (*acetyl-CoA acetyl transferase 2* [*ACAT2*], *3-hydroxy, 3-methylglutaryl CoA synthase 1* [*HMGCS1*], *HMG-CoA reductase* [*HMGCR*], and *farnesyl diphosphate synthase* [*FDPs*]) ($P < 0.1$), whereas some other cholesterol biosynthesis- and ketogenesis-related genes tended to be increased in DG (*sterol regulatory element binding transcription factor 2* [*SREBF2*] and *HMG-CoA lyase* [*HMGCL*]) ($P < 0.1$). Furthermore, the proton and cholesterol efflux–related genes were increased (Na^+/H^+ *exchanger 3* [*NHE3*] and *ATP-binding cassette 1* [*ABCA1*]) in UG ($P < 0.05$), whereas *monocarboxylate transporter 4* (*MCT4*) showed a tendency to be decreased in DG ($P < 0.1$). These results suggest DG heifers may have greater intracellular cholesterol and a reduction in intracellular pH, which might imbalance the epithelial homeostatic status. Pathway analysis showed that the differentially expressed genes in DG were involved in the "T cell receptor signaling" and "complement and coagulation cascades" pathway, whereas UG might activate cell repair function through "p53 signaling pathway" and cell cycle arrest. Overall, the different gene networks controlling fatty acid metabolism and cholesterol homeostasis among individuals might account for the animal variation in ruminal responses during high-grain diet adaptation in beef cattle.

Key Words: beef cattle, high-grain diet, rumen transcriptome

1515 Dose response effect of acetate on milk fat synthesis in lactating dairy cows. N. L. Urrutia*[1], M. Baldin[1], J. Y. Ying[2], Y. Fan[1,3], K. J. Harvatine[1], and J. Carvalho[1], *[1]Penn State University, University Park, PA, [2]Penn State University, State College, PA, [3]China Agricultural University, Beijing, P. R. China*.

Acetate is the main source of energy and substrate for milk fat synthesis in the dairy cow; however, the effect of acetate supply on milk fat synthesis has not been investigated in high-producing cows. The objective was to investigate the dose-dependent effect of acetate on milk fat synthesis. Six ruminally cannulated multiparous lactating Holstein cows were randomly assigned to treatments in a 4 × 4 Latin square design. Treatments were 0 (control), 5, 10, and 15 mol/d of acetate. Acetate was neutralized to pH 6.1 with sodium hydroxide and continuously infused into the rumen in 5 L/d for 4 d with 7-d washout periods. Milk samples were collected daily. Blood and rumen samples were collected twice (before noon and after noon) on the last day of treatment. Time course data was analyzed as repeated measures in SAS and all other data was analyzed using JMP Pro. The model included the random effect of cow and period and the fixed effect of treatment. Rumen concentration of acetate ($P < 0.01$) and acetate:propionate ratio ($P < 0.001$) linearly increased before feeding (before noon) and rumen concentration of acetate ($P < 0.001$), butyrate ($P < 0.05$), and total VFA ($P < 0.01$) linearly increased after feeding (after noon) as acetate dose increased. Acetate infusions linearly increased rumen pH before feeding ($P < 0.005$). Dry matter intake, milk yield, and protein yield and concentration were not affected by treatments. Acetate dose had a quadratic effect on milk fat yield ($P < 0.001$) and a linear effect on milk fat concentration ($P < 0.001$). Fat yield increased 7, 16, and 14% and fat concentration increased 6, 9, and 11% at 5, 10, and 15 mol/d, respectively, compared with the control. Acetate linearly increased yield and concentration of palmitic acid and yield of de novo synthetized fatty acids (both $P < 0.001$). Acetate infusions had no effect on plasma NEFA, glucose, glucagon, or insulin but linearly increased plasma βHBA after feeding ($P < 0.01$). These results demonstrate that acetate supply has an impact on milk fat synthesis under normal dietary conditions and suggest that milk fat yield and concentration may be improved through dietary strategies that increase rumen acetate production.

Key Words: acetate, milk fat synthesis, rumen infusion

1516 Lipogenic gene network expression in mammary tissue in response to abomasal infusion of casein, glucose, and acetate into feed-restricted lactating cows. M. A. C. Danes*[1,2], F. Batistel[3], G. A. Broderick[4], M. A. Wattiaux[5], and J. J. Loor[3], *[1]Federal University of Lavras, Lavras, Brazil, [2]University of Wisconsin, Madison, [3]University of Illinois, Urbana, [4]Broderick Nutrition & Research, LLC, Madison, WI, [5]University of Wisconsin-Madison, Madison*.

Nutrients that are building blocks of the main milk components also can work as regulators of the synthesis of these products through cell signaling pathways regulated at the transcriptional level. Six Holstein multiparous cows, averaging 40 kg milk/d, were used in a 6 × 6 Latin square with 14-d periods. Cows were fed the same diet for 10 d in each period, after which they were feed restricted for 4 d to 85% of ad libitum intake and abomasally infused with 1 of 6 treatments: acetate (A) or glucose (G), each at 5% of ad libitum ME intake (Mcal/d); casein (C) at 15% of ad libitum MP intake (g/d); A + C (AC); G + C (GC); or a saline solution (S; negative control). The mean milk fat yield was 1.58, 1.55, 1.42, 1.65, 1.51, and 1.41 kg/d for A, G, C, AC, GC, and S, respectively. Mammary tissue was biopsied on the last day of each period. The expression of lipogenic gene networks was evaluated via quantitative RT-PCR of 11 genes. Data were log2 transformed and analyzed using the GLIMMIX procedure of SAS. Infusion of all nutrients upregulated ($P < 0.05$) *ACSS2*, *ACACA*, and *FASN*, which are involved in acetate activation and de novo fatty acid synthesis. Surprisingly, A alone did not cause a greater effect than C and G, but when AC was infused, the expression of these genes was the greatest (approximately 2- to 3-fold greater), suggesting a role of AA in regulating fatty acid synthesis. This was even more evident in the upregulation ($P < 0.05$) by AC of *FABP3*, encoding a cytosolic transport protein required for use of fatty acids in triacylglycerol synthesis. Acetate and AC upregulated *IDH1* (approximately 2- to 5-fold), which encodes the main enzyme responsible for NADPH synthesis in mammary cells. This response agreed with the gene data indicating an overall stimulation of fatty acid synthesis especially in the AC treatment. There was no treatment effect ($P > 0.05$) on *AGPAT6*, *DGAT1*, *LPIN1*, and *PPARG*. Unexpectedly, A downregulated ($P < 0.05$) the lipogenic transcription factor *SREBF1*, which previously has been associated with fatty acid synthesis regulation in mammary tissue during milk fat depression. However, the fact that AC induced a strong tendency ($P = 0.08$) for upregulation (2-fold) of the transcription regulator *RXRA* compared with S underscores a potentially important role in the nutritional regulation of milk fat synthesis. Results underscore the role of nutrients in regulating mammary fatty acid synthesis at the transcriptional level.

Key Words: milk fat synthesis, nutrigenomics

1517 The effects of feeding increasing concentrations of corn oil on energy metabolism and nutrient balance in finishing beef steers. K. E. Hales*, A. P. Foote, T. M. Brown-Brandl, and H. C. Freetly, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

The use of added fat source is common in high-concentrate finishing diets. The objective of our experiment was to determine if feeding increasing concentrations of added dietary corn oil would decrease enteric methane production, increase the ME:DE ratio, and improve retained energy in finishing beef steers. Four treatments were used in a replicated 4 × 4 Latin square ($n = 8$; initial BW = 397 kg ± 3.89). Data were analyzed using a Mixed model with the fixed effects of period and dietary treatment and random effects of square and steer within square. Treatments consisted of 1) 0% added corn oil (Fat-0), 2) 2% added corn oil (Fat-2), 3) 4% added corn oil (Fat-4), and 4) 6% added corn oil (Fat-6). Dry matter intake or GE intake did not differ across diets ($P > 0.39$). As a proportion of GE intake, fecal energy loss and DE loss did not differ by treatment ($P > 0.27$); however, urinary energy loss tended to linearly decrease as corn oil increased in the diet ($P = 0.09$). Additionally, methane energy respired linearly decreased as corn oil increased in the diet ($P < 0.01$). No differences were detected in ME loss as a proportion of GE intake ($P > 0.98$); however, the ME:DE ratio linearly increased as corn oil increased in the diet ($P < 0.01$). No differences in retained energy or heat production as a proportion of GE intake were noted ($P > 0.59$). Dry matter digestibility did not differ across diets ($P > 0.36$). Digestibility of NDF as a proportion of intake quadratically responded, increasing from 0% corn to 4% corn oil and decreasing thereafter ($P = 0.02$). Furthermore, ether extract digestibility as a proportion of intake quadratically increased, increasing from 0 to 4% corn oil inclusion before reaching a plateau ($P < 0.01$). No differences were detected in OM digestibility across treatments ($P > 0.35$). From these data, we interpret that adding dietary fat decreases urinary energy loss and enteric methane production while decreasing NDF digestibility when included at more than 4% of dietary DM. Moreover, the ME:DE ratio linearly increases as dietary fat increases. The USDA is an equal opportunity provider and employer.

Key Words: dietary fat, energetics, finishing cattle

1518 Isolation and comparison of expression of novel glucose transporters, GLUT3 and GLUT14, in bovine uteroplacental tissues from days sixteen to fifty of gestation. M. S. Crouse*, J. S. Caton, K. J. McLean, P. P. Borowicz, L. P. Reynolds, C. R. Dahlen, and A. K. Ward, *Department of Animal Sciences, North Dakota State University, Fargo*.

Glucose transporters *GLUT3* and *GLUT14* previously have not been isolated in ruminant utero-placenta. The glucose transporter *GLUT14* is a duplicon of *GLUT3* with 95% shared homology. We hypothesized that maternal nutrition and day of gestation would impact mRNA expression of *GLUT3* and *GLUT14* in heifers and that there would be a difference in mRNA expression between the two transporters. Crossbred Angus heifers (n = 49) were synchronized, bred via AI, assigned to nutritional treatment (CON = 100% of requirements to gain 0.45 kg/d and RES = 60% of CON), and ovariohysterectomized on d 16, 34, or 50 of gestation (n = 6 to 9/d); nonpregnant (NP) controls were not bred and ovariohysterectomized on d 16 of the synchronized estrous cycle (n = 6). The resulting treatment arrangement was a 2 × 3 factorial + 1. Utero-placental tissues (caruncle [CAR], intercaruncular endometrium [ICAR], fetal membrane [chorioallantois] [FM], cotyledon [COT], intercotyledonary placenta [ICOT], and amnion [AMN]) were obtained from the pregnant uterine horn immediately after ovariohysterectomy. For NP controls, only CAR and ICAR were obtained. Comparison of expression across tissues was achieved by using NP CAR and ICAR tissues as the baseline. For FM, COT, ICOT, and AMN, NP endometrium served as the baseline. Expression of *GLUT3* was greater ($P < 0.05$) on d 50 in CAR compared with d 16 CAR. In FM, *GLUT3* was greater ($P < 0.05$) on d 16 compared with to d 50 FM. There also was a significant day × tissue interaction for *GLUT3*, which was greater ($P < 0.01$) in d 50 CAR compared with all other tissues and days. Expression of *GLUT14* in CAR was greater ($P < 0.05$) on d 50 compared with d 16 and 34. Direct comparison of the two genes showed that *GLUT14* expression was 5-fold greater ($P < 0.01$) than *GLUT3* expression across all days, tissues, and treatments. There was a significant gene × tissue interaction ($P < 0.01$), such that *GLUT14* was greater in ICAR and intermediate in CAR compared with FM and compared with *GLUT3* in all tissues. These data demonstrate that glucose transporters *GLUT3* and *GLUT14* are expressed in ruminant utero-placenta and also support our hypothesis that the magnitude of mRNA expression of *GLUT3* differs from that of *GLUT14*. There were no effects, however, of nutritional treatment or day of gestation within gene.

Key Words: early gestation, facilitated transporters, glucose

1519 Does microbial contamination affect in situ estimation of crude protein degradability of concentrate feedstuffs? A. C. B. Menezes*[1], S. C. Valadares Filho[2], P. P. Rotta[3], S. A. Santos[4], D. Zanetti[5], M. V. C. Pacheco[1], B. C. Silva[5], H. M. Alhadas[1], J. M. V. Pereira[1], and P. Pucetti[1], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Colorado State University, Fort Collins, [4]Universidade Federal da Bahia, Salvador, Brazil, [5]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*.

Microbial contamination (MC) is an important source of errors in in situ methods, thereby resulting in underestimation of CP degradability as well as overestimation of RUP content. The aim of this study was to use ^{15}N to estimate the MC of fractions soluble (a), potentially degradable (b), and the rate of digestion of the fraction b (kd) of CP as well as to estimate the necessary incubation time to estimate the RDP of energy and protein feeds considering two outflow rates (0.05 and 0.08 h^{-1}). Twelve concentrates were evaluated: six energy concentrates—wheat bran, rice meal, ground corn, ground sorghum, ground corn cob, and soybean hulls—and six protein concentrates—cottonseed meal 38% CP, soybean meal, ground bean, peanut meal, sunflower meal, and corn gluten meal. The feeds were divided into 4 groups and they were ruminally incubated in 4 crossbred bulls for 0, 2, 4, 8, 16, 24, 48, and 72 h. To estimate the MC of the incubated residues, ruminal bacteria were labeled with ^{15}N via continuous intraruminal infusion of $^{15}(NH_4)_2SO_4$. Ruminal digesta was collected for the isolation of bacteria before the first infusion of ^{15}N and after the infusion of ^{15}N during the collection period. There was no difference ($P = 0.74$) in the parameters a, b, and kd, corrected and uncorrected for MC. All the feeds followed an exponential model of degradation and the model fitted well to the data, except for corn gluten meal; probably, the maximum incubation time used here (72 h) was not long enough to allow an accurate estimation of degradation profile. The cluster analysis allowed ($R^2 = 0.944$) grouping feeds into three different groups according to the necessary incubation time to estimate RDP. The first was formed by the high-starch energy concentrates (15.4 ± 0.46 h), the second by the low-starch energy concentrates (6.8 ± 0.60 h), and the third by the protein concentrates (9.9 ± 0.41), considering kp 0.05 h^{-1}. In conclusion, the MC was low and nonsignificant, so correction of ruminal protein degradation is irrelevant for the concentrate studied. However, the chemical composition of these feeds resulted in different incubation times to estimate RDP content, and it needs to be considered in techniques used to estimate CP digestibility in the rumen and intestines.

Key Words: microbial contamination, protein, rumen degradable protein

1520 Effect of concentrate type (starch vs. fiber) and bicarbonate addition in grass silage–based diets on performance, diet digestibility, and enteric methane emissions in lactating dairy cows. A. Bougouin*, A. Ferlay, M. Doreau, Y. Rochette, S. Rudel, C. Lascoux, and C. Martin, *INRA-UMR1213 Herbivores, Saint-Genes-Champanelle, France*.

Cereals and corn silage diets are extensively used for high-yielding dairy cows and it is well established that altering dietary starch and fiber proportion results in methane (CH_4) emissions mitigation. With grass silage-based diets, quantitative evidence of CH_4 emissions reduction with high-starch concentrate is lacking. Therefore, the objective was to compare the effects of fiber-rich (F) or starch-rich (S) diets based on grass silage, supplemented or not with bicarbonate (Fb and Sb), on CH_4 emissions, diet digestibility and performance in dairy cows. Four multiparous lactating Holstein cows were used in a 4 × 4 Latin square design experiment of 4 periods of 4 wk each. Four dietary treatments were assigned based on grass silage 42%, hay 8%, and 50% F or S concentrate (DM basis), supplemented or not with sodium bicarbonate (1% DMI). Bicarbonate was used as a digestive regulator to lower the risk of ruminal acidosis appearance. Intake and milk production were measured daily and milk composition was measured weekly during the experiment. Methane production and diet digestibility were measured simultaneously for the last 5 d of each period when cows were in open respiration chambers. Feed efficiency (fat- and protein-corrected milk/DMI) was calculated using data from wk 4. Data were analyzed using mixed-effect models with cows as a random effect and period and treatments as fixed effects. Orthogonal contrasts were used to evaluate diet type or bicarbonate supplementation effects. The S and Sb diets induced less daily CH_4 emissions (417.5 and 393.9 g/d, respectively) than F and Fb diets (487.9 and 506.4 g/d, respectively) as well as a significant decrease in CH_4 intensity (−14% in g/DMI and −20% in g/FPCM). Dry matter intake was reduced by 3.5% with the starch diets compared with fiber diets ($P < 0.05$). Total tract digestibility of nutrients (DM, OM, and starch) and GE were lower ($P < 0.05$) for F and Fb diets than for S and Sb diets. Feed efficiency and milk yield and fat content were not different between starch and fiber diets ($P > 0.05$) but milk protein content was greater for the starch diets (+3%; $P < 0.05$). Bicarbonate had no effect on diet digestibility and CH_4 emissions ($P > 0.05$). However, milk fat content was higher ($P = 0.05$) with Sb than S, F and Fb diets. Feeding 50% starch-rich concentrate with grass silage diets, with or without bicarbonate, is an effective dietary approach for reducing methane emissions without altering diet digestibility and milk performance of dairy cows.

Key Words: concentrate type, dairy cow, methane emissions

1521 Validation of the GreenFeed system against model-predicted methane emissions. P. Huhtanen[1], M. Ramin[1], and A. N. Hristov*[2], *[1]Swedish University of Agricultural Sciences (SLU), Umeå, Sweden, [2]The Pennsylvania State University, University Park*.

The GreenFeed (GF) system (C-Lock Inc., Rapid City, SD) was introduced to estimate methane (CH_4) emission by measuring gas concentrations and flux when cattle visit a GF. The objective of the present study was to validate CH_4 measured with the GF system with model-predicted CH_4 emissions. Evaluation was based on 55 treatment means from dairy and beef cattle studies, in which CH_4 emission was measured by GF. Methane emission was predicted with the models of Yan et al. (2000; models Y1 and Y2), Ellis et al. (2007; E), Jentsch et al. (2007; J), and Ramin and Huhtanen (2013; R1 and R2). If the parameter values required in the models were not reported, tabulated values were used. A concentration of 18.5 MJ GE/kg DM was assumed for models based on GE intake. The evaluation was based on root mean squared prediction error (RMSPE) expressed as a proportion of observed mean. The RMSPE was divided into errors resulting from mean bias, slope bias, and random error across regression line. Observed mean (SD) CH_4 emission, DMI, and dietary concentrations of CP and NDF were 386 g/d (103), 18.4 kg/d (5.6), 172 g/kg DM (34), and 401 g/kg DM (81), respectively. Mean CH_4 emission estimated by GF was close to values predicted by models Y, J, and R that were developed from respiration chamber data (Table 1). However, observed CH_4 values were much higher than those predicted by model E, which was developed from

Table 1521. Predicted CH_4 emission (observed, 386 g/d).

					Distribution of MSE			P-value	
Model	Predicted CH4, g/d	R^2	RMSPE	% of mean	Mean bias	Slope bias	Random error	Mean bias	Slope bias
Y1	395	0.898	34.2	8.9	0.062	0.019	0.919	0.07	0.31
Y2	394	0.925	28.6	7.4	0.066	0.007	0.927	0.06	0.53
J	371	0.949	28.7	7.4	0.281	0.091	0.628	<0.01	<0.01
E	294	0.900	103.1	26.7	0.800	0.104	0.095	<0.01	<0.01
R1	382	0.952	23.2	6.0	0.034	0.037	0.929	0.18	0.15
R2	376	0.954	24.1	6.2	0.180	0.006	0.814	<0.01	0.55

data determined by different techniques. The RMSPE ranged from 6 to 9% of observed mean except model E, with most of the error due to random variation. The RMSPE was smaller when the effect of feeding level was taken into account compared with a model based only on intake (Y2 and J vs. Y1 and E). The RMSPE was further reduced when the effects of diet digestibility and composition were taken into account in addition to intake (R1 and R2 vs. the others). It is concluded that CH_4 emissions estimated by GF were consistent with values predicted by models derived from large data sets from respiration chamber studies.

Key Words: GreenFeed, methane, model

1522 Influence of colostrum on the microbiological diversity of the developing bovine intestinal tract.

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The timely acquisition of high-quality colostrum is a proven factor in promoting intestinal health in young calves, including supporting epithelial function, host metabolism, immune development, and microbial colonization. Mucosal microbial colonization is influenced by the birth environment and local factors (e.g., temperature, pH, host epithelia types, etc.). We studied the impact of colostrum on the choreography of the neonatal calf microbiome. Twelve healthy, male Holstein calves were separated from their dams immediately following birth; fed 4 L of aseptically collected, high-quality colostrum; and housed, monitored, and fed separately for the remainder of the experiment. Postpartum maternal udder and vaginal scrapings were sampled. Fecal samples were collected throughout the experiment. Three animals were euthanized for necropsy, and intestinal samples were collected after colostrum administration (Day 1) and progressively during the trial (Days 3, 7, and 21). The V3 to V4 region of the microbial 16S rRNA gene was sequenced from digesta, mucosal scrapings, and feces. Mean diversity indices were highest in maternal udder (mean 217 OTU) and vaginal scrapings (mean 152 OTU) followed by colostrum samples. In calf samples, diversity increased over time in all locations; duodenal (mean 122 OTU) and proximal jejunal samples (mean 217 OTU) had the highest diversity. Calf duodenal, middle jejunal, and ileal (Day 7) digesta samples and fecal samples were most similar to maternal colostrum samples using Bray–Curtis dissimilarity. When clustering with multidimensional scaling (MDS) by OTU abundance, there was some clustering by location of sample: intestinal samples, stomach samples, and maternal samples clustered somewhat together, respectively. The proximal jejunum had the highest diversity at the phylum level and contained phyla Acidobacteria and Actinobacteria, which were not observed in abundance elsewhere. Firmicutes increased along the digestive tract (proximal to distal), along which Bacteroidetes and Proteobacteria decreased, the latter of which was much higher in mucosal scrapings ($P < 0.05$). Shifts in community diversity were observed in the first few days after birth, and neither digesta nor mucosal microbiota had distinguished themselves by 21 d (LDA, PERMANOVA, and ANOSIM). A large proportion of genera in colostrum, udder, vagina, and intestinal samples could not be classified. In combination, these results indicate that colostrum contributes significantly to the trajectory of the intestinal microbiome of the young calf. Further studies are needed to identify the mechanism and clinical significance of these results and to explore the identity and importance of the unknown taxa.

Key Words: host-associated microbiome

1523 Effects of starch feeding on lipopolysaccharide concentrations in rumen fluid and feces in fresh dairy cows.

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The objectives of this study were to determine 1) the effect of dietary starch content on the concentrations of lipopolysaccharide (LPS) endotoxin in rumen fluid and feces of lactating dairy cows during 21 d after calving and 2) the correlation between rumen and fecal LPS concentrations. Multiparous ruminally cannulated Holstein cows ($n = 16$) were fed a close-up diet (44% NDF and 16% starch, DM basis) for 21 d before expected calving. For the first 21 d after calving, cows were fed either a low-starch diet (37% NDF and 21% starch, DM basis) or a high-starch diet (32% NDF and 27% starch, DM basis). Rumen and fecal samples were collected at 6 h after feeding on d −14, 1, 2, 3, 4, 5, 6, 7, 9, 13, 17, and 21. Data were analyzed as a completely randomized design by ANOVA with the MIXED procedure of SAS with model effects of treatment, day, and treatment × day, with day treated as a repeated measurement. Across days after calving, LPS concentrations in the rumen were higher (12,793 vs. 6,592 EU/mL; $P < 0.01$) for the cows on the high-starch diet compared with cows on the low-starch diet. Cows on the high-starch diet also had a higher LPS concentration in feces during this period (11,885 vs. 7,129 EU/mL; $P < 0.05$). Day after calving did not affect the LPS concentration in rumen fluid. However, days after calving affected this concentration in feces ($P < 0.01$) due to a relatively low fecal LPS concentration at Day 1 after calving. The concentrations of LPS in rumen fluid and in feces were positively correlated ($r = 0.35$, $P < 0.001$). Our results show that feeding higher starch during the first 3 wk of lactation increased LPS concentrations in rumen fluid and feces, indicating a greater risk for compromised rumen health and inflammation.

Key Words: fresh cows, lipopolysaccharide, starch

1524 Correlations between the abundance of specific ruminal bacteria with milk production and total tract digestibility of dairy cows fed live or killed yeast.

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Ruminal nutrient metabolism and animal performance depend on the abundance and diversity of ruminal bacteria. The objective of this study was to examine the correlation between the abundance of different ruminal bacteria and total tract nutrient digestibility and milk production of dairy cows fed diets supplemented without or with live or killed *Saccharomyces cerevisiae*. Four ruminally cannulated lactating cows (284 + 18 DIM) were assigned to 4 treatments arranged in a 4 × 4 Latin square design with four 21-d periods. Cows were fed a nonacidotic total mixed ration (46.8% corn silage, 8.5% wet brewers' grain, and 44.7% concentrate, DM basis). The diet was not supplemented with yeast or supplemented with a low dose of live yeast (5.7×10^7 cfu/d), a high dose of live yeast (6.0×10^8 cfu/d), or a high dose of killed yeast (6.0×10^8 cfu/d before heating at 80°C). Ruminal fluid was collected 0, 2, 4, 6, 8, and 10 h after the morning feeding on d 21 and strained through cheese cloth to separate solid and liquid fractions. Microbial diversity was examined by Illumina MiSeq sequencing of the V4 region of the 16S rRNA gene. Data were analyzed using R (R Core Team, 2013). In the ruminal solid fraction, the *Fibrobacter* abundance was correlated ($r = 0.60$, $P < 0.05$) with milk fat concentration. Unknown genera in family Lachnospiraceae and RFP12 were negatively ($P < 0.05$) correlated with NDF digestibility ($r = -0.52$ and -0.56, respectively). An unknown genus (UT) in family Paraprevotellaceae was negatively ($P < 0.05$) correlated with milk fat and protein content ($r = -0.56$ and -0.52, respectively) and NDF digestibility ($r = -0.65$), whereas a UT in family Clostridiaceae was negatively correlated with CP digestibility ($r = -0.59$, $P < 0.05$). In the liquid fraction, *Prevotella* was negatively correlated with DMI and milk protein and fat content ($r = -0.64$, -0.59, and -0.53, respectively; $P < 0.05$). Unknown genera in families Succinivibrionaceae and Ruminococcaceae were positively correlated ($P < 0.05$) with ADF digestibility ($r = 0.63$) and milk yield ($r = 0.49$), respectively, whereas a UT in family Lachnospiraceae was negatively correlated with DM digestibility ($r = -0.56$, $P < 0.05$). This study revealed several uncultured or unknown ruminal bacteria that appear important as candidates for future studies because of their correlation with one or more indices of dairy cow performance.

Key Words: correlation, milk production, rumen bacteria

1525 Inhibiting the growth of *Escherichia coli* O157:H7 in alfalfa silage with silage additives.

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This study examined if adding microbial inoculants or propionic acid to alfalfa silages contaminated with *Escherichia coli* O157:H7 would inhibit the growth of the pathogen during or after ensiling. Alfalfa forage was harvested at the early bloom stage, wilted to a DM of 54%, chopped to 19-mm lengths, and ensiled after treatment with one of the following: 1) distilled water (Control), 2) 1×10^5 cfu/g of *E. coli* O157:H7 (EC), 3) EC and 1×10^6 cfu/g of *Lactobacillus plantarum* (EC+LP), 4) EC and 1×10^6 cfu/g of *Lactobacillus buchneri* (EC+LB), and 5) EC and 2.2 g/kg of propionic acid (EC+ACID). Each treatment was ensiled in quadruplicate in laboratory silos for 0, 3, 7, 16, and 100 d and analyzed for EC counts, pH, and organic acids. In addition, samples from d 100 were analyzed for counts of yeasts and molds and aerobic stability. Data were analyzed using the GLIMMIX procedure of SAS. The pathogen was detected in all silages until d 7, but by d 16, it was not detected in those treated with EC+LB and EC+LP, although it was still detected in EC and EC+ACID silages. However, by d 100, the pathogen was not detected in any silage. The rate of pH decrease to 5.0 was fastest for the EC+LP silage (7 d) followed by the EC+LB silage (16 d). Nevertheless, all silages had attained a pH less than 5.0 by d 100. The rapid decrease in pH in EC+LP and EC+LB silages was associated with higher ($P < 0.05$) lactate and acetate concentrations, respectively, relative to the other silages during the early fermentation phase (d 3 to 16). Propionic acid was detected only in the EC+ACID silage. Yeast counts were lowest ($P < 0.05$) in EC+LB and EC+ACID silages. Subsamples of all d -100 silages were reinoculated with 1×10^5 cfu/g of EC immediately after silo opening. When the pathogen was subsequently enumerated after 168 h of aerobic exposure, it was not detected in silages treated with EC+ACID, EC+LB, or EC+LP, which all had pH values less than 5.0, whereas the EC silage had a pH value of 5.4 and 2.3 log cfu/g of the pathogen. Certain bacterial inoculants can hasten the inhibition of *E. coli* O157:H7 during ensiling, and like propionic acid, they can also prevent its growth on silage contaminated with the pathogen after ensiling.

Key Words: alfalfa, *Escherichia coli* O157:H7, microbial inoculants

1526 Partial replacement of ground corn by citrus pulp or steam-flaked corn fed at two concentrate levels on rumen parameters and kinetics. V. B. Ferrari*, N. R. B. Cônsolo, F. Rodriguez, J. F. Penso, M. O. Frasseto, and L. F. P. Silva, *University of Sao Paulo, Pirassununga, Brazil*.

The objective of this study was to evaluate three nonstructural carbohydrate (NSC) sources and two levels of concentrate on rumen parameters and kinetic of beef steers, having sugarcane silage as roughage source. Six rumen-cannulated Nellore steers, 345.10 ± 14 kg initial BW and` 20 mo old, were individually fed and assigned to 2 noncontemporary 6 × 6 Latin squares (LS) in a 3 × 2 factorial arrangement of treatments. Treatments consisted of three sources of NSC—ground corn (GC) and 70% of GC replaced by pelleted citrus pulp (PCP) or by steam-flaked corn (SFC)—and 2 levels of concentrate in diet (CONC)—either 60 (60C) or 80% (80C) on a DM basis. The experiment had 6 periods of 14 d. Samples of ingredients, orts, and rumen contents were analyzed for chemical composition. Rumen fluid was collected for rumen pH, short-chain fatty acids (SCFA), and ammonia nitrogen ($N\text{-}NH_3$) analyses. Statistical analysis was conducted using PROC MIXED of SAS and the model included fixed effects of CONC, NSC, and interaction (CONC×NSC) as well as random effects of period, animal(LS), and LS. Treatment effects were considered significant at $P \leq 0.05$. Increasing concentrate from 60C to 80C decreased NDF turnover rate ($P < 0.01$) and rate of passage (k_p) ($P < 0.01$). It also decreased DM and NDF intake ($P < 0.01$). Partial replacement of GC by either SFC or PCP decreased DM and CP intake ($P < 0.01$). The PCP increased NDF turnover rate ($P = 0.02$) and decreased k_p ($P < 0.01$) compared with GC. There was a CONC × NSC effect ($P < 0.05$) on rumen mass of OM, DM, and FDN, where PCP with 60C decreased these parameters. Rumen mass of iNDF was not influenced by any treatment ($P > 0.05$). Pelleted citrus pulp increased rumen pH ($P < 0.01$) and acetic acid ($P < 0.01$), decreased propionic acid ($P < 0.01$), and, consequently, increased A:P ratio ($P < 0.01$). The PCP increased total tract digestibility of DM ($P = 0.01$) and NDF ($P < 0.01$) compared with GC. Partial replacement of GC by SFC decreased acetic acid ($P < 0.01$), increased starch digestibility ($P = 0.05$), and decreased rumen $N\text{-}NH_3$ ($P = 0.03$). In conclusion, replacing GC with PCP in sugarcane silage based diets reduced intake and rate of passage but increased rumen pH and digestibility. Replacing GC by SFC increased starch digestibility and reduced rumen $N\text{-}NH_3$.

Key Words: carbohydrate source, concentrate levels, sugarcane silage

1527 Recovering lactating dairy cows from diet-induced milk fat depression using corn with different starch degradabilities. B. M. Koch, L. E. Koch*, W. C. Bridges, and G. J. Lascano, *Clemson University, Clemson, SC*.

Milk fat depression (MFD) is a condition where milk fat synthesis is impeded by ruminal biohydrogenation intermediates and continues to be a problem in the dairy industry. The objective of this experiment was to determine the effects of feeding a high- or low–rumen degradable starch diet after diet-induced MFD. Six rumen cannulated Holstein cows (416.58 ± 25.23 kg $BW^{0.75}$ and184.33 ± 29.6 DIM) were used in a crossover design consisting of covariate, induction, and recovery periods. All cows were fed a high-fiber control diet for 10 d during the covariate period and then switched to a high-PUFA and low-fiber diet for 10 d to induce MFD. After induction, cows were switched to one of two recovery diets with the incorporation of low- or high–degradable starch corn sources (LDS: 35% and HDS: 75% 7-h starch degradability) for 18 d. Samples were collected every 3 d throughout the duration of the trial. All dependent variables were analyzed using PROC MIXED of SAS including the covariate period as a fixed effect and repeated measures. Starch level was similar (25%; $P = 0.76$) in all treatments; however, crude fat level was greater for the induction diet compared with HDS and LDS (9.89 vs. 4.47 HDS and 4.92 LDS). There was no treatment effect on DMI but the effect of day on DMI was significant across treatments ($P < 0.01$). No treatment differences were detected for CP, crude fat, ADF, starch, sugar, and ash intakes but there was a significant increase of all nutrient intakes on Days 16, 22, and 28 ($P \leq 0.01$). Milk yield, protein, lactose, and solids-not-fat were not affected by treatment but were markedly decreased by day ($P < 0.01$). Milk fat decreased during induction ($P < 0.01$) and was significantly reduced by Day 7 and 10 ($P \leq 0.01$). Total fatty acids less than C16:0 and *cis*-9, *trans*-11 CLA were not affected by treatment but increased on Days 4, 7, and 10 of induction ($P \leq 0.01$). *Trans*-10, *cis*-12 CLA was not different for HDS or LDS, yet there was a tendency of days to differ ($P = 0.09$), with Day 7 and 10 of induction having a greater concentration. Milk fatty acid profiles of the recovery diets were similar, milk yield was not affected, and DMI did not vary by treatment during this experiment. This suggests that using corn sources with starch degradability of up to 75% may be incorporated into rations to recover milk fat to normal levels.

Key Words: milk fat depression, polyunsaturated fatty acids, starch degradability

1528 Effects of field pea supplementation on digestibility and rumen volatile fatty acid concentration of diets containing high- and low-quality forages. H. L. Greenwell*[1], J. L. Gramkow[2], M. L. Jolly-Breithaupt[1], J. C. MacDonald[1], and K. H. Jenkins[3], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Lincoln, NE, [3]University of Nebraska, Scottsbluff, NE*.

Five ruminally fistulated steers (initial BW = 202 kg; SD = 20 kg) were used in a 5 × 6 Latin rectangle to evaluate the effects of supplementation on total tract digestibility of diets containing either high- or low-quality forages. Treatments were set up as a 2 × 3 factorial (forage quality × supplement type). The first factor was high-quality forage (HQ; 50% alfalfa and 50% sorghum silage, DM basis) or low-quality forage (LQ; 50% brome grass hay and 50% wheat straw, DM basis). The second factor was one of three supplements: control (CON), dry-rolled corn (DRC), or field peas (FP). Steers were supplemented at 0.43% of BW (DM basis). Periods lasted 14 d with a 9-d adaptation period and 4-d collection period. Data were analyzed using the mixed procedure of SAS and evaluating significance at $\alpha = 0.05$. There were no interactions between forage quality and supplement type on digestibility ($P \geq 0.25$). Dry matter intake, DM digestibility (DMD), OM intake (OMI), and OM digestibility (OMD; $P < 0.01$) were greater with HQ forage (6.13 kg/d, 63.1%, 4.96 kg/d, and 64.2%, respectively) than with diets containing LQ (4.71 kg/d, 49.1%, 3.60 kg/d, and 50.1%, respectively). The FP supplement ($P \leq 0.03$) increased DMI and OMD (6.14 ± 0.512 kg/d and 61.6 ± 1.94%, respectively) over steers receiving DRC (5.33 kg/d and 56.1%, respectively) or CON (4.80 kg/d and 53.8%, respectively); DRC and CON did not differ in intake or OMD. The acetate-to-propionate ratio (A:P) was affected by both forage and supplement where HQ was less than LQ (3.61 ± 0.05 and 4.09 ± 0.05, respectively) and DRC supplement produced lower A:P (3.58 ± 0.07) than FP and CON (3.99 and 3.97 ± 0.07, respectively), which were similar. Propionate proportions differed, with HQ tending ($P = 0.06$) to have greater concentrations than LQ. There was a supplement effect ($P = 0.01$) where DRC increased propionate proportion over CON and FP (18.88, 17.96, and 17.72 ± 0.27%, respectively). Acetate proportions ($P < 0.01$) were greater for the LQ forage (72.3 ± 0.58%) than for the HQ forage diet (64.8 ± 0.58%). A supplement effect was observed for acetate ($P < 0.01$), with CON and FP values greater than DRC. Supplementing FP in low- or high-quality diets increases DMI and OMD and may be an acceptable supplement for beef cattle.

Key Words: cattle, field peas, forage quality

1529 Effect of live yeast fed to natural-program beef steers during the finishing phase. L. A. Ovinge*, J. O. Sarturi, M. L. Galyean, P. R. B. Campanili, and L. A. Pellarin, *Texas Tech University, Lubbock*.

Growth performance, carcass characteristics, nutrient digestibility, and feeding behavior were evaluated in natural-program beef cattle fed steam-flaked corn–based finishing diets with 3 inclusion levels of live yeast (ABVista Inc., United Kingdom; 0, 25, and 50 g/steer daily). Steers ($n = 144$; 341 ± 20 kg) were blocked by BW and assigned to treatments in a randomized complete block experimental design. The natural program did not include the use of implants, ionophores, and antibiotics. Live yeast was included in a premix (cottonseed meal carrier) at 1% of the diet (DM basis). Data were analyzed using the GLIMMIX procedure of SAS with pen used as the experimental unit. Feed efficiency tended to be improved (quadratic, $P = 0.08$) between d 0 and 183, with steers fed 25 g/d of live yeast having a 4.3% greater G:F than the average of other treatments. Linear increases in premium Choice ($P < 0.01$) and Choice ($P = 0.05$) carcasses were observed as live yeast increased in the diet. Total tract nutrient digestibility increased (quadratic, $P < 0.01$) as live yeast increased, with steers fed 25 g/d having greater digestible DM (5.4%), OM (4.8%), NDF (22.1%), ADF (19.9%), hemicellulose (22.7%), CP (6.2%), and ether extract (2.5%) than the average of steers in the other treatments. Rumination (11%), eating time (8%), and chewing activity (20%) were not affected by treatments (% of 24-h evaluation). Live yeast included at 25 g/d in the finishing diet of natural-program beef steers improved dietary nutrient digestibility (except starch) and carcass quality grade and tended to improve gain efficiency, without affecting feeding behavior.

Key Words: digestibility, live yeast, natural program

1530 Effects of calcium–ammonium nitrate on in vitro fermentation of bahiagrass hay with supplemental molasses. D. D. Henry*[1], F. M. Ciriaco[1], R. C. Araujo[2], M. E. Garcia-Ascolani[1], P. L. P. Fontes[1], N. Oosthuizen[1], C. D. Sanford[1], T. M. Schulmeister[1], M. Ruiz-Moreno[1], G. C. Lamb[1], and N. DiLorenzo[1], *[1]University of Florida, North Florida Research and Education Center, Marianna, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil*.

A randomized complete block design was used to determine the effects of increasing amounts of calcium ammonium nitrate (CAN) on in vitro fermentation of bahiagrass hay (*Paspalum notatum*). In vitro fermentation consisted of 100 mL of a 4:1 buffer:ruminal fluid inoculum and 0.7 g of a substrate composed of 80:20 bahiagrass hay:molasses (DM basis) incubated for 48 h in 125-mL serum bottles. Three days (block) of incubation were performed. Duplicate bottles in each day were randomly inoculated and received 1 of 4 treatments: 1) negative control (no added NPN; NEG), 2) control (0.75% urea in

the substrate DM; CTL), 3) 1.2% CAN (0.38% urea and 1.2% CAN in the substrate DM; 1.2CAN), and 4) 2.4% CAN (2.4% CAN in the diet DM; 2.4CAN). Treatments CTL, 1.2CAN, and 2.4CAN were isonitrogenous. Two ruminally cannulated Angus crossbred steers (348 ± 29 kg BW) fed bahiagrass hay ad libitum and 2.27 kg (as is) of a 50:50 molasses:crude glycerol mixture, daily, were used as ruminal fluid donors. In vitro OM digestibility (IVOMD) was determined using the same amounts of substrate and inoculum from the in vitro batch culture. Data were analyzed using the mixed procedure of SAS with the fixed effect of treatment and the random effect of day. Means of duplicate bottles within day were considered the experimental unit. Contrasts were used to determine the effect of NPN (NEG vs. others), linear effects of CAN, and quadratic effects of CAN. Gas production increased ($P = 0.023$) when adding NPN (295 vs. 301 ± 2.0 mL/g of OM incubated for NEG vs. NPN, respectively) and linearly decreased ($P < 0.001$) as nitrate amounts increased. Adding NPN increased ($P = 0.015$) IVOMD, whereas a linear ($P = 0.001$) decrease occurred as nitrate increased; however, no difference ($P = 0.351$) was observed between CTL and 1.2CAN. Methane production linearly decreased ($P = 0.001$) with the addition of nitrate (4.81 vs. 0.65 ± 0.325 mmol/g substrate fermented for CTL vs. 2.4CAN, respectively). There was no effect ($P > 0.05$) of NPN or nitrate on total VFA (m*M*), acetate:propionate ratio, or molar proportions of any VFA analyzed. Added NPN improved the IVOMD of bahiagrass hay as expected in a CP-deficient forage. Inclusion of 2.4CAN reduces IVOMD and methane production, whereas 1.2CAN also reduces methane production without affecting IVOMD, implying a potential intervention to decrease methane emissions.

Key Words: fermentation, nitrate, nonprotein nitrogen

1531 A meta-analysis to estimate the net macromineral (calcium, phosphorus, magnesium, sodium, and potassium) requirements for maintenance in beef cattle. L. F. Costa e Silva*[1], S. C. Valadares Filho[2], P. P. Rotta[3], M. I. Marcondes[4], D. Zanetti[1], F. A. S. Silva[1], and M. V. C. Pacheco[1], *[1]Universidade Federal de Viçosa, Viçosa, Brazil, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [4]Departamento de Zootecnia, Universidade Federal de Viçosa, Viçosa, Brazil*.

To predict mineral requirements for beef cattle, the factorial method has been the most used. A meta-analysis was used to estimate the net macromineral (Ca, P, Mg, Na, and K) requirements for maintenance and retention coefficient in Nellore cattle. A database composed by 278 animals from 8 studies conducted in tropical conditions was developed, being 134 bulls, 73 steers, and 71 heifers. Also, animals were from the following genetic groups: Nellore ($n = 196$), Zebu × Holstein ($n = 46$), Angus × Nellore ($n = 18$), and Simmental × Nellore ($n = 18$). Variables such as mineral intake and mineral excretion as feces and urine were collected where retained mineral was calculated by difference between mineral intake and mineral excretion. Therefore, the linear regression between retained mineral and mineral intake, as milligrams per kilogram BW, was performed to achieve the net mineral requirement for maintenance and retention coefficient where the intercept and slope were considered the net requirement for maintenance (NRM) and retention coefficient (RC) of each mineral, respectively. Then, the NRM for Ca, Na, and K were 9.85, 4.47, and 16.28 mg/kg BW, these values being below those recommended by the beef cattle NRC system of 15.4, 15.0, and 38 mg/kg BW. Considering a 300-kg animal, the NRM for Ca would be 2.95 and 4.62 g/d when estimated by this new proposal and the beef cattle NRC system. This shows that the Ca supply to meet endogenous losses is overestimated, which could reduce Ca excretion via feces to environment. Moreover, the NRM for P and Mg were 19.0 and 1.87 mg/kg BW, which are close to the recommendations of the beef cattle NRC system of 16.0 and 3.0 mg/kg BW. However, the RC for Ca, P, and Mg were 59.1, 79.6, and 23.5%, respectively, which are close to the recommendations of the beef cattle NRC system of 50, 68, and 17%, whereas the RC for Na and K were 34.2 and 48.8%, respectively, which are below those recommend by the beef cattle NRC system of 91 and 100%. Therefore, we believe that these values for the net macromineral requirement for maintenance and retention coefficient can improve the understanding of dietary mineral requirements of beef cattle.

Key Words: meta-analysis, mineral requirements, Nellore

1532 Effect of micronutrient source on mineral status and performance of steers fed low- or high-sulfur diets. S. J. Hartman*, O. N. Genther-Schroeder, and S. L. Hansen, *Iowa State University, Ames*.

The objective was to determine effects of hydroxy (HYD) or inorganic (ING) trace minerals within low- or high-S diets on mineral status and performance of beef steers. Forty-eight Angus-crossbred steers were blocked by BW (316 ± 2.8 kg) and assigned to a 2 × 2 factorial with low (0.25%; LS) and high S (0.53%; HS; additional S as $CaSO_4$). Trace minerals (TM) were supplemented as 10 mg Cu, 30 mg Zn, and 20 mg Mn per kilogram DM from ING (sulfates) or HYD (IntelliBond; Micronutrients USA LLC, Indianapolis, IN). Growing period (GP; 84 d) diets were corn silage based and finishing period (FP; 78 d) diets were corn based with 12% hay. Steers (6/pen) were fed via GrowSafe bunks, and the experimental unit was steer ($n = 12$/treatment). Plasma and liver mineral concentrations were determined at trial initiation and at the end of GP and FP. Data were analyzed as a 2 × 2 factorial using SAS; initial plasma and liver mineral concentrations were covariates in analysis.

High S decreased ($P < 0.01$) end of GP and FP liver Cu concentrations and tended ($P \leq 0.1$) to decrease plasma Cu at these times. At the end of GP, HS decreased ($P = 0.04$) plasma Zn concentrations and tended to decrease ($P = 0.1$) liver Zn concentrations. Final liver Cu concentrations were greater in ING steers than in HYD steers ($P < 0.01$). Liver Mn concentrations displayed S × TM effects ($P = 0.05$) at the end of GP and FP, where LS-HYD had greater Mn concentrations than HS-HYD, HS-ING, and LS-ING at the end of GP; however, HS-HYD final Mn concentrations tended to be greater than LS-HYD and LS-ING tended to be greater than HS-ING and LS-HYD. Growing period ADG and G:F displayed TM × S effects ($P \leq 0.06$) where LS-HYD had better efficiency and gain than LS-ING and HS-ING. Overall, HS-HYD was less efficient than HS-ING ($P = 0.02$) and LS-HYD ($P = 0.06$). Overall DMI, ADG, final BW, HCW, and marbling scores were not different ($P \geq 0.12$) due to treatment; however, steers consuming ING had larger REA ($P = 0.02$) than those fed HYD, and HS decreased ($P = 0.03$) back fat and yield grade compared with LS. In this study HS decreased markers of Cu and Zn status, and differential effects of ING vs. HYD minerals were noted, although all steers maintained adequate status.

Key Words: beef, sulfur, trace mineral

1533 Effect of anionic salts on rumen fermentation in a continuous culture system. A. L. Kenny*[1], J. L. Purdom[1], M. M. Masiero[1], J. P. Jarrett[2], T. J. Wistuba[2], and M. S. Kerley[1], *[1]University of Missouri, Columbia, [2]Phibro Animal Health Corporation, Quincy, IL*.

The objective was to determine if anionic salt products (AS), commonly used to lower dietary cation–anion difference (DCAD) in prefresh dairy cattle diets, altered ruminal digestion, microbial fermentation, or microbial yield in a single-flow continuous culture system. Two consecutive experiments were conducted using 24 fermenters inoculated with rumen fluid from two lactating Holstein cows. For Exp. 1, fermenters were fed a basal diet twice daily (47.12 g DM/d; 37% wheat hay, 26% corn silage, 12.5% soybean meal, 11% soy hulls, and 13.5% supplement on a DM basis). Treatments (0.19 g/d) were added directly to randomly assigned fermenters (4/treatment) and consisted of control (CON; basal diet only), soybean meal (SBM), urea (URE), chloride and sulfur containing AS blend (CSB), glutamic acid fermentation product (GAF), and hydrochloric acid based product (HCB). In Exp. 2, the same basal diet was used except CSB and GAF treatments were blended to the basal diet at 0.077 and 0.146 g/d, respectively, and other treatments were blended to achieve 0.19 g/d (representing approximate adjustments for equivalent DCAD content from respective AS). Diets were fed for 7 d with 4 d of adaptation and 3 d of sampling. Passage rate was 5.47% for Exp. 1 and 4.83% for Exp. 2. Fermenter samples for VFA and ammonia analysis were collected at 0 and 4 h after the morning feeding. Outflow was collected daily, and fermenter content was collected at the end of the experiment. Data were analyzed as a completely randomized design with fermenters as the experimental unit, using the MIXED procedure of SAS (version 9.3; Cary, NC). In Exp. 1, NDF digestibility (%) tended to be lower ($P = 0.088$) for GAF (31.9) and HCB (33.0) compared with the other treatments except SBM (37.4). Ammonia concentration (mg NH_3 N/dL) for URE was greater (22.2; $P < 0.01$) than for the other treatments, with CSB greater (19.5; $P < 0.04$) than SBM (18.3) and CON (18.5). These differences were not found in Exp. 2. In both experiments, there were no effects on OM, CP, or ADF digestibility; microbial efficiency; microbial flow; or VFA. Differences in NDF digestibility and ammonia concentration between Exp. 1 and Exp. 2 may be due to run-to-run variability. In conclusion, adding anionic salt products to a prefresh dairy cattle diet had no detrimental effects on ruminal digestibility or microbial fermentation and yield.

Key Words: anionic salts, continuous culture, rumen fermentation

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1534 Effects of prepartum dietary cation–anion difference and source of vitamin D on dairy cows: Vitamin D, mineral, and bone metabolism. R. M. Rodney*[1,2], N. Martinez[3], E. Block[4], L. L. Hernandez[5], C. D. Nelson[6], P. Celi[7], J. E. P. Santos[6], and I. J. Lean[1,2], *[1]University of Sydney, Camden, Australia, [2]Scibus, Camden, Australia, [3]Department of Animal Sciences, University of Florida, Gainesville, [4]Church and Dwight Animal Nutrition, Ewing, NJ, [5]Department of Dairy Science, University of Wisconsin, Madison, [6]University of Florida, Gainesville, [7]Faculty of Veterinary and Agricultural Sciences, The University of Melbourne, Parkville, Australia*.

This 2 × 2 factorial study evaluated the effects of feeding dairy cows diets containing either calcidiol or cholecalciferol (3 mg/11 kg of diet DM) and positive (+130 mEq/kg) or negative (−130 mEq/kg) dietary cation–anion difference (DCAD) on vitamin D, mineral, and bone homeostasis during transition. Pregnant Holstein cows ($n = 79$) were blocked by parity and milk yield and randomly allocated to treatments from 255 d of gestation until calving. All groups of cows were then fed on identical lactating cow diets until 49 d after calving. Blood samples were taken thrice weekly prepartum and after calving until d 30 of lactation, with additional samples taken at 0, 1, and 2 d postpartum, for analysis. Milk yield and composition were recorded for the first 49 DIM. Feeding calcidiol increased concentrations of calcidiol pre- (235.1 ± 6.18 vs. 60.3 ± 6.25 ng/mL) and postpartum (214.8 ± 4.85 vs. 59.13 ± 4.90 ng/mL) and calcitriol prepartum (55.66 ± 1.62 vs. 51.05 ± 1.64 ng/mL) when compared with feeding cholecalciferol. Feeding negative vs. positive DCAD increased prepartum

concentrations of calcitriol (58.0 ± 1.61 vs. 48.3 ± 1.65 pg/mL) but decreased calcidiol (136.0 ± 6.17 vs. 160.4 ± 6.26 ng/mL) and cholecalciferol (6.8 ± 0.41 vs. 9.7 ± 0.42 ng/mL) prepartum and calcidiol, cholecalciferol and calcitriol postpartum (131.3 ± 4.84 vs. 144.4 ± 4.91 ng/mL, 3.7 ± 0.28 vs. 4.9 ± 0.28 ng/mL, and 98.0 ± 4.29 vs. 117.5 ± 4.34 pg/mL, respectively). After calving, calcitriol was higher in parous than nulliparous cows. Blood calcium increased in cows fed calcidiol (2.45 ± 0.02 vs. 2.34 ± 0.02 and 2.27 ± 0.01 vs. 2.25 ± 0.01 m*M* for pre- and postpartum, respectively). Calcium concentrations in the negative DCAD group were lower before calving, compared with the positive DCAD group (2.36 ± 0.2 vs. 2.43 ± 0.2 m*M*), but higher postpartum (2.29 ± 0.01 vs. 2.23 ± 0.01 m*M*). Feeding negative DCAD lowered blood pH (7.44 ± 0.01 vs. 7.49 ± 0.01) compared with positive DCAD prepartum but not postpartum. There was no effect of vitamin D or DCAD on blood osteocalcin, PTH, adiponectin, leptin, or serotonin concentrations. Nulliparous cows had higher blood concentrations of osteocalcin and crosslaps than parous cows. Cows fed calcidiol produced 3.70 ± 1.2 kg/d more 3.5% fat- and energy-corrected milk than those receiving cholecalciferol.

Key Words: calcidiol, calcium, dietary cation–anion difference

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1535 The net macromineral (calcium, phosphorus, magnesium, sodium, and potassium) requirements for growth in beef cattle estimated by meta-analysis.

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To predict mineral requirements in beef cattle, the factorial method has been the most used. A meta-analysis was used to estimate the net macromineral (Ca, P, Mg, Na, and K) requirements for growth in Nellore cattle. A database composed by 873 animals from 21 studies conducted in tropical conditions was developed, being 411 bulls, 255 steers, and 157 heifers. Also, animals were from the following genetic groups: Nellore (n = 473), Zebu × Holstein (n = 149), and beef crossbred cattle × Nellore (n = 250). The net mineral requirement was calculated using the following allometric model: $Mi = a \times EBW^b$, in which Mi is the amount of each mineral in the body, EBW is the empty body weight, and a and b are parameters of the model. When differences were observed for sex (bulls, steers, and heifers) and genetic group (Zebu, dairy crossbred, and beef crossbred cattle), distinct equations were separately generated. For crossbreeding, differences between dairy crossbreeds and beef crossbreeds were not verified ($P > 0.05$) for any mineral, which allowed us to analyze genetic group such as Zebu and crossbred cattle. Moreover, the allometric plateau method was used to reach the empty body weight at which animals achieve maturity for mineral retention and, after this point, there are only mineral requirements for maintenance. Therefore, differences regarding sex were observed for Ca and Na, allowing us to generate different equations for bulls, steers, and heifers. Also, from the database used in this study, bulls establish their need for Ca and Na when they reach 432 and 424 kg of EBW, respectively, whereas for steers, the EBW to reach maturity of these minerals were 421 and 481 kg, respectively. For heifers, the EBW were 432 and 405 kg for Ca and Na, respectively. In the case of P, Mg, and K, differences were verified for genetic group where zebu cattle establish the need for P, Mg, and K for growth when the EBW is 522, 427, and 460 kg, respectively. Moreover, considering crossbred cattle, the estimate of EBW for reaching maturity of P, Mg, and K is 469, 433, and 492 kg, respectively. Therefore, we believe that the equations for the net macromineral requirement for growth can improve the understanding of dietary mineral requirements of beef cattle and contribute to correct supply of minerals in diet reducing losses and environment pollution.

Key Words: beef cattle, mineral, requirement

1536 The effect of decreasing dietary cation–anion difference in the prepartum diet on urine mineral excretion and blood energy metabolite concentrations in multiparous Holstein cows.

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The objective of this study was to determine the effect of decreasing dietary cation–anion difference (DCAD) in the prepartum period on prepartum urine mineral excretion and concentrations of energy metabolites in plasma in the periparturn period. Multiparous Holstein cows (n = 89) were randomly allocated to one of three prepartum diets with decreasing DCAD, CON (+18.3 mEq/100 g DM), MED (+5.9 mEq/100 g DM), or LOW (−7.4 mEq/100 g DM), beginning at 24 d before expected parturition and individually fed. Cows were fed a common postpartum diet from parturition until 63 d in milk. Urine samples collected 1x before treatment assignment and 1x/wk prepartum were analyzed for mineral and creatinine concentrations. Blood samples were collected 1x before treatment assignment, 2x/wk prepartum, 2x/24 h postpartum, and 3x/wk through 21 d postpartum. Repeated

measures analysis was conducted using the MIXED procedure of SAS with linear and quadratic effects of decreasing prepartum DCAD as contrasts. Pearson's correlation coefficient for the association between urine pH and urine Ca-to-creatinine ratio was determined using the CORR procedure of SAS. Least squares means or geometric means and 95% confidence intervals are presented. No difference in prepartum or postpartum concentrations of NEFA or β-hydroxybutyrate was observed for the treatment groups. A trend for a quadratic effect on postpartum plasma glucose was observed (CON = 50.0 mg/dL [48.6–51.4], MED = 50.8 mg/dL [49.4–52.1], and LOW = 48.6 mg/dL [47.2–50.0]; $P = 0.09$). No effect of treatment on Mg excretion was observed; however, as calving approached, the ratio of urine Mg to creatinine decreased in all groups ($P < 0.01$). A quadratic effect on mean ratio of urine Ca to creatinine was observed (CON = 0.03 [0.02–0.04], MED = 0.07 [0.06–0.09], and LOW = 0.33 [0.27–0.44]; $P < 0.01$). A quadratic effect on estimated grams of Ca excreted, based on a creatinine excretion rate of 29 mg/kg of BW per day, also was observed (CON = 0.7 g/d [0.6–0.9], MED = 1.7 g/d [1.4–2.0], and LOW = 8.2 g/d [6.8–10.0]; $P < 0.01$). Urine pH and urine Ca-to-creatinine excretion ratio were highly correlated ($r = -0.81$, $P < 0.01$). Feeding decreasing DCAD prepartum did not significantly alter concentrations of energy metabolites in plasma in the peripartum period. Urine Ca excretion greatly increased when cows were fed the lowest DCAD, suggesting greater Ca flux prepartum, which likely contributed to improved Ca status postpartum.

Key Words: dietary cation–anion difference, energy metabolism, mineral excretion

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1537 The effect of decreasing dietary cation–anion difference in the prepartum diet on plasma haptoglobin concentrations and incidence of cytological endometritis in multiparous Holstein cows. B. M. Leno*[1], C. M. Ryan[1], R. O. Gilbert[2], K. Zanzalari[3], D. Kirk[4], J. D. Chapman[4], and T. R. Overton[1], *[1]Cornell University, Department of Animal Science, Ithaca, NY, [2]Cornell University College of Veterinary Medicine, Department of Clinical Sciences, Ithaca, NY, [3]Phibro Animal Health Corp., Quincy, IL, [4]Phibro Animal Health Corporation, Quincy, IL*.

The objective of this study was to determine the effect of decreasing dietary cation–anion difference (DCAD) in the prepartum period on concentration of haptoglobin in plasma in the peripartum period and incidence of cytological endometritis. Multiparous Holstein cows ($n = 89$) were randomly allocated to one of three prepartum diets with decreasing DCAD, CON (+18.3 mEq/100 g DM), MED (+5.9 mEq/100 g DM), or LOW (−7.4 mEq/100 g DM), beginning at 24 d before expected parturition and individually fed. Cows were fed a common postpartum diet from parturition until 63 d in milk. Plasma samples were analyzed for haptoglobin concentrations at wk −1 and d 3, 5, 7, and 14. A low-volume uterine lavage was conducted at approximately 8 d in milk (range 4–12 d; first lavage) and again at approximately 50 d in milk (range 40–60 d; second lavage). Cytology slides were prepared and 200 cells (excluding erythrocytes) were counted per slide to determine the percent polymorphonuclear leukocytes (PMN). The MIXED procedure of SAS, with linear and quadratic effects of decreasing prepartum DCAD as contrasts, was used to analyze plasma haptoglobin as a repeated measure and percent neutrophils present at the first and second lavage. Geometric means and 95% confidence limits are presented. Fisher's exact test was conducted to determine associations of treatment with incidence of cytological endometritis (CE) at second lavage (>10% PMN) using the FREQ procedure of SAS. A linear trend for lower plasma haptoglobin with decreasing DCAD was observed (CON = 0.7 mg/mL [0.6–0.8], MED = 0.6 mg/mL [0.5–0.7], and LOW = 0.6 mg/mL [0.5–0.7]; $P = 0.12$). No effect of prepartum DCAD on percent PMN at first or second lavage was observed. Incidence of CE was not different between treatment groups (CON = 10/30, MED = 7/30, and LOW = 9/29; $P = 0.70$). Decreasing prepartum DCAD did not alter PMN presence in endometrial cytology or incidence of cytological endometritis but tended to reduce haptoglobin in the peripartum period, suggesting decreased inflammation in those cows.

Key Words: cytological endometritis, dietary cation–anion difference, haptoglobin

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1538 Influence of molybdenum concentration, pH, and transit time on the in vitro bioaccessibility of sulfur. J. Hawley* and E. B. Kegley, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

In vitro bioaccessibility (IVBA) methods are useful to provide knowledge on possible interactions between antagonists and the factors involved in digestion on the potential to influence the physiological solubility of minerals for absorption into the animal. This study was conducted to evaluate the influence of Mo concentration, pH, and transit time on the S IVBA of S sources frequently used in beef cattle rations. In vitro digestions ($n = 540$) were used in a 3 × 5 × 3 × 3 factorial arrangement of treatments (4 replicates/treatment) to determine the effects of Mo concentration (no additional Mo [No Mo], 1 [Low Mo] ppm Mo added, or 5 [High Mo] ppm Mo added) on the S IVBA of S sources (no S source [Control], corn gluten feed [CGF], dried distillers' grains [DDG], chemical grade sodium sulfate [Na_2SO_4–CG], or feed grade sodium sulfate [Na_2SO_4–FG]) using hydrochloric acid solutions (pH = 2, 4, or 6), transit times (0.5, 2, or 6 h), and agitation to simulate the physiologic conditions that occur in the gastrointestinal environment. Sulfur IVBA in the processed samples was estimated by dividing extractable S in the in vitro digestions by

the S concentration in the S source being assayed. Sulfur and Mo concentrations were determined by inductively coupled plasma spectroscopy. Sulfur IVBA differed ($P < 0.0001$) by S source (0.0, 44.7, 42.9, 106.1, and 102.9% S for Control, CGF, DDG, Na_2SO_4–CG, and Na_2SO_4–FG, respectively). A Mo concentration× S source interaction was observed for S IVBA ($P < 0.0001$). The addition of High Mo to CGF and DDG decreased S IVBA, whereas the S IVBA of Na_2SO_4–CG was not affected by Mo concentration. Increased transit time for No Mo and Low Mo increased S IVBA and was greatest for Low Mo at 6 h; however, High Mo was not affected by transit time ($P < 0.0001$; Mo concentration × transit time interaction). A S source × transit time interaction was observed for S IVBA ($P < 0.0001$). Increased transit time increased the S IVBA of CGF and DDG, whereas the S IVBA of Na_2SO_4–FG was not affected by transit time. These findings indicate a complex interrelationship exists between the physiochemical properties of S sources, Mo antagonism, and ruminal factors on S bioaccessibility.

Key Words: antagonism, in vitro bioaccessibility, sulfur

1539 Bovine hair mineral concentrations as potential indicators of mineral status. J. Hawley* and E. B. Kegley, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

This study was designed to assess the efficacy of bovine hair mineral concentrations as an indicator of mineral status. Thirty-six primiparous beef heifers of predominantly Angus breeding were stratified by BW, BCS, and anticipated calving date and assigned to 12 pens (3 heifers/pen) for a 260-d maternal nutrition study. Pens were randomly assigned to 1 of 4 treatments (2 × 2 factorial): 1) 0.15% S and 6 mg Cu/kg, 2) 0.15% S and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$), 3) 0.55% S (from Na_2SO_4) and 6 mg Cu/kg, or 4) 0.55% S (from Na_2SO_4) and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$). A cracked corn and soybean meal basal ration delivered each treatment starting at 170 ± 16 d of gestation through 150 ± 16 d in lactation. Heifers had ad libitum access to mixed grass pasture. Heifer blood, hair, and liver samples were collected on d 55 and 112 ± 16 relative to parturition, and progeny blood, hair, and liver samples were collected on d 59 and 114 ± 6 relative to birth. Point-biserial correlation (r_{bp}) analysis was used to determine the correlation between hair mineral concentrations and age. Pearson's correlation (r) analysis was performed to determine the correlation between bovine hair mineral concentrations and traditional mineral status indices. Indices that showed significant correlation were analyzed by simple linear regression to determine the working relationship between indices. Age influenced hair mineral concentrations. Progeny exhibited greater hair Cu ($r_{pb} = 0.47$, $P < 0.0001$) and Zn ($r_{pb} = 0.38$, $P < 0.0001$) concentrations. Heifer hair Cu concentrations were positively correlated with plasma Cu ($r = 0.70$, $P < 0.0001$) and liver Cu ($r = 0.59$, $P < 0.0001$) concentrations. Progeny hair Cu concentrations were negatively correlated with plasma S ($r = -0.55$, $P < 0.0001$) and positively correlated with liver Cu ($r = 0.32$, $P < 0.05$) concentrations. Regression equations revealed heifer hair Cu concentrations accounted for 49 and 35% of the variability in plasma and liver Cu concentration, respectively. Progeny hair Cu concentrations accounted for 30 and 10% of the variability in plasma S and liver Cu concentrations, respectively. Results suggest that bovine hair mineral concentrations alone do not provide sufficient information to assess mineral status; however, they may be useful when combined with other traditional mineral status indices to assess mineral status with greater precision.

Key Words: beef cattle, hair, mineral concentrations

1540 Effects of diets containing either traditional anionic salts or a commercial anionic supplement on feed intake and energy balance of prepartum dairy cows. F. S. Strydom*[1], J. N. Nothnagel[1], and J. P. Swiegers[2], *[1]Nova Feeds, Malmesbury, South Africa, [2]Ruminant Nutrition Consultancy, Bethlehem, South Africa*.

Anionic supplements are fed to prepartum (PP) dairy cows to reduce dietary cation–anion difference (DCAD) and improve calcium status at calving. Traditional anionic salts (AS) can reduce DMI, presumably due to poor palatability. Commercial

Table 1540.

DMI, kg/d (LS Mean)	AS	SC	AS v SC (Adj P value)
3rd week PP	12.6	13.5	1.00
2nd week PP	11.4	13.2	0.622
1st week PP	9.7	11.7	0.053
3 week average	11.4	12.8	0.0004
EB, Mcal/d (LS Mean)			
3rd week PP	-0.02	+0.99	1.0000
2nd week PP	-1.74	-0.29	1.0000
1st week PP	-6.22	-2.82	0.122
3 week average	-2.68	-0.51	0.0039

Table 1541.

Table 1. Effect of level of prepartum DCAD and duration (Dur) of feeding on intake and blood measures

	Treatment					P value		
Prepartum	S -60	S -160	L -60	L -160	SEM	Dur	DCAD	Dur x DCAD
DMI (-21 to -1), kg/d	12.1	9.9	11.4	10.0	0.6	0.45	<0.01	0.29
Urinary pH	6.19	5.38	6.41	5.47	0.09	0.10	<0.01	0.47
Blood pH	7.419	7.382	7.413	7.384	0.007	0.80	<0.01	0.58
Blood HCO_3^-, m*M*	26.2	22.6	25.7	23.8	0.5	0.49	<0.01	0.13
Base excess, m*M*	1.62	-2.40	1.04	-1.43	0.63	0.75	<0.01	0.21
Blood iCa, m*M*	1.26	1.29	1.25	1.28	0.01	0.44	<0.01	0.93
Postpartum								
Blood pH	7.448	7.452	7.444	7.454	0.003	0.74	0.05	0.47
Blood pCO_2, mm Hg	41.9	41.7	41.6	42.5	0.5	0.73	0.49	0.34
Blood HCO_3^-, m*M*	29.3	29.1	28.6	30.1	0.4	0.59	0.07	0.02
Base excess, m*M*	5.17	5.51	4.56	6.11	0.37	0.99	0.01	0.10
Blood iCa, m*M*	1.12	1.13	1.13	1.13	0.02	0.81	0.66	0.70

anionic supplements purportedly are more readily consumed, but there is little research to support this assertion. Twenty-nine pregnant multiparous Holsteins were used to examine the effects of AS or a commercial anionic supplement (SoyChlor [SC]) on DMI and energy balance (EB) during the last 3 wk of pregnancy. The AS supplement consisted of 55% ammonium chloride, 29% magnesium sulfate, and 16% ammonium sulfate. At dry off, each cow entered a communal pen and was accustomed to a Calan gate feeder. The far-off dry period diet was a total mixed ration without anionic supplementation. At 21 d before expected calving date, cows were alternately assigned to a treatment. The AS or SC was incorporated into the diet to yield a calculated DCAD [(Na + K) − (Cl + S)] of −120 mEq/kg. Urine pH was monitored to ensure similar metabolic acidification among the two PP groups. Individual DMI was measured daily. Diet energy content (estimated using the CNCPS version. 6.5 model) and DMI allowed calculation of EB. Data were analyzed using the Mixed procedure of SAS. Post hoc testing of means was done using Bonferroni's procedure. Overall treatment and treatment by week effects for each of the three PP weeks were examined. Least squares means are in the table. Over the entire PP period, cows supplemented with SC had higher DMI ($P < 0.001$) and EB ($P < 0.004$) than cows supplemented with AS. Dry matter intake and EB declined for both groups as the PP period progressed toward calving.

Key Words: anionic supplement, dry matter intake, energy balance

1541 Effect of level of dietary cation–anion difference and duration of prepartum feeding on calcium and measures of acid–base status in transition cows. C. Lopera*[1], R. Zimpel[1], F. R. Lopes Jr.[1], W. G. Ortiz[1], B. N. Faria[1], M. R. Carvalho[1], A. Vieira Neto[1], M. L. Gambarini[2], E. Block[3], C. D. Nelson[1], and J. E. P. Santos[1], *[1]University of Florida, Gainesville, [2]Federal University of Goiás, Goiânia, Brazil, [3]Church and Dwight Animal Nutrition, Ewing, NJ.*

Objectives were to determine the effects of extending the feeding of acidogenic salts prepartum at two levels of negative dietary cation–anion difference (DCAD) on mineral metabolism and acid–base status in dairy cows. One hundred twelve Holstein cows at 230 d of gestation were blocked by lactation (1 vs. >1) and 305-d milk yield and, within each block, randomly assigned to one of four treatments arranged as 2 × 2 factorial with two levels of DCAD (−60 vs. −160 mEq/kg) and two durations (DUR) of feeding the negative DCAD, short (S; 21 d) or long (L; 42 d). Cows in S received an isonitrogenous and isocaloric diet with a DCAD of +130 mEq/kg from 233 to 254 d of gestation. Therefore, during the first 21 d of the experiment, cows were fed one of three DCAD diets, +130, −60, or −160 mEq/kg, whereas during the last 21 d of gestation, they were fed either −60 or −160 mEq/kg. Urine was collected twice weekly, and pH was measured. Cows were weighed and their BCS was assessed once weekly prepartum. Intake of dry matter (DMI) was measured daily. Blood was sampled from the jugular vein at 250, 269, and 272 d of gestation and on d 0, 1, 2, 3, and 4 postpartum and analyzed for concentrations of ionized Ca (iCa), blood gases, pH, base excess, and bicarbonate (HCO_3^-). Data were analyzed by ANOVA with repeated measures using the MIXED procedure of SAS. Intake of DM

in the first 21 d in the experiment decreased ($P < 0.01$) by reducing the DCAD and averaged 11.8, 10.9, and 10.4 kg/d for cows fed +130, −60, and −160 mEq/kg, respectively. Similarly, urinary pH decreased ($P < 0.01$) with a reduction in DCAD and averaged 8.11, 6.59, and 5.67 for cows fed +130, −60, and −160 mEq/kg, respectively. Results for the last 21 d of gestation and first 4 d postpartum are depicted in Table 1. Reducing the level of negative DCAD from −60 to −160 mEq/kg reduced DMI, induced a more exacerbated metabolic acidosis prepartum, and increased the concentration of iCa in blood. Extending the duration of negative DCAD had minor impacts on blood iCa and measures of acid–base status.

Key Words: acidogenic salts, dietary cation–anion difference, prepartum

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1542 Effects of concentrate type and chromium propionate supplementation on insulin resistance parameters, milk production, and reproductive outcomes in lactating dairy cows consuming excessive energy.

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This experiment compared insulin resistance parameters, milk production, and reproductive outcomes in lactating dairy cows consuming excessive energy and receiving, in a 2 × 2 Latin square design, the following treatments: 1) concentrate based on ground corn (CRN; $n = 13$) or citrus pulp (PLP; $n = 13$) and 2) supplemented ($n = 14$) or not ($n = 12$) with 2.5 g/d of chromium propionate. Twenty-six multiparous, nonpregnant, lactating Gir × Holstein cows (average 80 d in milk on d 0) were offered corn silage for ad libitum consumption (d 0 to 180). Cows individually received concentrate formulated to allow diets to provide 160% of their daily NE_L requirements. Cow BW, BCS, and milk production were recorded weekly. Blood samples were collected weekly before the morning concentrate feeding. Glucose tolerance tests (GTT) were performed on d 0, 60, 120, and 180, by infusing cows with 0.5 g of glucose/kg of BW. Follicle aspiration for in vitro embryo production was performed on d 0, 80, and 160. No treatment differences were detected ($P \geq 0.25$) for BW and BCS during the experiment. Milk production and milk fat and solid concentrations were similar ($P \geq 0.24$) between treatments. However, CRN had greater ($P = 0.01$) milk protein compared with PLP cows (3.54 vs. 3.14%, respectively; SEM = 0.08). Within weekly samples, concentrations of serum insulin and glucose as well as revised quantitative insulin sensitivity check index and insulin:glucose ratio were similar among treatments ($P \geq 0.40$), whereas CRN had less serum NEFA concentrations compared with PLP cohorts (0.178 vs. 0.219 mmol/L; SEM = 0.008). No treatment differences were detected ($P \geq 0.35$) on number of viable oocytes collected and embryos produced within each aspiration. During the GTT, no treatment differences were detected ($P \geq 0.16$) for serum glucose concentration, glucose clearance rate, glucose half-life, and insulin:glucose ratio ($P \geq 0.16$). Serum insulin concentrations were less ($P = 0.05$) in CRN cows supplemented with chromium propionate compared with nonsupplemented CRN cohorts (9.01 vs. 13.61 ng/mL, respectively; SEM = 1.73), whereas chromium propionate supplementation did not impact serum insulin within PLP cows ($P = 0.68$). In summary, concentrate type altered milk protein content and serum NEFA concentrations in lactating dairy cows consuming excessive NE_L and impacted the effects of chromium propionate supplementation on serum insulin response to a GTT but did not influence milk yield or reproductive responses.

Key Words: chromium, dairy cows, energy intake, insulin resistance

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1543 Regulatory effect of dietary intake of chromium propionate on function of monocyte-derived macrophages from Holstein cows in mid lactation.

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Chromium (Cr) has been reported to improve insulin sensitivity and cattle performance. However, its effect on bovine macrophage metabolic and inflammatory response is unknown. The objective was to characterize the effect of dietary Cr on cow performance and the immunometabolic response of polarized macrophages ex vivo. Twelve healthy primiparous and 16 multiparous Holstein cows (143 ± 37 DIM) were enrolled. Cows were fed a common diet once daily that was top-dressed with 200 g of ground corn containing no Cr (CTL) or chromium propionate (CrP; 8 mg of Cr/cow per day) for 35 d. Cows were weighed at 0, 17, and 35 d of supplementation. On the same days, blood monocytes were isolated and cultured to obtain 3 monocyte-derived macrophage phenotypes: M0 (nonstimulated), M1 (interferon-γ polarized), and M2 (interleukin-4 polarized). The experiment was set in a randomized complete block design. Neither DMI nor milk yield were affected by CrP or its interactions. Similarly, plasma concentrations of glucose, insulin, and NEFA were not affected by CrP or its interaction with parity. Across parities, CrP increased expression of *IGFI* (fold change [FC]: 1.7; $P = 0.03$) in M0 and increased expression of *CXCL11* (FC: 2.2; $P = 0.07$) and *SLC2A3* (FC: 2.1; $P = 0.06$, only at 17 d of feeding) in M2. For primiparous cows, CrP compared with CTL tended to reduce the production of nitrate in M2 (266 vs. 532 n*M*; $P = 0.14$) and to increase the expression of *IGFI* in M2 at 17 d of supplementation (FC: 3.4; $P = 0.06$). For cows supplemented with CrP but not with CTL, primiparous cows compared with multiparous cows tended to have greater BW gain (37.8 vs. 0.6 kg; $P = 0.07$), better efficiency of BW gain ($P = 0.08$), greater blood monocyte number

(1.31 vs. 0.85 × 10^3/μL; $P = 0.10$), greater glucose in media in M2 ($P = 0.11$), and lower tumor necrosis factor-α in media in M1 (24.6 vs. 61.1 pg/mL; $P = 0.12$). In addition, at 17 d of supplementation, *SLC2A5* expression tended to be greater in M1 (FC: 10.6; $P = 0.13$) and in M2 (FC: 8.8; $P = 0.07$) and IGFI tended to be greater in M2 (FC: 3.5; $P = 0.06$). Regardless of parity, the minor effects observed may indicate potential regulatory mechanisms of Cr on the immunometabolic response of monocyte-derived macrophages via regulation of insulin and IGF-I on glucose transporters.

Key Words: chromium, lactating cows, macrophage

1544 Influence of supplementary zinc- and chromium–amino acid complexes on growth performance and carcass characteristics of finishing cattle fed zilpaterol hydrochloride.

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Eighty bullocks (528.27 ± 26.81 kg) were used to determine the influence of supplementary chromium (Cr) and zinc (Zn) from AA complexes on growth performance and carcass characteristics of cattle during a finishing period, which included feeding zilpaterol hydrochloride (ZIL). Bullocks were individually weighed and blocked by weight at study initiation. Groups of five bullocks were placed in 16 dirt-floor pens (6 by 12 m). Pen was the experimental unit. Pens within a block were randomly assigned to treatments as follows: 1) basal diet (13.5% CP and 2.15 Mcal NE_m/kg DM) that provided 30 mg of inorganic Zn/kg DM from $ZnSO_4$ plus an additional 40 mg Zn/kg DM from $ZnSO_4$ provided through a hand-fed supplement (control; CTR), 2) basal diet plus 40 mg Zn/kg DM provided from Zn methionine complex (ZnM; ZINPRO 120; Zinpro Corp., Eden Prairie, MN), 3) CTR plus 0.40 mg Cr/kg DM provided from Cr methionine complex (CrM; Micróplex; Zinpro Corp., Eden Prairie, MN), and 4) basal diet plus 40 mg Zn/kg DM from ZnM and 0.40 mg Cr/kg DM from CrM (ZCM). Diets provided equivalent supplemental levels of 70 mg Zn/kg DM. All bullocks were supplemented with 0.15 mg ZIL/kg BW (Zilmax; Merck Animal Health, Summit, NJ) for 30 d with a 3-d withdrawal before harvest. Zilpaterol, ZnM, and CrM were top-dressed in the feed bunk. Data were analyzed by ANOVA as a mixed model, for a randomized complete block design with a 2 × 2 factorial arrangement of treatments. The model included the random effect of block and fixed effects of ZnM, CrM, and ZnM × CrM interaction. Bullocks receiving ZnM gained faster than CTR ($P = 0.04$; 1.87 vs. 1.55 kg/d, respectively) and exhibited an improved ($P = 0.05$) gain:DM feed efficiency ratio (0.21 vs. 0.16 kg). Dietary ZnM tended ($P = 0.06$) to improve the observed/expected ratio of NE_m (1.21 vs. 1.01) and NE_g (1.27 vs. 1.02) compared with CTR, respectively. Zinc source had no effect on DMI ($P = 0.97$). Feeding CRM had no effect on performance variables ($P > 0.15$). The HCW was similar for bullocks fed $ZnSO_4$ or ZnM (366 and 372 kg, respectively). Carcass dressing percentage tended ($P = 0.10$) to be increased by ZnM compared with CTR (64.5 vs. 63.7%, respectively). The results suggest that ZnM supplementation may contribute to an incremental improvement in growth performance of finishing beef cattle fed ZIL.

Key Words: feedlot performance, zilpaterol hydrochloride, zinc

1545 Effect of peripartum source of dietary calcium and magnesium and postpartum level of magnesium on dry matter intake, performance, and plasma minerals in multiparous Holstein cows.

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The objective of this study was to determine the effect of source of dietary Ca and Mg in the peripartum period and level of Mg postpartum on DMI, milk production and composition, and plasma macromineral concentrations. Multiparous Holstein cows ($n = 41$) were randomly assigned to one of two prepartum diets beginning at 21 d before expected parturition in which supplemental Ca and Mg were provided primarily from common sources (C; calcium carbonate and magnesium oxide) or MIN-AD (M; Papillon Agricultural Company, Inc., Easton, MD). At calving, cows remained on the same source assignment and were further randomized to receive Mg at 0.45 (C-HM, $n = 11$; M-HM, $n = 9$) or 0.30% of DM (C-LM, $n = 11$; M-LM, $n = 10$). Cows were fed individually through 42 d in milk (DIM), and blood samples were collected 2x/wk prepartum and daily from d 0 through 7 postpartum. Repeated measures data were analyzed with the MIXED procedure of SAS. Actual postpartum Mg intake, based on 21-d average DMI and diet analyses, were 84, 71, 103, and 71 g/d for C-HM, C-LM, M-HM, and M-LM, respectively. Prepartum, cows fed M had increased DMI (17.9 ± 0.3 vs. 17.0 ± 0.3 kg/d; $P = 0.05$) and energy balance (10.0 ± 0.4 vs. 8.7 ± 0.4 kg/d; $P = 0.03$). An interaction of source, level, and week was found for postpartum DMI in wk 1 to 6 ($P = 0.03$), reflecting increased DMI during wk 2 for cows fed M-HM. No effects on postpartum energy balance were observed. There was no effect on milk yield postpartum. A source × time interaction for fat yield ($P = 0.01$), 3.5% fat-corrected yield ($P = 0.03$), and energy-corrected yield ($P = 0.02$) was detected such that cows fed M had higher yield, especially in wk 1 postpartum. No effects of treatment on plasma Ca concentrations were observed. Cows fed higher Mg tended to have higher plasma Mg postpartum (1.71 ± 0.03 vs. 1.64 ± 0.03; $P = 0.09$) and cows

fed M tended to have higher plasma P postpartum (4.67 ± 0.14 vs. 4.35 ± 0.13; $P = 0.09$). Overall, cows fed M had increased DMI in parts of the transition period and increased fat- and energy-corrected yield. Plasma Ca was not influenced by dietary source and level of Mg; however, plasma Mg was increased by feeding higher Mg postpartum and plasma P was increased by feeding M in the transition period.

Key Words: magnesium, mineral source, transition cow

1546 Effects of mineral supplementation on pre- and postpartum primiparous beef heifer performance and progeny preweaning performance.

J. Hawley*, E. B. Kegley, and J. G. Powell, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

A study was conducted to determine the effect of mineral supplementation on primiparous beef heifer pre- and postpartum and progeny preweaning performance. Thirty-six primiparous beef heifers (20 ± 0.5 mo of age) of predominantly Angus breeding were stratified by BW (398 ± 24.9 kg), BCS, and anticipated calving date and assigned to 12 pens (3 heifers/pen) for a 260-d study. Pens were randomly assigned to 1 of 4 treatments (2 × 2 factorial): 1) 0.15% S and 6 mg Cu/kg, 2) 0.15% S and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$), 3) 0.55% S (from Na_2SO_4) and 6 mg Cu/kg, or 4) 0.55% S (from Na_2SO_4) and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$). A cracked corn and soybean meal–based supplement delivered each treatment starting at 170 ± 16 d of gestation through 150 ± 16 d in lactation. Heifers grazed mixed grass pasture and were provided access to predominantly fescue hay in quantities sufficient to ensure ad libitum forage intake. A 7-d controlled internal drug release $PGF_{2\alpha}$ protocol was used to synchronize estrus. Heifer BW and BCS were collected on d −113, −112, −85, −57, −29, 1, 27, 56, 85, 113, 149, and 150 ± 16 relative to parturition. Calf BW was collected on 0, 31, 59, 86, 115, 141, and 150 ± 6 d relative to birth. Orthogonal contrasts were used to determine the effects of Cu vs. S supplementation. Gestation length was not influenced ($P = 0.52$) by mineral supplementation. Mineral supplementation did not influence ($P \geq 0.40$) heifer BW, ADG, or BCS. Synchronized estrus response was not influenced ($P \geq 0.68$) by mineral supplementation; however, reproductive tract scores (Cu main effect, $P = 0.09$) and synchronized conception rates (Cu main effect, $P = 0.07$) tended to be greater for heifers supplemented with Cu. For calf birth weight, progeny from heifers fed 0.15% S and supplemented with Cu tended to have greater birth weights; however, supplemental Cu decreased birth weights for progeny from heifers fed 0.55% S (Cu × S interaction, $P = 0.09$). Progeny ADG trended to be greater from heifers supplemented with Cu (Cu main effect, $P = 0.13$). Results of this study suggest mineral supplementation may influence primiparous beef heifer postpartum reproductive and progeny preweaning performance.

Key Words: beef heifers, mineral supplementation, progeny

1547 Effects of mineral supplementation on pre- and postpartum primiparous beef heifer mineral status and progeny preweaning mineral status.

J. Hawley*, E. B. Kegley, and J. G. Powell, *Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville*.

A study was conducted to determine the effect of mineral supplementation on primiparous beef heifer pre- and postpartum and progeny preweaning mineral status. Thirty-six primiparous beef heifers (20 ± 0.5 mo of age) of predominantly Angus breeding were stratified by BW (398 ± 24.9 kg), BCS, and anticipated calving date and assigned to 12 pens (3 heifers/pen) for a 260-d study. Pens were randomly assigned to 1 of 4 treatments (2 × 2 factorial): 1) 0.15% S and 6 mg Cu/kg, 2) 0.15% S and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$), 3) 0.55% S (from Na_2SO_4) and 6 mg Cu/kg, or 4) 0.55% S (from Na_2SO_4) and 12 to 14 mg Cu/kg (6 to 8 mg from $Cu_2[OH]_3Cl$). A cracked corn and soybean meal–based supplement delivered each treatment starting at 170 ± 16 d of gestation through 150 ± 16 d in lactation. Heifers had ad libitum access to mixed grass pasture. Heifer mineral status was assessed in blood samples collected on d −113, −85, −57, −29, 1, 27, 56, 85, 113, and 150 ± 16; in liver biopsy samples collected on d −113, −57, 1, 56, and 113 ± 16; and in colostrum samples collected 24 h relative to parturition. Heifer Se status was assessed in blood samples collected on d −113 ± 16, −13 ± 13, and 150 ± 16 relative to parturition. Progeny mineral status was assessed in blood samples collected on d 0, 31, 59, 86, 115, 141, and 150 ± 6 and in liver biopsy samples collected on d 7, 59, and 115 ± 6 relative to birth. Progeny Se status was assessed in blood samples collected on d 150 ± 6. Orthogonal contrasts were used to determine the effects of Cu vs. S supplementation. Heifers supplemented 0.55% S exhibited lower plasma and liver Cu concentrations (S main effect, $P < 0.05$). At parturition, heifers supplemented with 0.55% S exhibited lower plasma Cu concentrations (S main effect, $P < 0.01$). Supplemental Cu tended to increase colostrum Cu concentrations in heifers fed 0.55% S but lower colostrum Cu concentrations in heifers fed 0.15% S (Cu × S interaction, $P = 0.08$). Progeny from heifers supplemented with 0.55% S exhibited lower plasma Fe, serum Se, and liver Cu concentrations (S main effect, $P < 0.05$). Results of this study suggest mineral supplementation may influence primiparous beef heifer pre- and postpartum and progeny mineral status.

Key Words: beef heifers, mineral status, progeny

1548 Relative bioavailability of selenium sources for beef cattle. M. A. Zanetti*[1], J. S. Silva[2], J. C. D. C. Balieiro[1], and J. A. Cunha[2], *[1]University of São Paulo – USP/FZEA, Pirassununga, Brazil, [2]FZEA-USP, Pirassununga, Brazil*.

Recent research conducted at FZEA-USP, Pirassununga, Brazil, demonstrated that it is possible to reduce the cholesterol in bovine meat using high levels of organic selenium (Zanetti et al., 2014). This study aimed to compare the bioavailability of high levels of organic and inorganic selenium using muscle concentration. The study used 63 Nellore cattle of approximately 24 mo of age and 350 kg live weight, in a feedlot during 84 d, in individual pens. The animals (9/treatment) were submitted to one of the seven diets: control diet without additional supplementation of selenium, control diet + 0.3 mg Se kg DM in the form of sodium selenite, control diet + 0.3 mg of Se kg DM in the form of organic selenium, control diet + 0.9 mg Se kg DM in the form of sodium selenite, control diet + 0.9 mg Se kg DM in the form of organic selenium, control diet + 2.7 mg Se kg DM in the form of sodium selenite, and control diet + 2.7 mg Se kg DM in the form of organic selenium. The organic selenium used was yeast selenium. Diets were formulated according to NRC (1996) recommendations, and the roughage:concentrate ratio was 30:70. Corn silage was used and the concentrate was a mixture of corn grain and soybean meal. The control diet had 0.065 mg of Se/kg of DM. Animals were weighed at the beginning of the experiment and every 28 d. Food intake was monitored daily and offered in amounts to leave 10% orts. At the end of the experiment (84 d), the animals were slaughtered and muscle samples were taken for selenium analysis, according to Whetter and Ullrey (1978). The bioavailability was calculated by the technique of slope ratio assay (Ammerman et al., 1995). Linear regression was performed with the general linear models procedure (Proc GLM) of SAS (2004) to characterize muscle Se concentrations. The slopes estimation with SE were 0.028 ± 0.005 for the sodium selenite and 0.123 ± 0.005 for the yeast source. The difference between the slopes was significant ($P < 0.0001$). The relative bioavailability estimated by muscle selenium concentration for the yeast selenium in relation to the sodium selenite was 4.39 or 439%, when using diets high in concentrate and with high selenium levels. Acknowledgments: FAPESP.

Key Words: feedlot, muscle selenium, sodium selenite, yeast selenium

1549 Hydroxy trace mineral supplementation lowers proportion of low-quality embryos in postpartum dairy cows. A. H. Souza*[1], C. D. Narciso[2], G. E. Higginbotham[3], E. Martinez[2], R. Ruggeri[2], and E. O. S. Batista[4], *[1]Ceva Animal Health, Libourne, France, [2]Sequoia Veterinary Services Inc., Tulare, CA, [3]Micronutrients, Indianapolis, IN, [4]University of Sao Paulo, Pirassununga, Brazil*.

Objectives of this study were to test whether type of mineral source fed after calving (0 to 70 DIM) could improve quality of in vivo produced embryos from superovulated dairy cows. Postpartum Holstein cows (n = 82) received the same basic TMR (NRC 2001) composed (DM kg/d) of alfalfa hay (3.6), corn silage (3.2), haylage (1.4), wheat silage (1.5), flaked corn (4.4), canola meal (2.7), distillers' (1.7), almond hulls (2.7), corn gluten feed (2.0), EnergII (0.1), and mineral source (0.6). Animals were blocked by parity and calving date and randomly assigned to 2 dietary treatments differing only in type of supplemented mineral source, as follows: 1) hydroxy (HYD) (hydroxyl sources of Cu, Mn, and Zn) and 2) combination (COM) (sulfate sources of Mn, hydroxyl sources of Cu, and 75% zinc sulfate/25% organic Zn). Data was analyzed with the PROC GLIMMIX of SAS and cows were treated as a random experimental unit. Cows were superovulated with a modified 5-d double Ovsynch protocol associated with 400 mg/cow of FSH (Folltropin), and uterine content was flushed 6 d after synchronized ovulations. A single batch of FSH and frozen semen from a single sire (15×10^6 sptz/straw from Select Sires Inc.) were used to minimize variation due to FSH batch and service sire. In addition, a single treatment-blinded technician graded all embryos. There were no overall differences between groups in CL number, fertilization efficiency, or production of transferable embryos. Surprisingly, HYD supplementation significantly reduced the proportion of degenerated embryos in relation to all structures (HYD = 27.3 ± 4.5 vs. COM = 44.4 ± 6.2; $P = 0.03$) or fertilized structures (HYD = 34.8 ± 5.7 vs. COM = 52.2 ± 6.9; $P = 0.04$). In addition, further analysis indicated that HYD increased the proportion of cows that yielded more than 80% of good quality, freezable embryos (HYD = 32.4% vs. COM = 16.6%; $P = 0.04$). These results were unrelated to level of milk production and/or parity number of the superovulated cow. Also, conception results after transferring HYD (59.2%; n = 71) or COM (56.4%; n = 55) embryos to Holstein recipient heifers did not differ (P = 0.72). In conclusion, these findings support the hypothesis that feeding hydroxy minerals can improve embryo quality in postpartum dairy cows. Future research is needed to explore a possible positive impact of hydroxy mineral supplementation on conception results of artificially inseminated cows.

Key Words: dairy cow, embryo quality, hydroxy mineral

1550 Effects of zinc amino acid complex on mammary epithelium and dairy food chemistry.

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Objectives of this study were to determine effects of supplemental zinc level and source on mammary epithelial barrier integrity and milk chemistry in dairy cattle. In a mouse model, moderate zinc deficiency was shown to dramatically impact milk secretion and mammary gland involution. In addition, through multiple pathways, zinc is known to impact apoptosis in mammary and other epithelial tissues. To test for similar effects in cattle, 12 multiparous Holstein cows in mid to late lactation (132 ± 21 DIM) were blocked by milk production and randomly assigned to treatment sequence in a replicated 3 × 3 Latin square experiment. Each treatment period lasted 21 d (17 d of acclimation and 4 d of sampling). Treatments consisted of 1) 0.97 g zinc/d provided as $ZnSO_4$ (approximately 30 mg zinc/kg diet DM; 30-ZS), 2) 1.64 g zinc/d as $ZnSO_4$ (60-ZS), and 3) 0.55 g zinc/d provided as $ZnSO_4$ plus 1.13 g zinc/d provided as a zinc methionine complex (60-ZM; Zinpro Corp., Eden Prairie, MN). Treatments were also balanced for metabolizable methionine using Smartamine M (Adisseo Inc., France). Cows were housed in individual tie stalls, given ad libitum access to water, and fed a balanced basal ration twice daily. Treatments were provided daily in an oral bolus and contained all supplemental trace minerals except for selenium, which was included in the grain mix. Measurements were analyzed with a mixed model using fixed effects of treatment, period, and their interaction and the random effect of cow. Significance was declared at $P < 0.05$ and tendencies at $P < 0.10$. Feed intake tended to increase for 60-ZS cows ($P = 0.06$) and 60-ZM cows tended to have increased milk fat percentage ($P = 0.08$) compared with 30-ZS cows. No other effects on milk composition, yield, or production efficiency were observed. No effects of treatments were observed on heat coagulation time or the percent of NPN in the milk. Plasma electrolyte, lactose, and α-lactalbumin levels as well as transcript abundance of genes implicated in zinc transport (ZnT2), tight junction formation (occludin), and apoptosis (clusterin) were also unaffected by treatment. In conclusion, zinc supplementation of dairy rations at 60 ppm as opposed to 30 ppm did not appear to impact the integrity of the blood milk barrier or dairy food properties of milk.

Key Words: epithelial integrity, trace mineral, zinc

1551 Effects of sulfur on the nutrition value of dried distillers' grains with solubles for beef cattle.

L. He*, *China Agricultural University, Beijing, P. R. China*.

To investigate the effects of sulfur levels and sources on the nutrition value of corn dried distillers' grains with solubles (DDGS) for beef cattle, in vitro cultivation setting three sulfur levels (0.346, 0.692, and 1.038%) and four sulfur sources (Na_2SO_4, Na_2SO_3, $Na_2S_2O_3$, and Na_2S) without regard of interactions was conducted for 72 h with rumen fluid collected from Simmental × Limousin steers in triplicate and monitoring the fermentation parameters (DM digestibility [DMD], gas production [GP], VFA, and ammonia nitrogen [NH_3–N]) and model predicted indicators (OM digestibility [OMD], ME, NE, microbial protein [MP], and gas yield [GY]). The results showed that the sulfur content of DDGS used in livestock ranged from 0.346 to 1.038% on a DM basis; high sulfur level (0.692 and 1.038%) only decreased ($P < 0.05$) asymptotic gas production (b). As to the effects of sulfur sources, Na_2SO_4 and Na_2S produced more GP ($P < 0.05$) along with a faster rate ($P < 0.01$) than those of Na_2SO_3 and $Na_2S_2O_3$, whereas Na_2SO_3 had the highest b and the inverse for Na_2SO_4 ($P < 0.01$); Na_2SO_4 and Na_2S also had a higher ($P < 0.01$) OMD, ME, NE (for maintenance and growth), and GY_{24} and a lower ($P < 0.01$) DMD_{24} and MCP than those of Na_2SO_3 and $Na_2S_2O_3$; no significant response of VFA and NH_3–N to sulfur levels and sources was found ($P > 0.05$). These results suggest that DDGS with different sulfur content ranging from 0.346 to 1.038% have a similar feed value and that dietary sulfur source exerts a great effect on its nutrition value for beef cattle.

Key Words: dried distillers' grains with solubles, in vitro fermentation, sulfur

1552 Effects of sulfur on the in vitro fermentation profile of dried distillers' grains with solubles.

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This study was conducted to investigate the effects of sulfur on the nutrition values of dried distillers' grains with solubles (DDGS) for beef cattle by in vitro rumen fermentation. In vitro cultivation was conducted in triplicate with the rumen fluid collected from 3 Simmental steers, and the gas production (GP) was recorded until 72 h of incubation, setting DDGS as the fermentation substrate with different sulfur levels (0.346, 0.692, and 1.038%, on a DM basis) and various sulfur sources (Na_2S, $Na_2S_2O_3$, Na_2SO_3, and Na_2SO_4). The filtrate of the fermentation fluid was used to determine ammonia nitrogen (NH_3–N), VFA, and DM digestibility (DMD), finally calculating OM digestibility (OMD), ME, NEm and NEg, and microbial CP production (MCP) with the monitored parameters. The results showed that in vitro gas production parameters (b and c) of DDGS were significantly influenced by its sulfur

source ($P < 0.01$) but not sulfur level ($P > 0.05$), being that the sulfur from Na_2SO_3 developed the slowest gas production rate (c) (0.018/h) with the highest asymptotic gas production (b) (60.20 mL/g) and the inverse for Na_2SO_4 (0.049/h and 42.77 mL/g). What is more, sulfur from Na_2SO_4 and Na_2S produced higher ($P < 0.05$) GP than those of Na_2SO_3 and $Na_2S_2O_3$ at 12, 24, and 48 h, whereas there was no difference ($P > 0.05$) found in different sulfur levels. Sulfur from Na_2SO_4 and Na_2S also had higher ($P < 0.01$) DMD, OMD, ME, NEm, and NEg than that of Na_2SO_3 and $Na_2S_2O_3$. As to the VFA profile, sulfur from Na_2SO_4 tended ($P = 0.09$) to produce a lower total VFA (29.10 mmol/L) than the others (37.34, 39.10 and 37.98 mmol/L), and there was no difference ($P > 0.05$) in the individual fatty acid proportion. These results suggest that DDGS with different sulfur concentration ranging from 0.346 to 1.038% have a similar in vitro rumen fermentation profile, whereas its sulfur source exerts a great effect on the fermentation, indicating that the valence state of sulfur in DDGS makes a big difference to its nutrition value for beef cattle.

Key Words: dried distillers' grains with solubles, in vitro fermentation, sulfur

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1553 Supplementation with a blend of capsicum and artificial sweetener alters milk yield and nutrient partitioning in lactating dairy cows. E. H. Wall* and D. M. Bravo, *Pancosma, Geneva, Switzerland*.

Supplementation of lactating dairy cows with capsicum oleoresin (CAPS) or with SUCRAM (SUC; Pancosma, Geneva, Switzerland) increases milk and component yield; however, responses to the two additives fed in combination have not been described. Therefore, the objective of this experiment was to determine the effects of a CAPS-SUC blend on lactation performance of dairy cows. Primi- and multiparous lactating Holstein dairy cows were housed together in a free-stall pen and were milked using an automated milking system (AMS). During a 10-wk period, CAPS-SUC was blended with a carrier and was dispensed at the AMS for CAPS-SUC cows (n = 91) at a rate of 0.22 kg/d (doses of CAPS and SUC: 100 mg/d and 3.2 g/cow per day, respectively); control cows received no additive (n = 102). All cows were supplemented with 300 mg/d of monensin. Individual cow milk production and composition, milking frequency, and BW were recorded daily. Average DMI of the pen was monitored daily and did not change throughout the study. Supplementation with CAPS-SUC did not affect milking frequency (3.5 milkings/d; $P > 0.60$). There was a parity × treatment interaction for milk yield characterized by a decrease with CAPS-SUC in primiparous animals (34.7 vs. 32.1 kg/d; $P < 0.001$) but an increase in multiparous animals (41.4 vs. 44.6 kg/d; $P < 0.001$). Yield of milk fat (1.6 kg/d) and protein (1.2 kg/d) was not affected by treatment ($P > 0.10$). There was a treatment × parity × stage of lactation interaction for BW such that in cows less than 100 DIM, BW was increased with CAPS-SUC only in primiparous animals (590 vs. 616 kg; $P < 0.001$) whereas there was no effect in multiparous animals ($P > 0.30$). The prevalence of subclinical ketosis, indicated by milk fat-to-protein ratios, was decreased with CAPS-SUC (20 vs. 15%; $P < 0.01$). The decrease in milk yield of primiparous cows together with a corresponding increase in BW indicates that CAPS-SUC may have altered nutrient partitioning to support skeletal growth or accretion of tissue stores in those animals. This, taken together with the decreased incidence of ketosis and changes in milk production, reveals that CAPS-SUC can shift nutrient partitioning and consequent milk production performance of lactating dairy cows.

Key Words: feed additive, phytonutrient, SUCRAM

1554 Supplementation with rumen-protected capsicum oleoresin increases milk production and component yield in lactating dairy cows. E. H. Wall* and D. M. Bravo, *Pancosma, Geneva, Switzerland*.

Insulin responses in peripheral tissues of dairy cows are shifted so that availability of glucose is prioritized for milk synthesis during lactation. Supplementation of dairy cows with rumen-protected capsicum oleoresin decreased insulin responses and improved milk production performance. The objective of this experiment was to test the hypothesis that supplementation of rumen-protected capsicum oleoresin (RP-Caps; NexUlin; Pancosma) would increase milk production of dairy cows. Primi- and multiparous lactating Holstein cows were housed together in a free-stall pen and were milked using an automated milking system (AMS). During a 6-wk period, cows were blocked by stage of lactation (1–99 DIM, n = 67; 100–199 DIM, n = 63; and 200+ DIM, n = 66) and were randomly assigned to RP-Caps or control treatments. Rumen-protected capsicum oleoresin was blended with a carrier and was dispensed at the AMS for RP-Caps cows (n = 97) at a rate of 0.22 kg/d (100 mg/cow per day of RP-Caps); control cows (n = 99) received no additive. All cows were supplemented with 300 mg/d of monensin. Individual cow milk production and composition, milking frequency, and BW were recorded daily. Prevalence of subclinical ketosis was estimated by milk composition (fat/protein > 1.5). Average DMI of the pen was monitored daily and did not change throughout the study. Supplementation with RP-Caps did not affect milking frequency (3.6 milkings/d; $P > 0.50$). There were no parity × treatment interactions detected; however, there was an interaction between stage of lactation and treatment ($P < 0.001$) such that only cows in the 1 to 99 DIM group responded to RP-Caps whereas there was no effect of treatment in the other two groups ($P > 0.50$). In that group, milk production was increased in RP-Caps cows (40.7 vs. 44.4 kg/d; $P < 0.001$). Rumen-protected capsicum oleoresin had no effect on fat (4.5 vs. 4.4) or protein (3.09 vs. 3.10) percentages; therefore, the increase in milk production was accompanied with an increase in component and energy-corrected milk yield (46.2 vs. 50.0

kg/d; $P < 0.001$). The increase in milk and milk component yield was not accompanied by changes in BW (673 vs. 669 kg; $P > 0.30$) or prevalence of subclinical ketosis (22.1 vs. 23.9%; $P > 0.50$), indicating that metabolic status was maintained despite the increased nutrient output into milk. Responses to RP-Caps may be mediated by postruminal effects on insulin responses and augmented glucose sparing during early and peripeak lactation.

Key Words: feed additive, phytonutrient, postruminal effects

1555 WS Effects of increasing sugar beets on steer backgrounding performance. I. McGregor*, C. M. Page, W. C. Stewart, and M. Van Emon, *Montana State University, Bozeman*.

The objective of this study was to evaluate the effects of sugar beets on steer backgrounding performance. Forty-eight Angus steers (260.7 ± 3.43 kg) were used in a completely randomized design for a 50-d study. On d −1, steers were weighed and assigned to 1 of 8 pens (6 steers/pen) equipped with GrowSafe units and one of four dietary treatments on d 0 ($n = 12$ steers/treatment; 2 pens/treatment): 1) 0SB, a control diet with no sugar beets; 2) 15SB, 15% sugar beets substituted for barley on a DM basis; 3) 30SB, 30% sugar beets substituted for barley on a DM basis; and 4) 45SB, 45% sugar beets substituted for barley on a DM basis. Sugar beets directly replaced rolled barley on a DM basis. All dietary treatments were formulated to meet or exceed the nutrient requirements of a 295-kg steer gaining 0.91 kg/d. The MIXED procedure of SAS was used for statistical analysis. Initial BW, mid BW, final BW, period 1 and 2 ADG, and period 1 and 2 G:F were not different ($P \geq 0.33$) due to dietary treatment. There was a significant treatment × day interaction ($P < 0.001$) for DMI. On d 3, 19, 21, 23, 33, 44, and 45, 0SB DMI was reduced ($P \leq 0.05$) and increased ($P \leq 0.05$) on d 12, 20, and 47 compared with 15SB. On d 3, 19, 21, 33, 35, and 50, 0SB DMI was reduced ($P \leq 0.03$) and increased ($P \leq 0.01$) on d 9, 12, and 20 when compared with 30SB. On d 19, 21, 27, 33, 37, 38, and 45, 0SB DMI was reduced ($P \leq 0.05$) and increased ($P \leq 0.04$) on d 9, 24, and 35 when compared with 45SB. On d 35 and 37, 15SB DMI was reduced ($P \leq 0.002$) and increased ($P \leq 0.05$) on d 9 and 36 when compared with 30SB. On d 37 and 47, 15SB DMI was reduced ($P \leq 0.02$) and increased ($P \leq 0.03$) on d 1, 9, 44, and 46 when compared with 45SB. On d 45, 30SB DMI was reduced ($P \leq 0.03$) and increased ($P \leq 0.04$) on d 24 when compared with 45SB. These data suggest that backgrounding steers can be fed diets with up to 45% sugar beets on a DM basis without negatively impacting performance.

Key Words: backgrounding, steers, sugar beets

1556 Effects of red grape pomace to adapt beef cattle to finishing diets and spoilage mitigation strategies. L. A. Pellarin*[1], J. O. Sarturi[1], P. R. B. Campanili[1], L. A. Ovinge[1], B. C. Bernhard[1], B. J. Johnson[1], J. C. Brooks[1], and E. W. Hellman[2], *[1]Texas Tech University, Lubbock, [2]Texas A&M AgriLife Extension and Texas Tech University, Lubbock*.

The effects of red grape pomace to step-up beef steers to steam-flaked corn–based finishing diets on growth performance, carcass characteristics, nutrient digestibility, feeding behavior, and mitigation of pomace spoilage were evaluated. In Study 1, crossbred yearling steers ($n = 48$; 364 ± 41 kg) were blocked by BW and randomly assigned to 1 of 2 adaptation strategies, 1) traditional roughage sources (alfalfa hay/cottonseed hulls based) and 2) red grape pomace based, in a randomized complete block design. Both adaptation strategies decreased roughage as steam-flaked corn gradually increased in diets. Steers were fed once daily, following standard operations of the Burnett Center (Idalou, TX), a series of 5 diets consisting of four 7-d step-up diets and 1 common finishing diet (160 d), which did not contain pomace. In Study 2, red and white grape pomace were ensiled (18.9 L units; $n = 6$/treatment) following 1 of the 4 spoilage mitigation strategies: 1) control, 2) molasses, 3) inoculant (*Lactobacillus buchneri*), and 4) inoculant + molasses in a completely randomized design (2 × 4 factorial treatment arrangement). Data were analyzed using the GLIMMIX procedure of SAS. Intake, gain, and efficiency of steers during either adaptation or finishing phases were not ($P \geq 0.16$) negatively affected by red grape pomace when compared with a traditional adaptation strategy. Total tract apparent digestibility of DM, OM, EE, NDF, and ADF evaluated during the finishing phase was not ($P \geq 0.53$) affected by adaptation strategies, except by a subtle (99.46 vs. 99.03%) increase ($P = 0.01$) in starch digestibility for steers fed pomace when compared with a traditional adaptation strategy, respectively. Feeding behavior was not ($P \geq 0.21$) affected by adaptation strategies, except by steers fed the traditional strategy spending 17.3 and 18.4% more time ruminating and chewing on step-up diet 3 compared with the pomace strategy in the same phase ($P = 0.04$ and $P = 0.01$, respectively). After storage period (169 d), red grape pomace lost less DM compared with white pomace (7.87 and 11.37%, respectively; $P < 0.03$), whereas no differences among mitigation treatments were observed ($P = 0.52$). Red grape pomace strategy adapted beef steers to finishing diets without detrimental effects on growth performance and nutrient digestion when compared with a traditional alfalfa hay/cottonseed hulls approach. Grape pomace can be stored for long periods under anaerobic conditions with modest amount of DM losses; however, spoilage mitigation after silo opening must be further studied.

Key Words: adaptation, grape pomace, storage

1557 Effects of thyme (*Thymus vulgaris*) essential oil on feed intake and feeding behavior of Nellore steers. L. C. Roma Junior*[1], E. S. Castro Filho[2], |J. M. Bertocco Ezequiel[3], M. Almeida[4], and E. H. C. B. Van Cleef[2], *[1]Sao Paulo's Agency for Agribusiness Technology – APTA, Ribeirao Preto, Brazil, [2]Sao Paulo State University – UNESP, Jaboticabal, Brazil, [3]UNESP, São Paulo State University, Department of Animal Science, Jaboticabal, São Paulo, Brazil, [4]São Paulo State University, Jaboticabal, São Paulo, Brazil*.

The objective of this study was to evaluate the effects of increasing amounts of thyme (*Thymus vulgaris*) essential oil (TEO) on feed intake and feeding behavior of Nellore steers. Four ruminally cannulated steers (701 ± 37 kg BW) were assigned to a 4 × 4 Latin square design and were fed a total mixed ration containing 40% corn silage, 10% bermudagrass hay, and 50% commercial concentrate. Treatments consisted of a daily ruminal infusion of 0 (T0), 2 (T2), 4 (T4), or 8 (T8) g/animal per day of TEO. Each period lasted 21 d (13 d of adaptation and 8 d of data collection) and animals were fed once daily (0700 h). Feed delivered and feed refused were monitored every morning to calculate DMI. Feeding behavior observations were performed by 4 trained observers who recorded, each 5 min during 12 h (from 0600 to 1800 h), the following activities: interaction with feed bunk (IB), interaction with waterers (IW), ruminating standing (RS), ruminating laying (RL), standing still (SS), laying (LA), stereotypies (ST), and other activities (OA). The chewing activity was also evaluated with observations of number of chews per feed bolus, time spent chewing each feed bolus, and chews per time. Data were analyzed using the MIXED procedure and orthogonal contrasts were used to determine the linear, quadratic, and cubic effects of TEO and of T0 vs. TEO treatments. The infusion of TEO did not affect DMI of steers (average = 8.6 kg/d). Also, no effects of treatments were observed for IB, IW, RS, RL, LA, ST, and OA, and the averages were 183.3, 10.0, 37.5, 283.5, 92.5, and 112.5 min, respectively. The time spent on activity SS was linearly increased ($P = 0.03$) with increasing inclusion of TEO, showing a 20% increase from T0 to T8. Regarding the chewing activity, no alterations were observed, and the treatments' averages were 46 chews/feed bolus, 56 s/feed bolus, and 0.82 chews/s. Although TEO has known powerful antibacterial properties, it does not affect DMI, or most of the animal behavioral activities, when infused up to 8 g/d. (Financial support: FAPESP 2014/01212-4.)

Key Words: additive, medicinal plant, thymol

1558 Effects of functional oils or monensin on dry matter digestibility, milk yield, and composition of Holstein cows. F. P. Rennó*[1], E. F. Jesus[2], T. A. Del Valle[1], G. D. Calomeni[1], T. H. Silva[1], C. S. Takiya[1], T. H. A. Vendramini[1], P. G. D. Paiva[2], G. G. Silva[1], A. Saran Netto[3], and J. Torrent[4], *[1]School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil, [3]School of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, Brazil, [4]Oligo Basics Agroindustry, Cascavel, Brazil*.

Cashew nut shell liquid (CNSL) and castor oil have been defined as functional oils (FO) due to their antimicrobial, anti-inflammatory, antioxidative, and gastroprotective properties. Twenty-four multiparous cows (150.24 ± 61.43 d in milk and 29.1 ± 4.01 kg/d of milk yield) were used in a replicated 3 × 3 Latin square experiment with 21-d periods to compare the effects of FO or monensin (MON) supplementation on DM total apparent digestibility and milk yield and composition. Cows were assigned to one of these treatments: no additive (CON), supplementation of 500 mg/kg DM of FO (CNSL and castor oil as active ingredients; Essential; Oligo Basics, Cascavel, Brazil), and supplementation of 22 mg/kg DM of MON (Rumensin; Elanco Animal Health, São Paulo, Brazil). Diet was offered as a total mixed ration twice daily. Orts were weighed daily to determine feed intake, and samples of ingredients, orts, and feces were collected on Days 16, 17, and 18 of each period. Feces were collected every 9 h. All samples were analyzed for DM and indigestible NDF (iNDF) content. To obtain iNDF content, samples of ingredients, orts, and feces were placed in bags of nonwoven textile, incubated during 288 h in the rumen of two cows, and submitted to neutral detergent treatment. Fecal excretion was calculated based on iNDF intake and its concentration in feces. Cows were milked twice daily. Milk samples were automatically collected on Days 15, 16, and 17 of each period and analyzed fresh for fat, protein, and lactose by infrared methodology (Lactoscan; Entelbra, São Paulo, Brazil). Data were analyzed using PROC MIXED of SAS, and when treatment effects were significant, the PDIFF test was applied. Treatments did not affect DM intake or digestibility. Functional oils and MON increased ($P < 0.01$) milk (25.92, 27.17, and 27.13 kg/d for CON, MON, and FO, respectively), protein (0.78, 0.81, and 0.81 kg/d for CON, MON, and FO, respectively), and lactose (1.17, 1.22, and 1.22 kg/d CON, MON, and FO, respectively) yields. Cows supplied MON showed lower milk fat percentage compared with CON and milk fat from FO cows was not different from any of treatments (3.66, 3.46, and 3.60% for CON, MON, and FO, respectively). Cows supplemented MON produced milk with lower lactose concentration compared with FO cows. Monensin increased milk production with a decrease in milk fat percentage and FO increased milk production without affecting

milk fat percentage.

Key Words: castor oil, functional oil, ionophore.

1559 Effect of rumen-protected *Capsicum* oleoresin on immune responses in lactating dairy cows experimentally challenged with lipopolysaccharide.

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The objective of this experiment was to investigate the effects of rumen-protected *Capsicum* oleoresin (RPC) on immune responses in lactating dairy cows experimentally challenged with lipopolysaccharide (LPS). Nine multiparous Holstein cows (100 ± 9.1 d in milk and 665 ± 83.3 kg BW) were used in a replicated 3 × 3 Latin square design experiment balanced for residual effects with three 28-d periods. Treatments were 0 (control), 100, and 200 mg RPC/cow per day. Rumen-protected *Capsicum* oleoresin was mixed with a small portion of the total mixed ration and top-dressed. The basal diet consisted of (DM basis) 44% corn silage, 12% alfalfa silages, and 41% concentrate feeds and contained 16.1% CP and 30.9% NDF, and the NE_L and MP of the basal diet met the requirements of the cows. Bacterial LPS was intravenously administered at 1.0 μg/kg BW and blood samples were collected at 0, 2, 4, 8, and 24 h after administration. Dry matter intake, milk yield, and white blood cells including neutrophils, lymphocytes, monocytes, and eosinophils were decreased ($P < 0.01$) and rectal temperature, hemoglobin, and serum concentration of cortisol and haptoglobin were increased ($P < 0.01$) by LPS. Plasma concentration of thiobarbituric acid reactive substances, red blood cells, and platelets were not affected ($P \geq 0.13$) by LPS. Dry matter intake (25.7 kg/d; SEM = 1.73), milk yield (35.7 kg/d; SEM = 2.44), and milk composition were not affected ($P \geq 0.25$) by RPC after LPS challenge. Rectal temperature, white blood cells, red blood cells, hemoglobin, and platelets were also not affected ($P \geq 0.20$) by RPC, except lymphocyte counts were quadratically increased ($P = 0.02$) by RPC at 0 h. Compared with the control, RPC decreased ($P \leq 0.04$) serum concentrations of cortisol and haptoglobin and increased ($P < 0.01$) concentration of thiobarbituric acid reactive substances in plasma following LPS challenge. Collectively, feed intake, milk yield, rectal temperature, white blood cells, and red blood cells were not affected by RPC in dairy cows challenged by LPS. However, RPC increased concentration of thiobarbituric acid reactive substances in plasma and decreased cortisol and haptoglobin concentrations in serum. Data suggest that dietary supplementation of RPC increased oxidative stress in plasma and alleviated acute phase responses induced by LPS in lactating dairy cows.

Key Words: acute phase response, capsicum, lipopolysacharride

1560 Effects of cinnamaldehyde on performance of postweaned Holstein dairy heifers.

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Essential oils are secondary metabolites obtained from plants and are gaining interest because of their functions similar to ionophores. The objective of this 70-d study was to determine the effects of the essential oil cinnamaldehyde compared with the ionophore monensin sodium on performance of postweaned Holstein dairy heifers. Eighty-four 12-wk-old Holstein heifers (109 ± 7.50 kg) were housed in a naturally ventilated curtain side-wall barn in 12 pens with 7 heifers/pen (3.98 m^2/hd). Heifers were randomly assigned to 1 of 4 treatments in a completely randomized design: 1) control (CON; carrier, 908 g of ground corn), 2) monensin sodium (MON; 1 mg/kg of BW + carrier), 3) cinnamaldehyde (CIN1; 1 mg/kg of BW + carrier), or 4) cinnamaldehyde (CIN2; 2 mg/kg of BW + carrier). The treatments were mixed into a 20% CP whole shell corn and protein pellet mix fed daily at 2.27 kg/head per day. Heifers had access to free choice hay and water daily. Initial BW and hip heights (HH) were taken at the start of the study and biweekly thereafter until calves reached 22 wk of age. Blood samples were also taken on each weigh day to determine blood urea nitrogen, glucose, and insulin-like growth factor-1 (IGF-1) concentrations. Fecal samples were taken from 3 heifers/pen initially and then at wk 4, 8, and 10 of the study to determine coccidia count. There were no performance effects ($P > 0.05$) of cinnamaldehyde on growth, hay intake, HH, or blood metabolites compared with heifers offered MON or CON. Average daily gains were 0.98, 0.99, 1.01, and 1.03 kg/d and average hay intakes per pen were 17.08, 16.34, 18.11, and 17.60 kg/d for CON, MON, CIN1, and CIN2, respectively. Fecal samples by pens indicated the presence of viable coccidia, but the number of counts was low and not consistent across heifers within each pen. Feeding monensin sodium to postweaned dairy heifers did not affect any of the performance parameters measured when compared with the control. Under the conditions of this study, there were also no benefits of supplementing cinnamaldehyde into grain mixes for postweaned heifers. Increasing the dose of cinnamaldehyde or changing the way it was administered to feed may have resulted in a different outcome.

Key Words: cinnamaldehyde, heifer, monensin sodium

1561 Effects of essential oils and exogenous enzyme in feedlot finishing diets high in flint ground corn at different particle sizes during the adaptation period. M. A. P. Meschiatti[1], J. M. M. D. Moraes[1], T. S. Acedo[2], L. F. M. Tamassia[2], C. S. Cortinhas[2], V. N. D. Gouvea*[2], J. R. Dórea[3], and F. A. P. Santos[4], *[1]USP, Sao Paulo, Brazil, [2]DSM Nutritional Products SA, Sao Paulo, Brazil, [3]University of Wisconsin, Madson, [4]University of São Paulo, Piracicaba, Brazil*.

The objective of this study was to evaluate the interaction between two feed additives—MON (sodium monensin; Tortuga) vs. CRINA-RUM (the combination of essential oils: Crina Ruminants, DSM, and α-amylase; Ronozyme RumiStar)—and two different ground flint corn particle sizes—ground corn (GC = 1.82 mm average particle size) or coarsely ground corn (CGC = 2.53 mm average particle size)—on performance of finishing Nellore bulls during the adaptation period, the first 30 d. Two hundred fifty-six Nellore bulls (initial BW = 360 kg ± 38) were fed diets containing 82.5% ground corn (1.82 or 2.53 mm), 8.5% sugarcane bagasse, 5% soybean meal, 3% minerals and vitamin supplement, and 1% urea. Animals were blocked based on initial BW and randomly allocated in 48 pens. Treatments were GC + MON (1.82 mm ground corn and sodium monensin; 26 mg/kg DM), GC + CRINA-RUM (1.82 mm ground corn and the combination of essential oils [90 mg/kg DM] + α-amylase [560 mg/kg DM]), CGC + MON (2.53 mm ground corn and sodium monensin; 26 mg/kg DM), and CGC + CRINA-RUM (2.53 mm ground corn and the combination of essential oils [90 mg/kg DM] + α-amylase [560 mg/kg DM]). The DMI, ADG, and feed efficiency (G:F) were evaluated after 30 d of adaptation. The data were analyzed using PROC MIXED of SAS in a 2 × 2 factorial arrangement (2 ground corn particle sizes and 2 feed additives). Pen was considered the experimental unit. No interactions between feed additives and flint corn particle size were observed ($P > 0.05$). There was no effect ($P > 0.05$) of ground flint corn particle sizes on performance of the animals during the adaptation period. Animals fed with CRINA-RUM had 7.89% greater DMI (8.36 vs. 7.70 kg; $P < 0.05$) and 11.9% greater ADG (1.26 vs. 1.11 kg; $P = 0.08$) compared with animals fed MON, respectively. In conclusion, the use of essential oil combined with α-amylase improved animal performance during the adaptation period for animals fed ground flint corn grain.

Key Words: beef, Nellore, starch

1562 Effects of essential oils and exogenous enzymes on intake, digestibility, and rumen fermentation in finishing Nellore cattle. M. A. P. Meschiatti[1], L. A. Pellarin[1], C. D. A. Batalha[2], T. S. Acedo*[3], L. F. M. Tamassia[3], C. S. Cortinhas[3], V. N. D. Gouvea[3], F. A. P. Santos[2], and J. R. Dórea[4], *[1]USP, Sao Paulo, Brazil, [2]University of São Paulo, Piracicaba, Brazil, [3]DSM Nutritional Products SA, Sao Paulo, Brazil, [4]University of Wisconsin, Madson*.

The objective of this trial was to evaluate the combination of essential oils and exogenous enzymes on intake, digestibility, and ruminal fermentation in finishing Nellore cattle. Five Nellore steers (427 ± 52 kg BW) were fed isonitrogenous and isocaloric diets containing 82.5% corn, 8.5% sugarcane bagasse, 5% soybean meal, 3% mineral and vitamin supplement, and 1% urea. The treatments were MON (sodium monensin; Tortuga; 26 mg/kg DM), CRINA (essential oils; Crina Ruminants; DSM; 90 mg/kg DM), CRINA$^+$MON (90 and 26 mg/kg DM, respectively), CRINA$^+$RUM (CRINA + α-amylase; Ronozyme RumiStar; DSM; 90 and 560 mg/kg DM, respectively), and CRINA$^+$RUM+P (CRINA + RUM + protease; Ronozyme Proact; DSM; 90, 560, and 840 mg/kg DM, respectively). The experimental design used was a 5 × 5 Latin square. The 20-d experimental periods consisted of 15 d for adaptation followed by 5 d for collections. Data were analyzed using PROC MIXED of SAS and means were compared by Tukey test considering animal and period as random effects and treatments as fixed effects. Cattle fed CRINA$^+$RUM presented greater ($P < 0.01$) DM and total nutrient digestible (TND) intakes compared with MON (9.77 vs. 7.69 kg and 7.73 vs. 5.89 kg, respectively). CRINA increased ($P = 0.02$) total CP digestibility compared with MON (74.9 vs. 65.3%, respectively). The combination of CRINA$^+$RUM+P also increased ($P < 0.01$) total CP and the total carbohydrate digestibility in comparison with MON (75.0 vs. 65.3% and 91.0 vs. 84.8%, respectively). Total starch digested (kg) was greater ($P < 0.05$) for cattle fed CRINA$^+$RUM in comparison with MON (5.44 vs. 4.19 kg, respectively), although no difference ($P = 0.12$) in fecal starch was observed between the treatments. No difference in total NDF ($P = 0.73$) and EE ($P = 0.60$) digestibilities, ruminal pH ($P = 0.84$), and molar concentration of acetate ($P = 0.14$) were observed among the treatments. Animals fed CRINA$^+$RUM presented greater molar concentration of propionate ($P = 0.02$) and lower acetate-to-propionate ratio ($P = 0.04$), compared with CRINA$^+$RUM+P (41.5 vs. 27.7 m*M* and 1.48 vs. 2.2, respectively). Ruminal ammonia nitrogen was lower ($P = 0.05$) for animals fed CRINA$^+$RUM in comparison with animals fed CRINA$^+$MON (12.4 vs. 20.26 mg dL^{-1}). In conclusion, the use of essential oils and their combination with amylase increases the DM and TDN intakes and the amount of starch digested in the total tract compared with sodium monensin, presenting minor effects on fermentation parameters.

Key Words: amylase, protease, starch

1563 Effect of inclusion of *Acacia mearnsii* tannin extract on nitrogen and energy balance in growing beef cattle fed a low-protein corn silage diet.

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The study of tannins in animal feeds has primarily focused on the effects on digestibility, intestinal nutrient flow, and/or performance of ruminant animals; however, the overall impact on energetic efficiency in growing animals is not known. Eight Holsteins steers (BW = 332 ± 32.3 kg) were used in a replicated 4 × 4 Latin square design experiment to evaluate the effect of *Acacia mearnsii* tannin extract on energy metabolism and nitrogen balance. The experimental diets consisted of corn silage plus concentrate (10%) at 2 levels of intake with and without *A. mearnsii* tannin extract (3.9 g/kg of total dietary DM). The basal diet (DM basis) was formulated to be 36.2% DM, 8.1% MP, and 12.4% CP. The treatment structure was a 2 × 2 factorial: intake, 1.2 vs. 1.8 × NEm, and tannin addition vs. control. Each experimental period was 21 d with fecal and urine collections occurring Days 15 to 21. Respiratory gasses were measured d 19 to 21 by replacing the feed bunk with a respiration hood. Measures of inspired O_2 and expired CO_2, and CH_4 were continuously collected with samples analyzed at 9-min intervals. Whole-body heat production (HP) was calculated using the equation proposed by Brouwer. Data were analyzed for effects of intake, presence of tannin, and the interaction of intake × tannin. Treatment effects were considered significant at $P \leq 0.05$. Tannin extract addition did not affect ($P > 0.10$) any measure of nitrogen or energy balance. Tannins bind proteins, which are recovered in the fiber fraction of feces as such, and usually shift the N excretory pattern from urine to feces, being positive from the environmental point of view; however, this effect was not observed in the present study. As designed, all variables were higher with high intake ($P < 0.001$). There was no interaction between intake and tannin extract. More studies are needed to evaluate the mode of action of this phenolic compound on the use of energy in growing animals.

Key Words: heat production, intake, phenolic compounds

1564 Effects of condensed tannins on the ensiling and aerobic stability of purple prairie clover (*Dalea purpurea* Vent.) silage.

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Effects of condensed tannins (CT) on ruminal fermentation have been well documented, whereas little information is available on the effects of CT on ensiling. The objective of this study was to assess the effects of CT on ensiling and aerobic stability of whole-plant purple prairie clover (PPC) silage. The PPC contained approximately 55 g CT/kg DM, was harvested from 3 plots at the flowering stage, and was wilted in the field to DM of 35%. Forage was chopped to a theoretical length of 5 cm, divided into 2 portions, and ensiled without (Control) or with polyethylene glycol (PEG) in PVC laboratory silos (5/treatment). The PEG specifically inactivates the biological activity of CT. The silos were opened after 76 d of ensiling and the silage was subsampled for chemical characterization as well as assessed for aerobic stability over 14 d. Compared with PEG treated silage, Control silage had higher ($P < 0.001$) pH (5.02 vs. 4.61) and water soluble carbohydrates (2.40 vs. 0.26 g/kg DM) but contained less lactic acid (52.6 vs. 79.9 g/kg DM; $P < 0.01$), propionic acid (0.17 vs. 0.85 g/kg DM; $P < 0.05$), soluble N (0.29 vs. 0.40 g/kg DM; $P < 0.01$), NPN (0.35 vs. 0.44 g/kg DM; $P < 0.01$), ammonia N (2.7 vs. 3.3 g/kg DM; $P < 0.01$), and ochratoxin A (10.0 vs. 40.0 μg/kg DM; $P < 0.01$). Both silages had similar ($P > 0.05$) concentrations of total VFA, acetic acid, and deoxynivalenol. These results indicate that CT in PPC reduced protein degradation and decreased the activity of both lactic acid– and ochratoxin A–producing microorganisms. After 14 d of aerobic exposure, internal temperature of PEG-treated silage started to rise 12 h earlier than that of Control silage. This suggests that CT decreased microbial activity and improved the aerobic stability of PPC silage. This study demonstrated that plant CT could be used to improve silage quality by decreasing protein degradation and the activity of mycotoxin-producing microorganisms while improving the aerobic stability of silage.

Key Words: aerobic stability, condensed tannin, purple prairie clover, silage

1565 Effect of purple prairie clover (*Dalea purpurea* Vent.) and its condensed tannins on nutrient intake, digestibility, and growth performance of lambs. K. Peng*[1,2], D. C. Shirley[3], Z. Xu[2], Q. Huang[2,4], T. A. McAllister[5], A. V. Chaves[3], S. Acharya[2], S. Wang[1], and Y. Wang[2], *[1]College of Engineering, China Agricultural University, Beijing, P. R. China, [2]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [3]The University of Sydney, Faculty of Veterinary Science, School of Life and Environmental Sciences, Sydney, Australia, [4]College of Animal Science and Technology, Northwest A&F University, Yangling, P. R. China, [5]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, Lethbridge, AB, Canada*.

This study evaluated the effects of purple prairie clover (PPC; *Dalea purpurea* Vent.) hay and its condensed tannins (CT) on feed intake, nutrient digestibility, and growth performance of lambs. Alfalfa and PPC were harvested at full flower, sun cured to <12% moisture, baled, and stored in a shed for 120 d. Purple prairie clover contained about 5% CT at harvest. Thirty-six individually fed lambs were randomly allocated into three groups and fed TMR containing 40% (DM basis) of pelleted barley grain–based concentrate and 60% of alfalfa hay (Alf), PPC hay (PPC), or PPC hay along with polyethylene glycol (PPC-p) for 77 d. Polyethylene glycol (PEG) dissolved in water was sprayed onto TMR to neutralize PPC CT activity. Lambs were fed once daily, DMI was measured weekly, and ADG was determined biweekly. Fecal samples were collected in the fifth week for 5 d to estimate nutrients digestibility using AIA as a marker. The Mixed procedure of SAS was used to analyze the data with treatment as a fixed effect and lamb as a statistical unit. Alfalfa and PPC hay had similar DM, OM, N, NDF, and ADF content at feeding. Lambs fed the PPC-p diet exhibited greater DM (68.8 vs. 59.8 vs. 66.7%; $P < 0.01$), OM (71.2 vs. 60.8 vs. 66.9%; $P < 0.001$), and N (76.5 vs. 61.0 vs. 65.5; $P < 0.001$) digestibility than those fed the Alf or PPC diets and greater NDF (59.3 vs. 42.9; $P < 0.001$) and ADF (51.0 vs. 43.3; $P < 0.05$) digestibility than those fed the Alf diet. Digestibilities of OM and DM were greater ($P < 0.05$) for PPC than for the Alf diet, whereas N, NDF, and ADF digestibility were similar. Addition of PEG to the PPC diet increased ($P < 0.05$) N and NDF digestibility and tended ($P = 0.07$) to increase ADF digestibility but did not affect DM or OM digestibility. Although PPC hay had greater DM and OM digestibility than alfalfa hay, CT reduced the fiber digestibility of PPC hay. Lambs consuming Alf, PPC, and PPC-p diet had similar ($P > 0.05$) ADG (187.1 vs. 187.1 vs. 185.3 g/d) and feed efficiency (0.151 vs. 0.151 vs. 0.147) but lambs consuming PPC tended ($P = 0.093$) to eat less (1.10 vs. 1.18 vs. 1.18 kg DM/d). Purple prairie clover hay had superior nutritive value to alfalfa hay owing to its greater DM and OM digestibility but did not improve lamb growth performance, possible due to the detrimental impact of CT on N and fiber digestion.

Key Words: digestibility, growth performance, lamb, purple prairie clover

1566 Effect of dietary polyphenol, protected amino acid, and crude protein levels on in vitro rumen fermentation and crude protein digestibility. B. Choi*[1], J. Yang[1], C. Ryu[1], S. J. Shin[1], Y. Kim[1], J. Heo[2], S. Cho[3], and N. J. Choi[1], *[1]Chonbuk National University, Jeonju-si, the Republic of Korea, [2]Microbial Institute for Fermentation Industry, Sunchang-gun, the Republic of Korea, [3]CALS Co., Ltd., Seongnam-si, the Republic of Korea*.

The present study investigated the effect of polyphenol (PP), protected AA (PA), and CP levels on in vitro rumen fermentation to improve protein utilization efficiency of dairy cattle. Dietary polyphenol extracted from sweet chestnut and protected methionine and lysine were used. Two CP levels of basal diets were designed to 16 and 18%. A factorial experimental design ($2 \times 2 \times 4$) was used to evaluate the effect of PP, PA, CP, and their interactions on rumen fermentation. Four different levels of PP (0, 0.5, 1.0, and 1.5% in diet) and two levels of PA (0 and 2.5% in diet) were mixed with two basal diets. A total of 16 different experimental diets were prepared and subjected to in vitro rumen simulated fermentation. After 24 h of incubation, rumen fermentation parameters and CP digestibility were determined. Significant main effects of factors were detected ($P < 0.05$) in gas production parameters. Factors of CP level and PA elevated gas production, and gas production decreased as levels of PP increased. However, there was no significant interaction between these factors. The factors of CP level and PP showed significant main effects on methane production ($P < 0.05$). Methane production in 18% CP diets was greater than in 16% CP diets, and methane was decreased when PP levels increased. Total VFA (TVFA) production was affected ($P < 0.05$) by the levels of CP and PP. Higher CP levels showed greater TVFA production. Total VFA production was decreased when PP levels were increased. However, TVFA production was not changed until PP levels reached 0.5%. All factors showed significant main effects on in vitro DM digestibility (IVDMD) ($P < 0.05$), and significant interactions were detected between CP × PP and PA × PP ($P < 0.05$). In vitro DM disappearance was decreased when PP levels were increased. However, these decreasing patterns were altered by the levels of CP and PA. Increasing CP or PA levels slowed the decrement of IVDMD by PP, and CP digestibility showed patterns similar to those of IVDMD. Significant main effects were found for the levels of CP and PP ($P < 0.05$), and a significant interaction was detected between PA and PP ($P < 0.05$). When PP and PA were added in the diet together, they both decreased CP digestibility. These results indicate that polyphenol can alter the rumen fermentation, and 0.5% of polyphenol in a diet can increase

protein bypass to the intestine from the rumen without negative effects on rumen TVFA production.

Key Words: crude protein, in vitro, polyphenol, protected amino acid, rumen bypass

1567 The effect of addition of mulberry leaves silage in the diet of beef cattle on their growth and slaughter performance. H. Wu*, Q. Meng, L. Ren, and Z. Zhou, *China Agricultural University, Beijing, P. R. China*.

The objective of the present study was to evaluate the effect of adding different levels of ensiled mulberry leaves to the diet of beef cattle on their growth and slaughter performance. Eighty-eight beef cattle (44 Limousine crossbred cows and 44 local breed bulls) at the age of 30 ± 3.2 mo and with an initial BW of 468.0 ± 10.0 kg were divided into 4 groups (n = 22) in a randomized complete block design with sex as a block. Four levels of ensilaged mulberry (0, 7.5, 15.0, or 22.5% DM) were tested using the basal diets, with all the treatment groups being isonitrogenous and isoenergetic. The trial lasted for a total of 100 d including 10 d for adaptation and 90 d for data collection. At the end of the feeding trial, eight cattle from each treatment group were randomly selected and slaughtered for measurement of slaughter performance including HCW, bone weight, net meat weight, back fat thickness, and rib eye area. All statistical analyses were performed for a completely randomized block design using general linear models (GLM) procedures of SAS (2000). The differences between means were assessed by the Student–Newman–Keuls test and statistical significance was defined at $P < 0.05$. The results showed that the additions of ensilaged mulberry leaves at the tested levels did not results in significant ($P > 0.50$) difference in final BW, ADG, DMI, or feed conversion efficiency. The additions of ensilaged mulberry leaves were not accompanied by a significant ($P > 0.20$) change in carcass parameters except for increases in hot dressing percentage and rib eye area ($P < 0.01$), which were 54.0% and 62.2 cm^2, 57.1% and 75.5 cm^2, 56.8% and 75.4 cm^2, and 56.1% and 75.5 cm^2 for addition level from low to high, respectively. These results indicated that although ensiled mulberry silage may not significantly improve feed utilization, growth, or major carcass characteristics of beef cattle, it can be used as a resource of nutrients for beef cattle feeding.

Key Words: beef cattle, growth performance, mulberry leaves silage

1568 Supplementation of Korean honeysuckle (*Lonicera vesicaria*) extract in timothy hay on in vitro ruminal fermentation. I. D. Lee*[1], S. K. Lee[2], S. J. Lee[2], S. Y. Yang[3], S. S. Lee[1], and J. S. Eun[3], *[1]Division of Applied Life Science, Gyeongsang National University, Jinju, the Republic of Korea, [2]Institute of Agriculture and Life Science, Gyeongsang National University, Jinju, the Republic of Korea, [3]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan*.

Korean honeysuckle (*Lonicera vesicaria*; KH) is a traditional shrub and used as folk medicine in Korea. The KH is a rich source of ascorbic acid and phenolic components, particularly anthocyanins, flavonoids, and phenolic acids. These compounds reportedly have multiple biological activities, including strong antioxidant activity and antibiotic properties. Therefore, we performed an in vitro experiment to assess the effects of KH extract (KHE) on ruminal fermentation characteristics. Milled timothy hay (0.3 g DM) was incubated with buffer, ruminal fluid, and KHE at 0 (control) 3, 5, 7, or 9% DM. The experiment was conducted in a completely randomized design with 3 replications to test the 5 dose rates (DR) of KHE. Batch culture fermentation was conducted for 12, 24, and 48 h separately to measure gas production (GP), degradability of DM, methane (CH_4) production, and ammonia N (NH_3–N) concentration at the 3 predetermined time points. Degradability of DM linearly decreased (P = 0.02) with increasing DR of KHE at 24 h, with 2.5 percentage unit decreases at 7 and 9% KHE, but there was no effect of KHE on the DM degradability at 12 and 48 h. Production of GP was generally similar to the pattern of DM degradability, having a linear decrease (P = 0.01) mainly due to 9% KHE at 24 h. Concentration of NH_3–N linearly increased because of increasing KHE supplementation at 12 h, whereas it tended to decrease in a quadratic manner (P = 0.07) at 24 h. Supplementing KHE quadratically decreased ($P < 0.01$) CH_4 production at 12 h, and it elicited linear decreases ($P < 0.01$) on CH_4 production at 24 and 48 h. However, KHE supplementation greater than 5% did not further decrease CH_4 production. These collective results demonstrate that KHE supplementation affected in vitro ruminal fermentation in a dose-dependent manner and that KHE has a potential to function as a ruminal fermentation modifier to suppress CH_4 production with minimal effects on nutrient digestion in the rumen. The positive effects on NH_3–N and CH_4 may have been resulted from combined effects from condensed tannins and saponin in KHE.

Key Words: in vitro batch culture, Korean honeysuckle extract, methane

1569 Effects of an extract of plant flavonoids from *Citrus aurantium* on performance, eating and animal behavior, ruminal health, and carcass yield in Holstein bulls fed high-concentrate diets.
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This study evaluated the effects of an extract of plant flavonoids from *Citrus aurantium* (Bioflavex CA; 24% naringin) on performance, eating pattern, behavior, and carcass quality of Holstein bulls. Ninety-nine bulls (201.8 ± 3.30 kg BW and 154 ± 0.83 d of age) were randomly allocated to 1 of 6 pens and assigned to a control (C) or Bioflavex CA (BF; 0.4 kg/ton of Bioflavex CA added to the concentrate). Each pen (6 by 12 m) had one drinker, one separate straw feeder, and one single space feeder with lateral protections where concentrate (40% corn, 14% barley, 11% wheat, 23% corn gluten feed, 15% CP, and 2.88 Mcal of ME/kg) was offered. Concentrate intake was recorded daily, and BW and animal behavior by visual scan were registered fortnightly. Animals were slaughtered after 168 d of study (12 periods of 14 d), and HCW and carcass quality were recorded. Data were analyzed using a mixed-effects model with repeated measures. Throughout the study, 4 C and 1 BF bulls were removed, 2 of the 4 C bulls due to lameness. Concentrate intake (6.9 ± 0.12 kg/d for C and BF), concentrate efficiency (0.23 ± 0.031 kg/kg), and carcass weight (262 ± 2.3 kg for C and BF) were not affected by treatments. The ADG (1.67 and 1.63 ± 0.042 kg/d for C and BF, respectively) and final BW (487 and 478 ± 3.6 kg for C and BF, respectively) tended ($P = 0.07$) to be greater in C bulls than in BF bulls. An interaction between treatment and time was observed for most behavior parameters. During the growing phase (periods 1 to 8), C bulls performed more self-grooming and attempted less mounts ($P < 0.05$) compared with BF bulls. During finishing (periods 9 to 12), an interaction in meal duration ($P = 0.01$) was observed; meal duration was greater (periods 9 to 11) in BF bulls compared with C bulls. Moreover, during finishing, nonagonistic interactions, such as oral nonnutritive and social behaviors, were greater ($P < 0.05$) in C bulls than in BF bulls. In addition, agonistic interactions (fighting, butting, and chasing) and sexual behaviors (flehmen and complete mounts) were greater ($P < 0.05$) in C bulls than in BF bulls. In conclusion, when bulls were supplemented Bioflavex CA, meal duration increased and animals' agonistic and sexual interactions were less frequent compared with non-supplemented bulls during the finishing period.

Key Words: behavior, bulls, flavonoids, performance

1570 A blend of cinnamaldehyde, eugenol, and capsicum oleoresin improves milking performance in lactating dairy cows.
C. Oguey* and E. H. Wall, *Pancosma, Geneva, Switzerland*.

Supplementation with a blend of eugenol, cinnamaldehyde, and capsicum oleoresin (ECC; XTRACT Ruminant; Pancosma, Geneva, Switzerland) was previously shown to modulate rumen function and improve feed conversion efficiency in growing ruminants. This trial aimed to determine the productive implications of this response in dairy cows. Primi- and multiparous lactating Holstein dairy cows (mean parity = 2.43; mean DIM at trial start = 125 d) were housed together in a free-stall pen and were milked using an automated milking system (AMS). For 8 wk, ECC was blended with a carrier and was dispensed at the AMS for ECC cows ($n = 97$) at a rate of a rate of 0.22 kg/d (dose of ECC = 1,000 mg/cow per day); control cows ($n = 104$) received no additive. All cows were supplemented with 300 mg/d of monensin. Individual cow milk production and composition, milking frequency, and BW were recorded daily. Average DMI of the pen was monitored daily and did not change throughout the study. Data were analyzed using the mixed procedure of SAS with repeated measures. Regardless of parity, milk production was increased with ECC (35.5 vs. 37.5 kg/d; $P < 0.001$). There was a parity × treatment interaction for the effect of ECC on milk composition such that protein percent was decreased in primiparous animals (3.2 vs. 3.1%; $P < 0.001$) but not affected in multiparous animals ($P > 0.30$). Still, ECC increased protein yield (1.1 vs. 1.2 kg/d; $P < 0.001$) and did not affect fat yield (1.4 vs. 1.4 kg/d; $P > 0.50$). Therefore, there was an increase in energy-corrected milk with ECC (38.2 vs. 39.3 kg/d; $P < 0.001$). There was no effect of ECC on BW (673 vs. 674 kg; $P > 0.70$) or prevalence of subclinical ketosis (5.1 vs. 5.5%; $P > 060$). Interestingly, there was a parity × treatment interaction for number of milkings per day. In primiparous cows, ECC increased milking frequency (2.9 vs. 3.2; $P < 0.01$), whereas there was no effect in multiparous animals (3.5 vs. 3.6; $P > 0.30$). These findings reveal that supplementation with ECC, even on top of an ionophore, improves milk production performance of lactating dairy cows.

Key Words: automated milking system, performance, XTRACT

1571 Evaluation of a proprietary blend of essential oil and cobalt on a commercial dairy. O. J. Kuester*, *South Dakota State University, Brookings*.

A field trial was conducted for 7 mo on a commercial dairy equipped with two Lely robotic milking units to evaluate the response of feeding a proprietary essential oil and cobalt product (EOC) on the lactational performance of lactating Holstein dairy cows. Cows were divided between two pens (57 ± 2 cows and 59 ± 3 cows for treatment [EOC] and control [C] pens, respectively), based on cow parity (2.65 ± 1.52 and 2.33 ± 1.20), days in milk (DIM) (184 ± 103 and 154 ± 94.2), and milk production (35.4 ± 11.3 and 36.9 ± 11.3 kg/d) before study initiation. Cows were group fed either an EOC or C total mixed ration (TMR) 2x/d, and pen diets were switched after 4 mo of data collection. Production data was collected daily from Lely Time for Cows (T4C) robotic milking software and was reduced to weekly observations for each cow. Management level milk production was not different (P = 0.92) between EOC and C treatments (41.5 ± 1.91 and 41.4 ± 2.05 kg/d, respectively). Fat and protein percentages were not different between EOC and C treatments (P = 0.55 and 0.56, respectively) but were numerically higher for EOC-fed cows than for C-fed cows (3.39% fat and 2.99% protein vs. 3.36% fat and 2.97% protein, respectively). Total feed intake was not different between treatments (P = 0.16) but was numerically lower for EOC-fed cows (25.7 kg/d) than for C-fed cows (25.9 kg/d). Feed efficiency (FE) was not different between treatments (P = 0.73) but was numerically lower for cows fed EOC than for cows fed C (1.60 FE and 1.62 FE, respectively). Feeding the proprietary EOC product on a commercial dairy operation that used robotic milking units did not increase management level milk production or FE but numerically increased milk percentages of fat, protein, and total feed intake.

Key Words: cobalt, commercial dairy, essential oil, robotic milker

1572 Effects of feeding functional oils or monensin on feedlot performance and carcass traits of Nellore cattle. A. C. Melo*[1,2], M. C. Pereira[3], A. L. Rigueiro[1], D. H. M. Watanabe[1], M. M. Squizatti[1], L. A. Tomaz[1], J. V. Dellaqua[1], O. A. Souza[1], P. F. Santi[1], A. L. J. Lelis[1], A. F. Toledo[1], and D. D. Millen[1], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]Grant provided by São Paulo State Foundation (FAPESP), São Paulo, Brazil, [3]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil*.

This study, conducted at the São Paulo State University feedlot, Dracena campus, Brazil, was designed to test the effects of adding functional oils (Essential) or monensin (MON) on feedlot performance and carcass traits of Nellore cattle fed high-concentrate diets. Ninety-six 22-mo-old Nellore yearling bulls (377.9 ± 32.0 kg) were assigned to 24 pens (4 animals/pen) and used in a completely randomized block with 2 × 2 factorial arrangement of treatments, replicated 6 times. Factors were inclusion (DM basis) or not of functional oils or MON, at a dose of 500 or 27 ppm, respectively. Animals were adapted for 16 d to the high-concentrate diets fed. The finishing diet contained 68.5% cracked corn grain, 14.0% sugarcane bagasse, 14.1% cottonseed meal, 2.1% supplement, 0.8% urea, and 0.5% limestone (DM basis). Cattle were fed ad libitum three times daily for 105 d, and DMI was recorded daily. No significant (P > 0.10) functional oils main effect or interactions between functional oils and MON were observed for any of the feedlot performance and carcass traits variables evaluated: final BW (without functional oil = 503.6 kg and with functional oil = 505.1 kg), DMI (without functional oil = 9.6 kg and with functional oil = 9.6 kg), ADG (without functional oil = 1.2 kg and with functional oil = 1.2 kg), G:F (without functional oil = 0.126 kg/kg and with functional oil = 0.126 kg/kg), HCW (without functional oil = 280.9 kg and with functional oil = 281.0 kg), and dressing percentage (without functional oil = 55.8% and with functional oil = 55.5%). Also, no significant (P > 0.10) MON main effect was observed for final BW, ADG, HCW, and dressing percentage. However, the addition of MON reduced (P = 0.001) the DMI (without MON = 10.3 kg and with MON = 8.9 kg) and improved (P = 0.01) G:F (without MON = 0.117 kg/kg and with MON = 0.136 kg/kg). Cattle fed MON performed better than those animals not fed MON. On the other hand, feeding functional oils did not improve feedlot performance and carcass traits in this study.

Key Words: additives, feedlot, Nellore

1573 Influence of tannins extract and monensin supplementation on performance of feedlot heifers in Argentina. C. Cabral[1], A. Lopez Da SIlva[2,3], J. J. Couderc[3], D. Colombatto[4], and R. Barajas*[5], *[1]Indunor, S.A., Buenos Aires, Argentina, [2]Feedlot Don Corral de Corijunio S.A., Buenos Aires, Argentina, [3]Nowet S.A, Buenos Aires, Argentina, [4]Universidad de Buenos Aires, Buenos Aires, Argentina, [5]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico*.

Tannins extract and monensin have activity against several rumen bacteria that participate in feed-protein degradation; it was hypothesized that its effects could be synergistic. Three hundred forty-eight Angus heifers (207 ± 13.4 kg) were used to determine the influence of tannins extract and monensin supplementation on performance of feedlot heifers. The heifers were individually weighed and blocked by weight at study initiation. Groups of 29 heifers were placed in 12 dirt-floor pens (50 by 70 m). Pen was the experimental unit. Pens within a block were randomly assigned to treatments as follows: 1)

Table 1574. Effect of corn processing and dietary protein level on nitrogen (N) metabolism.

Items, g/d	SFC[1]			FGC		SEM	Contrast[1]		
	HP	LP		HP	LP		P	CP	P×CP
Intake N	698.40	619.60		736.00	670.20	21.33	<0.01	<0.01	0.66
Milk N	218.65	212.58		219.04	210.92	6.83	0.85	0.06	0.77
Fecal N	264.20	258.60		293.00	255.45	13.52	0.32	0.10	0.22
Urinary N	165.89	154.93		172.70	159.16	6.02	0.06	<0.01	0.65
Pollution N	430.09	413.53		465.70	415.52	15.22	0.14	0.01	0.18
Absorbed N	434.20	361.00		443.00	413.23	24.78	0.20	0.03	0.35
N efficiency, %	31.50	34.47		29.80	31.62	1.08	0.02	0.01	0.52

[1]Contrasts for P (corn processing effect), CP (protein level effect), and interaction (P×CP).

basal diet (14.1% CP and 1.75 Mcal NE_m/kg DM) plus 3.1 g of tannins extract (TE)/kg DM provided by ByPro (Indunor-Silvafeed; Buenos Aires, Argentina), 2) basal diet plus 35 mg of monensin (MON)/kg DM from Rumensin 200 (Elanco Animal Health, Indianapolis, IN), and 3) basal diet plus 3 g of TE and 35 mg of MON/kg DM (TEMO). Tannins extract and MON were top-dressed in the feed bunk. Data were analyzed by ANOVA as a mixed model, for a randomized complete block design. The model included the random effect of block and fixed effects of treatments (TE, MON, and TE + MON). Possible influence of initial weight was explored by covariance analyses. Heifers receiving TE had higher final weight than those received MON (P = 0.05; 316 vs. 306 kg) and gained faster (P = 0.04; 1.41 vs. 1.22 kg/d). Dry matter intake was not affected by treatments (P = 0.43). The gain:DM feed efficiency was better in heifers fed TE than in MON-supplemented heifers (0.17 vs. 0.15 kg). The observed:expected diet NE ratio was higher (P = 0.05) in TE heifers than in MON heifers (NEm, 0.97 vs. 0.93, and NEg, 0.96 vs. 0.90, respectively). The mean values of final weight, daily gain, DMI, feed efficiency, and NE exhibit by TEMO heifers were intermediate and not significantly distinct (P > 0.10) from those obtained by TE and MON heifers. The results suggest that TE supplementation may contribute to an incremental improvement in growth performance of beef cattle.

Key Words: feedlot performance, monensin, tannins

1574 Effects of different protein levels and corn processing methods on nitrogen metabolism in dairy cows and environmental pollution.
G. R. Ghorbani*, H. Rafiee, and M. Alikhani, *Isfahan University of Technology, Isfahan, the Islamic Republic of Iran*.

Eight midlactation Holstein cows averaging 105 ± 9 d in milk and 47.2 ± 3 kg of milk/d were assigned to a replicated 4 × 4 Latin square design (2 × 2 factorial) to study the effects of corn processing and protein level on nitrogen metabolism. Experimental diets contained either finely ground corn (FGC) or steam-flaked corn (SFC) based on either a low protein (LP; 14.8%) or a high protein (HP; 16.2%) content. Diets consisted of 40% forage, including 15% alfalfa hay and 25% corn silage. The concentrate contained soybean meal and urea as protein sources. Cows fed diets with a greater protein concentration had 11.2% greater N intake (717.2 vs. 644.9 g/d; P < 0.01), 7.8% greater urinary N (169.3 vs. 157.0 g/d; P < 0.01), 13.3% greater absorbed N (438.6 vs. 387.1 g/d; P < 0.01), and 8% greater pollution N (447.9 vs. 414.5 g/d; P = 0.01). Cows fed HP diets had lower milk N efficiency (30.6 vs. 33.0%; P = 0.01). Cows fed FGC rather than SFC had 6.7% greater N intake (703.1 vs. 659.0 g/d; P < 0.01), tended to have 3.4% greater urinary N excretion (165.9 vs. 160.4 g/d; P = 0.06), and had lower milk N efficiency (30.7 vs. 33.0%; P = 0.02). Results indicate that cows fed LP diets and SFC diets had greater N efficiency and reduced N loss.

Key Words: ground corn, level of protein, steam-flaked corn

1575 Eelative availability for lactating dairy cattle of methionine from two sources of ruminally protected methionine.
M. Ardalan*[1], C. F. Vargas Rodriguez[1], G. I. Zanton[2], M. Vázquez-Añón[3], E. C. Titgemeyer[1], and B. J. Bradford[4], *[1]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [2]USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI, [3]Novus International, Inc., St. Charles, MO, [4]Kansas State University, Manhattan*.

Our objective was to evaluate lactational responses of dairy cows to methionine (Met) provided from 2 rumen-protected (RP) Met sources. Twenty-one Holstein dairy cows (11 primiparous [137 DIM, 634 kg BW, and 3.6 BCS] and 10 multiparous [parity 2, 142 DIM, 670 kg BW, and 3.2 BCS]) were assigned to a treatment sequence in 4 replicated 5 × 5 Latin squares with 14-d periods. Treatments included 1) control; 2) and 3) 7.5 and 15 g/d, respectively, of a RP product (NTP-1401; Novus International, Inc., St. Charles, MO); and 4) and 5) 7.5 and 15 g/d, respectively, of a rumen-protected dl-Met product (Smartamine; Adisseo, Alpharetta, GA). By evaluation with CNCPS 4.0, the diet met MP and energy requirements when DMI was 25.6 kg/d for lactating Holstein cows

producing 45 kg/d milk with 3.5% fat and 3.0% true protein. Diets contained 16.1% CP and were predicted to be deficient in metabolizable Met (1.85% of MP) but sufficient in lysine (6.8% of MP). Feed intake and milk production were measured on d 11 to 14. Blood was collected on d 14. Dry matter intake, milk yield, energy-corrected milk (ECM), milk fat yield and percentage, and efficiencies of milk and ECM production were not affected by treatment ($P \geq 0.14$). Milk protein percentage and milk protein yield linearly increased with supplementation ($P < 0.01$), without differences between Met sources or interactions between source and level. Linear regressions of milk protein percentage and milk protein yield against supplement amount within source led to slope ratios (NTP-1401/Smartamine) of 95% for protein percentage ($P = 0.65$ for difference from 100%) and 84% for protein yield ($P = 0.60$ for difference from 100%), suggesting no differences between sources for increasing milk protein. Plasma Met concentrations were linearly increased ($P < 0.001$) by Met supplementation, with the increase being greater for Smartamine than for NTP-1401 ($P < 0.001$). Plasma d-Met was increased only by Smartamine. Plasma 2-hydoxy-4-methylthio-butyric acid (HMTBA) was increased only by NTP-1401. The sum of plasma Met and plasma HMTBA was linearly increased by Met supplementation ($P < 0.01$) with no difference between sources ($P = 0.89$). Our data demonstrated that supplementation of Met can improve milk protein percentage and yield. The 2 methionine sources did not differ in their effect on lactation performance or milk composition.

Key Words: dairy, methionine, milk protein

1576 Effects of rumen undegradable protein supplementation and ambient temperature on growth performance and blood metabolites in Korean cattle steers. H. J. Kang*, M. Y. Piao, H. J. Kim, and M. Baik, *Department of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul, the Republic of Korea*.

Under heat stress, RUP can have positive effects on milk production of dairy cow. This study was performed to evaluate whether rumen RUP supplementation and ambient temperature affects growth and blood metabolic parameters in Korean cattle. In Exp. 1, 14 Korean cattle steers (average 20.5 mo of age and 231.3 kg of BW) were divided into a conventional control diet group ($n = 7$) and a 0.55% RUP supplementation group ($n = 7$). Steers were allowed to receive daily an early fattening stage concentrate diet with the amount of 1.5% of BW using an automatic feeding station for 4 mo from July through October 2015, and they were allowed to receive a tall fescue with the amount of 0.75% of BW. Temperature data were analyzed by using one-way ANOVA, and growth and blood data were analyzed by using repeated-measured two-way ANOVA. Maximum ambient temperature and maximum temperature–humidity index (THI) were higher in July (30.6°C and 81.8, respectively), August (32.9°C and 80.7, respectively), and September (28.8°C and 80.3, respectively) than in October (19.8°C and 63.7, respectively). Blood was collected at starting day and at every 4 wk after 8 h fasting. Ruminally undegradable protein supplementation did not affect total feed intake, ADG, and feed efficiency (FE), although ambient temperature or month affected feed intake, ADG, and FE. Ruminally undegradable protein supplementation tended ($P = 0.08$) to decrease serum glucose concentrations, but it increased ($P = 0.006$) serum high-density cholesterol (HDL) concentrations. Ambient temperature or month affected ($P < 0.001$) both glucose and HDL concentrations. In Exp. 2, six Korean cattle steers (average 20.6 mo of age and 230.7 kg of BW) were raised in metabolic cages in a temperature-controlled room with air conditioning and heating system. Animals were divided into a conventional control diet group ($n = 3$) and a 0.55% RUP supplementation group ($n = 3$). In Exp. 2, steers were allowed to receive a same amount of the concentrate and the hay as that of Exp. 1. Experimental period 1 (P1) was 8 d with high temperature and period 2 (P2) was 8 d with normal temperature. Blood was collected at d 1 and 8 after 8 h fasting. Maximum ambient temperature and THI (34.4°C and 86.0) of P1 was higher ($P < 0.001$) than that (19.6°C and 67.0) of P2, respectively. In Exp. 2, RUP supplementation did not affect feed intake, ADG, FE, and blood parameters at both P1 and P2. In conclusion, RUP supplementation and ambient temperature affected blood parameters, although they did not significantly influence growth performance of Korean cattle.

Key Words: ambient temperature, beef cattle, blood metabolites, growth, rumen undegradable protein

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1577 Guanidinoacetic acid as a precursor for creatine in steers. M. Ardalan*[1], M. D. Miesner[2], C. D. Reinhardt[1], D. U. Thomson[3], C. K. Armendariz[1], and E. C. Titgemeyer[1], *[1]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [2]Department of Clinical Sciences, Kansas State University, Manhattan, [3]Department of Diagnostic Medicine/Pathobiology, Kansas State University, Manhattan*.

Guanidinoacetic acid (GAA) can be methylated to produce creatine. Because GAA supplementation bypasses the regulatory step in creatine formation, it may increase creatine availability. However, unregulated consumption of methyl groups may be problematic. We studied GAA supplementation in 7 steers maintained under conditions where methionine (Met) supply was purposefully limiting. Steers were limit-fed a soyhull-based diet and received abomasal infusions of AA to make methionine the solely limiting AA. Ruminal infusions of VFA and abomasal infusions of glucose provided energy. Factorial treatments (abomasally infused) included 0, 7.5, and 15 g/d GAA and 0 and 6 g/d l-Met. The experimental design

Table 1578. Dairy and Beef TMR CP and TAA population statistics.

Type	Parameter	n	Mean	St.Dev.	Min.	Max.
Beef	CP	9	13.2	1.2	11.2	14.7
Beef	TAA	9	11.1	1.1	9.3	12.7
Dry	CP	47	15.3	1.9	11.5	19.4
Dry	TAA	47	11.9	1.4	9.2	15.8
Lactating	CP	76	17.3	1.6	13.7	22.3
Lactating	TAA	76	14.0	1.2	10.4	18.7

was a split-plot, with Met main-plot treatments assigned in three 2 × 2 Latin squares. Subplot treatment was GAA, with amounts assigned to three 10-d subplot periods within each main-plot cell. Two steers received the same treatment sequence. Steers were housed in metabolism crates for measuring N retention over d 5 to 10. Jugular blood was collected on d 6, 8, and 10. Plasma GAA concentrations were increased by GAA supplementation ($P < 0.01$) but unaffected by Met ($P = 0.84$). Plasma creatine concentrations were increased by GAA supplementation ($P < 0.01$) but decreased by Met ($P < 0.01$). Plasma creatinine concentrations were unaffected by treatments ($P > 0.32$). Nitrogen retention was increased by Met ($P < 0.01$) but was not affected ($P > 0.28$) by GAA. There was, however, a tendency ($P = 0.10$) for N retention to demonstrate a Met × GAA interaction, with GAA linearly increasing N retention when 6 g/d Met was provided but decreasing N retention when no Met was supplemented. Urinary excretions of creatine and GAA did not demonstrate main effects of Met or GAA; however, both tended ($P < 0.10$) to be increased by GAA supplementation in the absence of supplemental Met but not affected by GAA when 6 g/d Met was supplemented. Urinary excretion of creatinine tended ($P < 0.10$) to be increased by GAA supplementation but was unaffected by Met. These data demonstrate that GAA can serve as a precursor to creatine in cattle and that metabolism of GAA and creatine are affected by methionine status. Supplementation of GAA did not affect N retention of growing steers, suggesting that either endogenous GAA production was adequate or longer periods may be required before responses are established.

Key Words: creatine, guanidinoacetic acid, methionine

1578 Total amino acid content variation for a commercial total mixed ration and relationship to crude protein. J. P. Goeser*[1,2], D. Sawyer[2], and G. A. Broderick[3], [1]*University of Wisconsin, Madison,* [2]*Rock River Laboratory, Inc., Watertown, WI,* [3]*Broderick Nutrition & Research, LLC, Madison, WI.*

Dairy cattle AA nutrition has evolved with NRC, CPM, and CNCPS model improvements. Ingredients rich in AA are added to dairy diets in precise amounts to better meet nutrient needs; however, animal health and performance still varies relative to expected responses when balancing for AA. The objective of this project was to describe total AA (TAA) population statistics and to determine if TAA varied relative to CP, for commercial TMR. Commercial TMR, $n = 141$, were selected from samples submitted to Rock River Laboratory for further analyses. Samples represented by dry, lactating dairy, finishing beef, and unknown TMR were dried using a microwave oven technique and ground (1 mm). TMR CP was determined as N × 6.25 after assaying N by a combustion technique. Total AA were determined after acid hydrolysis using *o*-phtaldialdehyde colorimetry. Type of TMR (beef, lactating, dry, and unknown) and CP were related to TAA using Fit Model function within JMP version 11.0; TMR type was considered random. Interactions and quadratic effects were tested. Residuals were visually assessed for normality using a residual by predicted plot. Commercial TMR CP and TAA (% of DM) and population statistics for all TMR except unknown are described in Table 1. Linear and quadratic relationships between CP and TAA were detected ($P < 0.05$). The quadratic effect was unanticipated and suggests a nonlinear relationship between TAA and CP. The model $R^2 = 0.78$, SE = 0.83, and parameter estimates (and SE) are as follows: 3.48 + CP × 0.58 (SE 0.04) + CP^2 × −0.02 (SE 0.01). That the slope estimate was <1.0 may partly be due to non-AA nitrogen in the form of urea, NH_3–N, or amide N present as glutamine and asparagine, all of which contribute N to CP but not to TAA equivalence. Results presented here demonstrate the variation in TAA contents of commercial farm TMR and may be useful when considering future model development and validation parameters. Furthermore, knowing TMR TAA in addition to CP may help improve on farm nutrition and troubleshooting.

Key Words: amino acid, protein, total mixed ration

1579 Impact of a rumen-protected methionine prototype on dairy cow performance, milk composition, and milk casein. A. M. Barnard*[1], B. A. Barton[2], C. A. Zimmerman[2], R. S. Ordway[2], and T. F. Gressley[1], [1]*University of Delaware, Newark,* [2]*Balchem Corporation, New Hampton, NY.*

Differences in the formulation of the protective matrix of methionine products may impact rumen degradation and intestinal availability. The objective of this study was to determine the effect of a rumen-protected methionine prototype on milk, milk protein, and casein yields. The study was conducted as a replicated 5 × 5 Latin square design in which 10 lactating,

Table 1579. Effect of methionine supplementation on production measures.

	Treatment						
		Methionine prototype					
	–Con	Met1	Met1.5	Met2	+Con	SEM	*P*-values
DMI, kg/d	28.17	28.76	28.48	28.47	29.28	0.71	0.59
Milk, kg/d	52.65	52.86	53.23	54.23	54.48	1.69	0.75
Fat, %	3.72	3.81	3.63	3.61	3.71	0.14	0.62
Fat, kg/d	1.97	1.99	1.92	1.94	1.99	0.07	0.84
Protein, %	2.64^{C}	$2.70^{A,B,C}$	2.72^{A}	$2.66^{B,C}$	$2.70^{A,B}$	0.02	0.05
Protein, kg/d	1.41^{B}	$1.43^{A,B}$	1.45^{A}	$1.43^{A,B}$	1.45^{A}	0.01	0.04
Casein, %	2.13^{C}	$2.18^{A,B,C}$	2.19^{A}	$2.14^{B,C}$	$2.18^{A,B}$	0.02	0.06
Casein, kg/d	1.14^{B}	$1.15^{A,B}$	1.17^{A}	$1.15^{A,B}$	1.17^{A}	0.01	0.06
Lactose, %	4.83	4.82	4.79	4.80	4.79	0.01	0.11
MUN, mg/dL	13.90	13.85	13.07	13.40	13.38	0.40	0.23
SCC	157.86	57.94	229.93	118.49	120.94	89.10	0.42

multiparous Holstein cows were assigned to either a methionine-deficient control ration (–Con), –Con supplemented with 0.09% Smartamine M (Adisseo, Antony, France; +Con), or the –Con supplemented with a rumen-protected methionine prototype (Balchem Corporation, New Hampton, NY) to provide either 1 (Met1), 1.5 (Met1.5), or 2 (Met2) times the amount of methionine supplied by Smartamine M. The ration was balanced with AMTS version 4.1.4 assuming 50.0 kg/d milk, 3.70% fat, 3.00% protein, and 740 kg BW. The –Con was formulated to have MP, MP methionine, and MP lysine balances of −32.5, −15.3, and +4.9 g/d, respectively. Supplementation of Smartamine M to the –Con resulted in formulated MP, MP methionine, and MP lysine balances of −16.2, +0.1, and +4.9 g/d, respectively. Periods were 14 d, and milk samples were collected on Days 11 to 14 of each period. Data collected during the last 4 d of each period were averaged by cow and analyzed using the Glimmix procedure of SAS. Data from two cows were removed before analysis due to illness. The model included a covariate (data collected during a 2-wk standardization period), fixed effects of treatment and period, and random effects of cow and cow within block. There were no treatment effects on DMI, milk yield, fat percentage, fat yield, lactose percentage, milk urea nitrogen (MUN), or somatic cell count (SCC) (Table 1). Treatment affected protein percentage ($P = 0.05$) and yield ($P = 0.04$) and tended to affect casein percentage ($P = 0.06$) and yield ($P = 0.06$). Relative to –Con, +Con and Met1.5 increased protein percentage by 0.06 ($P = 0.04$) and 0.08 ($P = 0.01$) units, respectively; protein yield by 0.04 kg/d for both treatments ($P = 0.01$); casein percentage by 0.05 ($P = 0.05$) and 0.06 ($P = 0.06$), respectively; and casein yield by 0.03 kg/d for both treatments ($P = 0.02$). The results suggest that Met1.5 was as effective at restoring methionine levels as +Con.

Key Words: bovine, methione, prototype

1580 Effects of feeding canola meal or wheat dried distillers' grains with solubles alone or in combination as the major protein sources on ruminal function and production in dairy cows.

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Canola meal (CM) is a good-quality protein supplement that is readily available and is used extensively in dairy cow diets in Canada and the United States. On the other hand, major growth of the ethanol industry in western Canada has resulted in large quantities of wheat dried distillers' grains with solubles (WDDGS) being available as an alternative protein supplement for dairy cows. Canola meal is an excellent source of limiting essential AA (e.g., lysine, histidine), whereas WDDGS has a greater CP content but is a poorer source of lysine; therefore, it is reasonable to consider that a judicious combination of CM and WDDGS as protein supplements may provide an optimal profile of essential AA that would improve milk production. The objective of this study was to determine the effects of feeding CM or WDDGS alone or in combination as the major sources of protein on ruminal fermentation characteristics and production in dairy cows. Fifteen lactating dairy cows (697 ± 46 kg BW and 76 ± 16 d in milk at the beginning of the experiment) were used in a replicated 5 × 5 Latin square design with 28-d periods (20 d of dietary adaptation and 8 d of measurements). Five cows in one Latin square were ruminally cannulated to facilitate ruminal sampling. The dietary treatments were 1) 100% CM as the major protein supplement, 2) 75% CM and 25% WDDGS, 3) 50% CM and 50% WDDGS, 4) 25% CM and 75% WDDGS, and 5) 100% WDDGS. Diets were isonitrogenous (17.6% CP) and were fed as TMR containing 50% forage and 50% concentrate. Dry matter intake (mean = 30 kg/d) was unaffected by diet. Milk production (40.4, 41.0, 41.2, 40.4, and 40.2 kg/d for the 100, 75, 50, 25, and 0% CM diets, respectively) was unaffected by diet. Milk composition was unaffected by diet; however, milk urea nitrogen linearly decreased ($P = 0.05$) as the dietary

proportion of CM decreased. Ruminal pH and concentrations of total and individual VFA were unaffected by diet. These results show that when dairy diets are formulated to contain 17.6% CP, CM or WDDGS can be fed alone or in combination as the major sources of protein and can support similar levels of milk production.

Key Words: canola meal, dairy cow, milk production, wheat dried distillers' grains with solubles

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1581 Relative bioavailability of l-carnitine delivered by ruminal or abomasal infusion or by encapsulation in dairy cattle. K. E. Olagaray*[1], J. E. Shaffer[1], C. K. Armendariz[2], A. Bellamine[3], S. Jacobs[3], E. C. Titgemeyer[1], and B. J. Bradford[1], *[1]Kansas State University, Manhattan, [2]Department of Animal Sciences and Industry, Kansas State University, Manhattan, [3]Lonza, Inc., Allendale, NJ.*

These studies evaluated the relative bioavailability of l-carnitine delivered by different methods in dairy cattle. In Experiment 1, 4 Holstein heifers were used in a split-plot design to compare ruminally or abomasally infused l-carnitine. The study included 2 main-plot periods, with infusion routes allocated in a crossover design. Within main-plot periods, each of 3 subplot periods consisted of 4-d infusions separated by 4-d rest periods. Subplot treatments were infusion of 1, 3, and 6 g l-carnitine/d. Doses increased within a period to minimize carryover. Treatments were delivered in two 10-h infusions daily. Blood was collected before the start of infusions and on d 4 of each infusion to obtain baseline and treatment l-carnitine concentrations. There was a dose × route interaction ($P < 0.05$) and route effect ($P < 0.01$) for increases in plasma carnitine above baseline, with increases above baseline being greater across all dose levels when abomasally infused compared with when ruminally infused. Results demonstrated superior bioavailability of l-carnitine when ruminal exposure was physically bypassed. In Experiment 2, 56 lactating Holstein cows (143 ± 72 DIM) were used in a randomized complete block design (blocked by parity and milk production) to evaluate 2 rumen-protected products compared with crystalline carnitine. Treatments were 1) control, 2) 3 g/d crystalline l-carnitine (crystalline), 3) 6 g/d crystalline, 4) 5 g/d 40COAT (40% coating and 60% l-carnitine), 5) 10 g/d 40COAT, 6) 7.5 g/d 60COAT (60% coating and 40% l-carnitine), and 7) 15 g/d 60COAT. Treatments were top-dressed to diets twice daily. The 14-d experiment included a 6-d baseline-measurement period with the final 2 d used for data and sample collection and an 8-d treatment period with the final 2 d used for data and sample collection. Plasma, urine, and milk samples were analyzed for l-carnitine. Crystalline ($P < 0.001$) and 40COAT ($P = 0.01$) linearly increased plasma l-carnitine, and 60COAT tended to linearly increase plasma l-carnitine ($P = 0.08$). Total daily excretion (milk + urine) of l-carnitine averaged 1.52 ± 0.04 g/d in controls, linearly increased with crystalline and 40COAT, and quadratically increased with 60COAT (all $P < 0.05$). Crystalline increased plasma l-carnitine and milk + urine l-carnitine more than 40COAT and 60COAT (all $P < 0.05$). In conclusion, preventing ruminal degradation of l-carnitine increased delivery of bioavailable carnitine to cattle, but effective ruminal protection and postruminal availability is challenging.

Key Words: bioavailability, dairy cow, l-carnitine

1582 Comparison of three levels of a rumen-protected methionine product on performance of lactating dairy cows. A. M. Barnard*[1], B. A. Barton[2], C. A. Zimmerman[2], R. S. Ordway[2], and T. F. Gressley[1], *[1]University of Delaware, Newark, [2]Balchem Corporation, New Hampton, NY.*

Because methionine is one of the limiting AA in the majority of dairy cow rations, rations are commonly supplemented with rumen-protected methionine products. The objective of this study was to evaluate the effect of a newly developed product, AminoShure-M (Balchem Corporation, New Hampton, NY), on performance of cows fed a methionine deficit ration. In a replicated 5 × 5 Latin square design, 19 multiparous cows were assigned to either a methionine-deficient control ration (–Con), the control ration supplemented with 0.09% Smartamine M (Adisseo, Antony, France) to serve as a positive control (+Con), or AminoShure-M to provide either 1.5 (ASM1.5), 1.75 (ASM1.75), or 2 (ASM2) times the amount of methionine supplied by Smartamine M. Periods were 14 d, and milk samples were collected on Days 11 to 14 of each period. Data collected during the last 4 d of each period were averaged by cow and analyzed using the Glimmix procedure of SAS. The model statement included a covariate (data collected during a 2-wk pretreatment period) and fixed effects of treatment and period. Cow and cow within block were included as random effects. There were no effects of treatments on milk yield, DMI, fat percentage, fat yield, lactose percentage, energy-corrected milk (ECM), ECM/DMI, fat-corrected milk (FCM), milk urea nitrogen (MUN) or somatic cell count (SCC). There was an effect of treatment on milk protein percentage ($P = 0.0001$) and protein yield ($P = 0.0001$). Compared with –Con, +Con increased protein percentage (2.77 vs. 2.66%; $P < 0.0001$) and yield (1.33 vs. 1.26 kg/d; $P < 0.0001$). ASM1.5 ($P = 0.003$), ASM1.75 ($P = 0.002$), and ASM2 ($P < 0.0001$) increased protein by 0.05, 0.06, and 0.08 percentage units, respectively, compared with –Con. ASM1.5 ($P = 0.001$), ASM1.75 ($P = 0.001$), and ASM2 ($P < 0.0001$) increased protein yield by 0.04, 0.04, and 0.05 kg/d, respectively, compared with –Con. +Con also increased protein by 0.06 and 0.05 percentage units compared with ASM1.5 ($P = 0.002$) and ASM1.75 ($P = 0.004$), respectively, but was not different from ASM2. +Con also increased protein yield by 0.03 kg/d compared with ASM1.5 ($P = 0.005$) and ASM1.75 ($P = 0.01$). Similar to protein percentage, ASM2 was not significantly different from +Con, suggesting that this ASM treatment was as

effective at restoring methionine levels as +Con.

Key Words: bovine, methionine, milk protein

1583 Evaluation of *Brassica carinata* meal as a protein supplement for growing beef heifers.

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Brassica carinata is a new oilseed crop in Florida with the potential of producing high-quality biodiesel for use as jet biofuel. A high-protein meal is obtained as a byproduct of oil extraction; however, this meal has not been tested as a potential supplement for growing beef cattle. The objective of this experiment was to determine the effect of supplementation with *B. carinata* meal (BCM) on animal performance, attainment of puberty, and blood profile in growing beef heifers consuming grass hay. Thirty-two Angus crossbred heifers (271 ± 42 kg initial BW) were stratified by initial BW and randomly allocated to a total of 10 pens in 2 BW blocks. Within block, pens were randomly assigned to one of two treatments: 0 (CTL) or 0.3% of BW/d (as fed) of BCM pellets. All heifers had ad libitum access to bahiagrass (*Paspalum notatum*) hay and water, and BCM pellets were supplemented daily in the pen. Body weight and blood samples were collected every 7 d for a duration of 70 d, before the daily supplementation. Plasma was collected for analysis of progesterone and blood urea nitrogen concentrations and glucose. Data were analyzed as a generalized randomized block design including block in the model as a random variable. Progesterone data were analyzed using the LIFETEST procedure of SAS to determine the effect of treatment on time to attainment of puberty. There was a difference ($P = 0.02$) in ADG between CTL (0.28 kg/d) and BCM (0.49 kg/d). Time to attainment of puberty did not differ between treatments ($P = 0.36$). Supplementing *B. carinata* meal at 0.3% of BW/d in growing heifers consuming bahiagrass hay is a viable option for increasing ADG without negatively affecting their interval to attainment of puberty.

Key Words: *Brassica carinata*, protein supplement, ruminants

1584 Effects of replacing soybean meal with canola meal or treated canola meal on nitrogen metabolism and total tract digestibility in lactating dairy cows.

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Canola meal (CM) has been shown to improve N efficiency in dairy cows when compared with soybean meal (SBM). Treating CM may increase its RUP fraction with the goal of increasing AA availability for absorption in the small intestine. The objective of this study was to evaluate the effects of feeding treated CM (TCM) on N metabolism and total tract digestibility of dairy cows. Thirty multiparous Holstein cows, averaging (means ± SD) 660 ± 55 kg BW, 119 ± 23 DIM, and 44.1 ± 7 kg milk/d, and 15 primiparous cows, averaging 592 ± 34 kg BW, 121 ± 19 DIM, and 33.5 ± 6 kg milk/d, were blocked in a randomized complete block design. Cows were fed a control diet for a 2-wk covariate period and then switched to the experimental diets for a 12-wk study; cows were individually fed in tie-stalls and had free access to water. Treatments differed only in CP source, which were SBM, CM, or TCM. The CM was treated by extrusion, with added molasses to promote the

Table 1584.

Table 1. Effect of soybean meal (SBM), canola meal (CM), or treated canola meal (TCM) on nitrogen metabolism and digestibilities

	Diet				Contrasts *P*-value	
Item	SBM	CM	TCM	SEM	SBM vs. CM+TCM	CM vs. TCM
N intake, g/d	653.0	691.9	691.9	22.7	0.17	1.00
Milk, kg/d	40.0	41.3	40.5	1.01	0.48	0.62
MUN, mg/dL	13.7	12.8	12.5	0.25	<0.01	0.43
DM digestibility, %	68.4	70.9	69.7	0.44	<0.01	0.08
OM digestibility, %	70.2	72.4	71.3	0.42	<0.01	0.07
CP digestibility, %	64.7	68.9	67.3	0.68	<0.01	0.09
NDF digestibility, %	45.1	49.1	47.1	0.80	<0.01	0.08
Fecal-N, g/d	206.5	201.9	210.2	8.01	0.96	0.47
Fecal-N, % of intake	31.6	29.2	30.3	0.45	<0.01	0.08
Urinary total N, g/d	219.4	221.3	215.5	7.25	0.92	0.57
Urinary total N, % of N intake	34.0	32.5	31.5	1.01	0.12	0.46
Urinary urea N, g/d	157.1	152.2	146.6	5.04	0.22	0.44
Urinary urea N, % of total urinary N	72.2	69.2	68.4	0.90	<0.01	0.52

browning reaction. All diets contained (DM basis) 30% alfalfa silage, 30% corn silage, 4% soy hulls, 2.4% mineral–vitamin premix, and 16% CP. The SBM diet contained 25% high-moisture corn (HMC) and 8.6% SBM; the canola diets contained 22% HMC and 11.4% CM or TCM. On the last day of wk 4, 8, and 12, spot urine and fecal samples were collected at 6 and 18 h after feeding. Data were analyzed using the MIXED procedure of SAS. Orthogonal contrasts were used to compare effects of different protein sources (SBM vs. CM + TCM and CM vs. TCM). Partial data are presented in Table 1. Compared with SBM, apparent digestibility of DM, OM, CP, and NDF was greater on both CM and TCM diets and there were trends for improved digestibilities when CM was compared with TCM. There were no differences for N intake, milk yield, and total N excreted in urine and feces; however, both canola diets decreased urinary urea N (% of total urinary N) and fecal N (% of total N intake) and decreased MUN concentration. No differences were observed between CM and TCM with regards to N utilization. Results from this experiment indicate that replacing SBM with CM or TCM in lactation diets improved digestibility and minimized environmental impact but that extrusion did not improve CM utilization.

Key Words: dairy nutrition, digestibility, nitrogen utilization

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1585 Impact of different diet crude protein levels and ruminally degradable protein:ruminally undegradable protein ratios on midlactation dairy cow performance: II. Dry matter intake, digestibility, and nitrogen balance.

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This study evaluated the impact of different CP levels and RDP:RUP ratios in the diets of 24 crossbred Holstein–Gir midlactating dairy cows. Animals were allotted for 60 d to 4 treatments on a complete random design ($n = 6$). Experimental diets were formulated using the CNCPS version 6.1 model to meet production requirements and to be isoenergetic and provide the same amount of MP. Crude protein concentrations were 12.4, 13.0, 13.6, and 15.4% on a DM basis. Ruminally degradable protein levels ranged from 5.6 to 9.7% DM and RUP ranged from 6.8 to 5.7 DM in relation to treatments with lower and higher CP levels, respectively. Soypass (Cargill) was used in substitution to soybean meal and urea to adjust RDP:RUP ratios. Parameters evaluated were DMI, CP intake (CPI), DM digestibility, nitrogen balance, microbial protein yield (MPY), and plasma urea nitrogen (PUN). Data were analyzed using PROC MIXED from SAS 9.0 on a split plot design. Dry matter intake did not differ among treatments and ranged from 20.0 to 21.6 kg/d, whereas CPI increased ($P < 0.01$) as diets' CP level increased (2.59–3.46 kg/d). Treatments did not affect DM digestibility (60.2–61.9%) but CP digestibility increased ($P < 0.04$) as RDP levels in the diets increased (58.2–67.2%). Treatments did not affect milk N (119–135 g/d) or N in feces (178–182 g/d). Urine N increased (116–247 g/d) as diets CP level increased ($P < 0.01$). Microbial protein yield was not affected by treatments. Plasma urea nitrogen values raised from 10.2 to 19.6 mg/dL as RDP levels increased ($P < 0.01$). Results show that formulating diets with more RUP sources can be an efficient tool to reduce N excretion and improve N balance. Reducing RDP and CP levels in the diets did not affect DMI and did not impair MPY.

Key Words: ruminally degradable protein, ruminally undegradable protein, nitrogen balance

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1586 Evaluation of protein supplementation in low- to medium-quality forage diets on intake and ruminal fermentation in steers.

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Four ruminally and duodenally cannulated steers (469 ± 37 kg initial BW) were arranged in a 4 × 4 Latin square to evaluate the impact of protein supplementation in low- to medium-quality forage diets on intake and ruminal fermentation. Protein supplement treatments included 1) high-fat dried distillers' grains (HDG; 10.8% fat), 2) low-fat dried distillers' grains (LDG; 5.7% fat), and 3) cottonseed meal (CSM; 3.0% fat). The basal diet (CON) consisted of low- to medium-quality chopped grass hay (8.3% CP and 64.9% NDF) fed ad libitum twice daily at h 0 and 12. Treatments were formulated to provide similar CP intake and were supplemented once daily to the basal diet: HDG at 0.8%, LDG at 0.7%, and CSM at 0.4% of BW. Each 21-d experimental period had 16 d of adaptation and 5 d of data collection. Intake data was collected d 17 to 21, and rumen fluid samples were collected on d 20 at h −2, 0, 2, 4, 6, 8, 10, and 12. Hay DMI was lower with supplementation of HDG ($P < 0.01$) verses CON and CSM but similar to LDG. However, hay DMI for LDG was not different ($P > 0.05$) than that for CON but lower ($P \leq 0.01$) than that for CSM. As expected, CP intake was greater ($P \leq 0.0001$) with protein supplementation than CON but not different among protein supplements. Fat intake was greatest to least for HDG, LDG, CSM, and CON, respectively ($P \leq 0.001$). Protein supplementation resulted in lower ($P \leq 0.05$) overall ruminal pH and over 2-fold greater ($P \leq 0.05$) ammonia concentration compared with CON. Overall ruminal pH was lowest for HDG compared with LDG, CSM, and CON (6.88, 6.23, 6.54, and 6.64 ± 0.09, respectively; $P = 0.0001$);

however, LDG and CSM were not different ($P > 0.05$) but lower ($P \leq 0.0001$) than CON. Total VFA production did not differ ($P = 0.46$) among treatments. Acetate proportions from greatest to least were CON, CSM, LDG, and HDG ($P \leq 0.03$). Propionate proportions from greatest to least were HDG, LDG, CSM, and CON ($P \leq 0.03$), with the exception of butyrate, which was not different between CSM and CON ($P = 0.26$). Supplementation of HDG, LDG, and CSM decreased ruminal pH and increased propionate while decreasing acetate proportions compared with no protein supplementation. Protein supplementation decreased hay consumption and the greatest decrease was observed with HDG supplementation.

Key Words: forage intake, protein supplementation, ruminal fermentation

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1587 The effect of increasing concentrations of different methionine forms and 2-hydroxy-4-(methylthio) butanoic acid on hepatic oxidative status and genes controlling methionine metabolism and transmethylation flux. Q. Zhang*[1], D. N. Luchini[2], and H. M. White[1], *[1]University of Wisconsin-Madison, Madison, [2]Adisseo S.A.S., Alpharetta, GA*.

The d-isomer of methionine (Met) cannot be directly utilized by the mammary gland in dairy cows; instead, it is transformed into l-Met, the proteogenic isomer, in the liver and other extramammary tissues. It remains unclear whether different Met forms and a Met hydroxy analog, 2-hydroxy-4-(methylthio) butanoic acid (HMB), are metabolized and function similarly in the liver. The objective of the present study was to examine the regulation of key genes in methionine regeneration, transulfuration, and transmethylation pathways and hepatic oxidative status in response to increasing doses of different Met forms. Hepatocytes isolated from 4 calves less than 7 d old were maintained as monolayer cultures for 24 h before addition of treatments. Treatments of (0, 10, 20, and 40 μM) d-Met, l-Met, dl-Met, dl-HMB, or a 1:1 mixture of dl-Met and dl-HMB were added to Met-free media in triplicate. After 24 h, cell lysates were collected for quantification of gene expression by quantitative PCR, and mRNA abundance was normalized to the mean of 3 reference genes. Cell culture media were collected for quantification of reactive oxygen species (ROS) by fluorometric assay. Data were analyzed with PROC MIXED of SAS 9.3. Analyses of covariance confirmed equivalent slopes of Met form and the final model included form, dose, and random effect of calf within form. Data are reported as least squares means ± SE. Neither Met form nor Met concentration affected ($P > 0.10$) ROS released from the cells. There was no main effect of Met form ($P > 0.10$) for any genes examined. The enzymes encoded by *betaine-homocysteine methyltransferase* (*BHMT*) and *5-methyltetrahydrofolate-homocysteine methyltransferase* (*MTR*) utilize betaine and 5-methyltetrahydrofolate, respectively, to regenerate Met from homocysteine. Increasing concentration of Met did not alter ($P > 0.10$) *MTR* expression (1.274, 1.269, 1.264, and 1.255 ± 0.257 arbitrary units [AU]) but decreased ($P < 0.05$) *BHMT* expression (1.308, 1.223, 1.138, and 0.968 ± 0.234 AU). Expression of glycine N-methyltransferase, the enzyme that controls transmethylation flux from S-adenosyl-methionine, was not affected (2.205, 2.157, 2.108, and 2.011 ± 0.735 AU; $P > 0.10$) by Met concentration. There was no effect ($P > 0.10$) of Met concentration on expression of cystathionine β-synthase (0.958, 0.972, 0.985, and 1.012 ± 0.168 AU), a key enzyme for the transulfuration pathway. The decrease in *BHMT* expression indicates decreased need for cellular Met regeneration with increasing Met concentration independent of Met form. The lack of differences among Met forms on regulating genes examined indicates that all Met forms were metabolized similarly within primary bovine hepatocytes and had similar sparing effects on Met regeneration in the liver.

Key Words: methionine isomer, methionine regeneration, 2-hydroxy-4-(methylthio) butanoic acid

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1588 Heat stress alters glucose homeostasis, hepatic heat shock proteins, and the immune system in lactating dairy cows. S. Quan[1,2], D. Bu*[1,3,4], Y. Zhang[2], J. Guo[1], S. Gao[1], and L. H. Baumgard[5], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, [2]The Animal Physiology and Biochemistry Laboratory of the Ministry of Agriculture in Nanjing Agriculture University, Nanjing, P. R. China, [3]Hunan Co-Innovation Center of Animal Production Safety, CICAPS, Changsha, P. R. China, [4]CAAS-ICRAF Joint Laboratory of Agroforestry and Sustainable Animal Husbandry, World Agroforestry Centre, East and Central Asia, Beijing, P. R. China, [5]Iowa State University, Ames*.

Experimental goals were to investigate glucose homeostasis, hepatic heat shock protein profiles, and circulating immune parameters in lactating dairy cows during heat stress (HS). Holstein cows ($n = 4$; 101 ± 10 DIM, 574 ± 36 kg BW, and 38 ± 2 kg milk/d) were used in a 2 × 2 crossover design during two experimental periods (each period lasted 10 d and were separated by 30 d) while housed in environmentally controlled chambers. Pair-fed, thermal-neutral control cows (PF) were exposed to constant 20°C and 40% humidity whereas HS cows were exposed to 36°C and 60% humidity from 0800 to 2000 h and 32°C and 60% humidity from 2000 to 0800 h with 12 h light and 12 h dark cycles. Blood and milk samples were collected on d 1, 4, 7, and 10 during both periods. Glucose tolerance test (GTT) was performed on d 6 of each period. Liver tissue was collected on d 10 of each period. Heat stress reduced milk yield (21.5%; $P < 0.05$) and lactose yield ($P < 0.05$; 300 g/d) compared with PF controls. Basal serum glucose decreased (30.1%; $P < 0.05$) and the rate of glucose

disposal following the GTT increased during HS (21.4%; $P < 0.05$). Serum IgA and TNF were reduced (38.1 and 23.4%, respectively) in HS cows ($P < 0.05$) compared with the PF controls but IgG, IgM, and IL-6 were similar between environments ($P > 0.05$). Liver HSP27 mRNA increased in the HS cows (51.2%; $P < 0.05$), but HSP70, HSP90, and HSF-1 did not differ between environments ($P > 0.05$). Heat stress markedly reduced mammary carbohydrate output, and the increased whole-body glucose utilization may be indicative of both an activated immune response and fuel required to mount and sustain a heat shock response.

Key Words: heat stress, glucose disposal, heat shock protein, immune activation, lactating cow

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1589 The effect of heat stress and jugular infusions of methionine, lysine, and branched-chain amino acids in lactating dairy cattle. K. Kassube*, J. Kaufman, K. G. Pohler, and A. G. Rius, *The University of Tennessee, Knoxville*.

Heat stress (HS) affects numerous physiological processes including nutrient partitioning and protein metabolism. Heat stress decreases production of milk and milk proteins and may benefit from supplementation of essential AA. The objective of this study was to determine the effect of jugular infusion of essential AA in lactating dairy cattle experiencing HS. Twelve multiparous lactating Holstein cows were used in a crossover design to evaluate the effect of two environments (thermoneutral [TN] and HS) and the absence or presence of AA infusion (NAA or AA [methionine {12 g}, lysine {21 g}, leucine {35 g}, isoleucine {15 g}, and valine {15 g} per day]). Thermal treatments were imposed from d 1 to 14 and jugular infusion of AA was from d 7 to 14. Temperature–humidity index values during TN never exceeded 66, whereas temperature–humidity index values during HS peaked at 76 and were above 68 for 14 h/d. Milk and blood samples were collected on d 5 to 7 and d 12 to 14. Data were analyzed using the Mixed procedure of SAS and reported as least squares means ± SEM. The HS treatment increased ($P < 0.05$) respiration rates and rectal temperatures (72.1 vs. 47.0 ± 3.9 breaths/min and 39.4 vs. 38.5 ± 0.017°C, respectively). Compared with TN treatment, HS decreased ($P < 0.05$) DMI (17.4 vs. 18.9 ± 0.41 kg/d), milk yield (29.3 vs. 32.1 ± 1.09 kg/d), milk protein yield (0.87 vs. 0.98 ± 0.05 kg/d), and lactose yield (1.41 vs. 1.55 ± 0.10 kg/d). Amino acid treatment decreased ($P < 0.001$) lactose yield (1.43 vs. 1.54 ± 0.10 kg/d) but had no effect on DMI and milk yield. Heat stress decreased ($P < 0.05$) milk protein percent (2.95 vs. 3.06 ± 0.06%). Amino acid treatment increased ($P < 0.001$) milk protein percent (3.04 vs. 2.96 ± 0.06%) and decreased ($P < 0.001$) lactose percent (4.82 vs. 4.87 ± 0.04%). Compared with the NAA treatment, AA did not affect milk fat yield in the TN treatment (1.33 vs. 1.33 ± 0.09 kg/d) but decreased milk fat yield in the HS treatment (1.18 vs. 1.32 ± 0.09 kg/d; interaction, $P < 0.05$). Compared with the NAA treatment, AA treatment increased milk urea nitrogen in the TN treatment (11.7 vs. 10.9 ± 0.77 mg/dL) but did not increase milk urea nitrogen in the HS treatment (12.3 vs. 12.8 ± 0.74 mg/dL; interaction, $P < 0.01$). Plasma glucose decreased 6.7% in the AA treatment (2.8 vs. 3.0 ± 0.05 mmol/L; $P < 0.001$). Insulin, NEFA, and β-hydroxybutyrate were not affected by treatments. In conclusion, HS elicited expected decreases in production; however, the infusion of essential AA did not improve milk yield and milk protein yield during HS.

Key Words: essential amino acids, heat stress

1590 Effect of experimental design on production responses in high-producing dairy cows fed two levels of metabolizable protein. G. I. Zanton*, *USDA-ARS, U.S. Dairy Forage Research Center, Madison, WI*.

Inferences about lactation responses to diet have been hypothesized to be affected by the use of changeover instead of continuous experimental designs; a direct test of this hypothesis has not been well studied. The objective of this study was to evaluate the effects of reducing MP on lactation performance when dairy cows are fed diets continuously or according to a changeover design. Forty-six multiparous, Holstein cows were fed a common diet for 14 d and then randomly assigned to a randomized completed block design (CONT; $n = 34$; initial mean ± SD: 2.9 ± 0.9 parity, 84 ± 30 d in milk, 720 ± 59 kg BW, and 58.1 ± 6.4 kg milk/d) or a balanced 2-treatment, 4-sequence, 4-period changeover design (CHANGE; $n = 12$; 2.7 ± 1.0 parity, 90 ± 32 d in milk, 709 ± 78 kg BW, and 56.7 ± 3.9 kg milk/d). Cows were fed once and milk thrice daily, received rBST every 14 d, and received a diet that was predicted to be either adequate (ADMP) or deficient (LOMP) in MP for 112 d or changing according to sequence for four 28-d periods. The base diet was formulated to contain (% DM) 37.5% BMR corn silage, 16% alfalfa silage, and 41% concentrate. Treatments differed by adding 5.5% expeller soybean meal to the base diet for ADMP or 5.5% soyhulls for LOMP. By design, chemical composition differed with 16.6 vs. 14.7% CP, 28.2 vs. 31.1% NDF, and 27.6 vs. 27.5% starch for ADMP vs. LOMP, respectively. Production data were analyzed for study d 22 to 28, 50 to 56, 78 to 84, and 106 to 112, corresponding to 21 d of adaptation and 7 d of measurement for cows in the changeover design. Statistical analysis was conducted using the mixed procedure of SAS as either a randomized complete block design or as a balanced changeover design where differences with $P < 0.05$ are considered significant. As shown in the table, response to dietary treatment was not different for BW, BW change, and DMI, irrespective of experimental design. Milk and protein yield and milk urea N concentration were reduced with LOMP compared with ADMP for both designs. Fat yield response to diet was not different for CONT whereas fat percent increased with LOMP. In contrast, fat yield was significantly reduced for cows fed LOMP in CHANGE with

Table 1590.

Table 1. Production responses for cows fed diets containing either adequate (ADMP) or low (LOMP) levels of MP either continuously for 112 d (CONT) or according to a 4-period changeover design (CHANGE)

	CONT				CHANGE				
	ADMP	LOMP	SEM	P_{MP}[1]	ADMP	LOMP	SEM	P_{MP}[1]	P_{CO}[1]
BW, kg	740	734	5	0.375	731	733	7	0.588	0.475
BW change, kg/28d	7.9	5.6	1.8	0.351	5.9	11.3	5.5	0.335	0.432
DMI, kg/d	28.9	30.7	0.7	0.062	30.0	30.5	0.7	0.277	0.122
Milk, kg/d	55.5	52.7	0.8	0.012	56.1	52.7	1.2	<0.001	0.961
Protein, kg/d	1.62	1.53	0.02	0.006	1.66	1.54	0.04	<0.001	0.531
Protein, %	2.93	2.92	0.02	0.860	3.03	2.99	0.04	0.099	0.356
Fat, kg/d	1.82	1.82	0.08	0.979	1.80	1.67	0.06	0.009	0.008
Fat, %	3.17	3.54	0.11	0.022	3.24	3.21	0.12	0.588	0.002
MUN, mg/dl	8.63	5.99	0.28	<0.001	8.58	5.80	0.36	<0.001	0.226

[1] P_{MP}: *P*-value for the effect of dietary treatment; P_{CO}: *P*-value for carry-over of previous treatment

no significant difference in fat percent for this design; significant carryover effect differences were observed. Under the conditions of this experiment, inferences on the response to different levels of MP were affected by the experimental design and the production variable of interest.

Key Words: experimental design, lactation, protein

1591 Meta-analysis of postruminal microbial nitrogen flows in dairy cattle.

1592 Prediction of crude protein and neutral detergent fiber content in *Pennisetum clandestinum* by near-infrared spectroscopy. A. Rivera*, *Universidad Nacional de Colombia, Medellin, Colombia*.

The objective of this study was to predict the CP and NDF content of *Pennisetum clandestinum* using near-infrared spectroscopy (NIRS).Three hundred fifty-four ($n = 354$) grass samples were collected from different dairy herds from northern Antioquia-Colombia, during 2015 and earlier 2016, which varied in soil types and fertility and grass growth stage and were analyzed at the Chemical Analysis and Bromatological Laboratory (certificate for ISOMEC 17025-2005) of the Universidad Nacional de Colombia at Medellin. Samples were dried to constant weight in a forced-air oven at 60°C for 48 h and then ground in a Wiley mill (1-mm sieve). Crude protein (N × 6.25) and NDF were analyzed following official methods. Content of CP ranged between 14 and 30.5%, with a mean of 23.07 ± 3.73%, and that of NDF ranged from 46.60 to 65.90%, with a mean of 56.22 ± 4.70%. Samples were randomized divided in two groups, and the first group ($n = 301$) was used for calibration and the second group for cross-validation ($n = 40$) and external validation ($n = 13$). Samples for calibration and cross-validation were scanned in an NIRS DS 2500 F monochromator (Foss-NIRsystem, Denmark) in the range of 1,108 to 2,492 nm for CP and 858 to 2,492 nm for NDF, with reflectance data collected every 8 nm. Modified partial least squares (MPLS) regression was applied to scatter-corrected spectra (SNV and detrend) and mathematical treatment (equation generation) was performed in the software WinISI version 4.8. The equations were selected by evaluating the statistical parameters (R^2 higher than 0.80, a SE of cross-validation [SECV] close to the SE of calibration [SEC], and a SE of reference database:SE of cross-validation [RPD] ratio greater than 3). As a result, the equation selected for CP was mathematically treated with derivative, 1; gap, 4; smooth, 3; smooth 2, 1; the mean was 22.48; SD 2,91; SEC 03253; SECV 0.439; and RPD 6.62 and correlation coefficients of calibration, cross-validation, and external validation were 0.977, 0.920, and 0.982, respectively. The equation selected for NDF was mathematically treated with derivative 1; gap, 4; smooth, 3; smooth 2, 1; the mean was 56.18; SD 4.56; SEC 1.571; SECV 1.770; RPD 2.75 and correlation coefficients of calibration, cross-validation, and external validation were 0.847, 0.727, and 0.781, respectively. According to these preliminary results, it was possible to predict reliably the CP content of *P. clandestinum*, but for NDF, further work is still needed.

Key Words: dairy, feed quality, forage analysis, near-infrared spectroscopy, nutrition

1593 Impact of metabolizable protein source on pancreatic enzyme activity in finishing cattle fed dry-rolled corn–based diets. E. J. Blom*[1], D. W. Brake[1], M. R. Fiene[1], J. A. Walker[1], F. E. Keomanivong[2], and K. C. Swanson[2], [1]*South Dakota State University, Brookings,* [2]*North Dakota State University, Fargo*.

Previous data indicate increases in MP flow from soybean meal can increase pancreatic amylase content in cattle fed corn-based diets. However, reports on effects of increased MP flows from different protein sources are limited. We evaluated effects of added MP from either dried distillers' grains or porcine blood meal and corn gluten meal to finishing cattle fed dry-rolled corn–based diets designed to meet CP requirements (CP = 13.7% DM) on pancreatic α-amylase and trypsin and duodenal maltase activity. Two hundred sixteen crossbred steers (362.3 ± 3.4 kg BW) were blocked by initial BW, randomly assigned to 18 pens, and adapted to 1 of 3 dietary treatments. Treatments were a dry-rolled corn–based diet with added urea to meet CP requirements (CON), a diet with supplemental dried distillers' grains (DGS) designed to provide an additional 200 g/d MP, and a diet designed to provide 100 g/d additional MP from blood meal and 100 g/d additional MP from corn gluten meal (BMCGM). Cattle were fed for 152 d and subsequently harvested in a commercial abattoir. At harvest, pancreata and duodenal tissues were collected from 2 steers randomly selected within each pen for enzyme analyses. Pancreatic protein concentration (114.2 ± 4.3 mg/g) was not affected (P = 0.26) by dietary treatment. Pancreatic α-amylase activity per gram tissue was less (P = 0.01) among cattle fed DGS compared with CON and BMCGM. Additionally, added MP from DGS tended (P = 0.07) to decrease pancreatic α-amylase activity per gram pancreatic protein. Greater MP flow from BMCGM increased (P = 0.02) pancreatic trypsin activity per gram tissue; however, increased MP from either BMCGM or DGS did not impact (P = 0.30) trypsin activity per gram pancreatic protein (120.9 ± 22.25 U/g). Additions of MP did not affect (P = 0.43) protein content in duodenal tissue (62.1 ± 2.67 mg/g). Similarly, duodenal maltase activity (227.6 ± 13.87 U/g duodenum and 4.30 ± 1.217 U/g duodenal protein) was not affected ($P \geq 0.29$) by additional MP from either BMCGM or DGS. These data indicate that pancreatic α-amylase and trypsin activity are impacted by amounts and source of MP in finishing cattle, which could potentially influence starch and protein digestion in the small intestine.

Key Words: cattle, metabolizable protein, pancreas

1594 Comparative effects of multiple sources of rumen-protected methionine on milk production and serum amino acid levels in midlactation dairy cows. Y. Zang[1], S. Saed Samii*[1], L. R. Tager[2], J. W. McFadden[1], and K. M. Krause[1], [1]*West Virginia University, Morgantown,* [2]*MarSyt, Elizabethtown, PA*.

Methionine (Met) and lysine (Lys) are limiting AA in dairy cow diets. Supplementation of rumen-protected (RP) Met and Lys can improve milk yield as well as yield and content of milk protein. Currently, multiple sources of RP-Met are available for supplementation; however, the comparative efficacy of these supplements to improve performance requires evaluation. Therefore, our objective was to characterize the production response of three RP-Met supplements in midlactation cows. Twelve multiparous Holstein cows (602 ± 46 kg BW and 174 ± 18 DIM) were used in a replicated 4 × 4 Latin square design with 21-d treatment periods. Dietary treatments included a corn silage and alfalfa haylage diet (control; no added Met) supplemented with one of three RP-Met sources (Novimet [Innovad], Smartamine M [Adisseo], and Mepron M85 [Evonik]). Treatments were designed to maintain a Lys:Met ratio of 2.9:1. For the control, Lys (RP-Lys; AjiPro) was added at 0.02% ration DM. For RP-Met supplementation, Met (RP-Met) was added at 0.03% ration DM. Cows fed RP-Met were provided Lys (RP-Lys) at 0.20% ration DM. Milk yields were recorded, and samples were collected during each period (d 19 to 21). Blood samples were collected on d 21 at 2, 4, and 6 h following feeding, and serum was pooled. Following solid-phase extraction, 21 serum AA were quantified using gas chromatography tandem mass spectrometry. Data were analyzed using a mixed model with repeated measures (fixed effects of treatment and period). Treatments had no effect on DMI or milk yield. Treatment did not modify milk fat, protein, or lactose yield; however, milk protein content was elevated with Smartamine M relative to control or Novimet (3.30 vs. 3.24 and 3.24% respectively; $P < 0.05$). Milk fat and lactose concentration were not modified with treatment. Treatment with RP-Met tended to increase milk urea nitrogen (P = 0.12). Smartamine M increased serum Met concentration (27.3 μ*M*) compared with the control (21.2 μ*M*), Novimet (22.7 μ*M*), or Mepron M85 (23.3 μ*M*) ($P < 0.001$). In a similar manner, Smartamine M lowered the serum Lys:Met ratio (4.5:1) compared with the control (5.2:1), Novimet (5.2:1), or Mepron M85 (5.1:1) ($P < 0.05$). Smartamine M was also able to enhance circulating glutamine relative to the control (320.8 vs. 289.5; P = 0.15). Treatment did not modify serum levels of all other AA, including Lys. We conclude that Smartamine M increased circulating Met and milk protein content more effectively than Novimet or Mepron M85.

Key Words: dairy cow, lysine, methionine

1595 Milk protein synthesis gene expression and mTOR phosphorylation in response to the "ideal" profile of Lys, Met, Thr, Phe, His, Val, Ile, and Leu in bovine mammary cells. X. Dong*[1,2], Z. Zhou[1], Z. Wang[2], B. Saremi[3], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]Sichuan Agricultural University, Ya'an, IL, [3]Evonik Industries AG, 63457 Hanau, Germany*.

Essential AA (EAA) are important for milk protein synthesis and potentially could alter phosphorylation of the key proteins in the mTOR pathway. We hypothesized that the EAA profile affects the mammary transcriptome and mTOR phosphorylation/total mTOR (PmTOR/TmTOR) in bovine MAC-T cells. The specific objective was to investigate how changing the ratio of Lys to Met, Thr, Phe, His, Val, Ile, or Leu affects mRNA expression of key milk protein synthesis genes and PmTOR/TmTOR. Experiment 1 consisted (n = 5 replicates/treatment) of a control medium (i.e., the "ideal" EAA ratio [IPAA; 2.9:1 Lys:Met, 1.8:1 Lys:Thr, 2.38:1 Lys:His, 1.23:1 Lys:Val, 1.45:1 Lys:Ile, 0.85:1 Lys:Leu, and 2.08:1 Lys:Arg]) or IPAA supplemented with Met to achieve a 2.5:1 Lys:Met ratio (LM2.5) and a 2.0:1 Lys:Met ratio (LM2.0). Data were analyzed using a MIXED model in SAS. Treatment means were generated using the LSMEANS option and separated when significant with the PDIFF option. Compared with IPAA, increasing exogenous Met (LM2.5 and LM2.0) led to greater ($P < 0.01$) *SLC3A2* (l-type AA transporter) but LM2.0 led to the lowest ($P = 0.05$) *MTOR* expression and a strong tendency ($P = 0.06$) for greater *EEF2* (translation elongation factor). Although *EIF4EBP1* (translation repressor) expression did not change ($P = 0.15$), PmTOR/TmTOR was lower ($P < 0.05$) with LM2.5 and LM2.0 compared with IPAA. Experiment 2 consisted (n = 5 replicates/treatment) of IPAA or IPAA supplemented with Thr, Ile, Val, and Leu to achieve a 1.3:1 Lys:Thr ratio (LT1.3), 1.29:1 Lys:Ile ratio (LI1.29), 1.12:1 Lys:Val ratio (LV1.12), and 0.78:1 Lys:Leu ratio (LL0.78). Compared with IPAA, an increase in Thr, Ile, Val, and Leu resulted in greater ($P < 0.01$) expression of *SLC3A2*, but only an increase in Ile upregulated ($P = 0.05$) *EIF4EBP1*. Expression of *MTOR* and *EEF2* did not change ($P > 0.10$) compared with IPAA. Only the increase in Ile (LI1.29) and Val (LV1.12) led to greater ($P < 0.01$) PmTOR/TmTOR, indicating the potential for enhancing protein synthesis compared with IPAA. Overall, the data from these experiments indicate that changes in EAA profile, particularly Lys:Met, Lys:Val, and Lys:Ile, may affect mammary epithelial cell protein synthesis at least in part through regulating AA transport and PmTOR/TmTOR.

Key Words: essential amino acid profile, protein synthesis, mammary cell

1596 Nitrogen excretion of lactating dairy cows fed an alfalfa hay– or birdsfoot trefoil hay–based high-forage diet. M. Ghelich Khan[1], S. Y. Yang[1], J. S. Eun*[1], and J. W. MacAdam[2], *[1]Department of Animal, Dairy, and Veterinary Sciences, Utah State University, Logan, [2]Department of Plants, Soils, and Climate, Utah State University, Logan*.

Legumes that contain condensed tannins (CT) may have lower protein degradability than alfalfa. The present study investigated the effects of feeding birdsfoot trefoil (*Lotus corniculatus* L.) hay (BFTH) on lactation performance and N utilization. Eight multiparous Holstein cows in mid lactation (150 ± 10.3 d in milk) were randomly assigned to 1 of 2 rations (AH-based TMR [AHT] or BFTH-based TMR [BFTHT]) in a crossover design with 2 experimental periods. Each experimental period lasted 16 d (14 d of adaptation and 2 d of total collection), and the 2 experimental periods were separated by a 7-d washout period. On the experimental diets, AH or BFTH was included at 40% DM to AHT or BFTHT, respectively. There were no treatment effects on DMI (21.4 vs. 20.7 kg/d; $P = 0.46$), milk yield (29.4 vs. 28.1 kg/d; $P = 0.47$), milk fat concentration (3.20 vs. 3.21%; $P = 0.40$), and milk protein concentration (3.20 vs. 3.16%; $P = 0.13$) for AHT and BFTHT, respectively. In addition, dietary treatments did not affect milk yield/DMI ($P = 0.59$) and energy-corrected milk yield/DMI ($P = 0.49$). In contrast, CP digestibility increased in BFTHT compared with AHT (69.1 vs. 64.8%; $P < 0.01$). Concentration of milk urea nitrogen decreased by feeding BFTHT compared with feeding AHT (11.9 vs. 13.3 mg/100 mL; $P < 0.01$), whereas total N excretion was similar ($P = 0.54$) between the diets. However, cows fed BFTHT excreted more N in feces (194 vs. 168 g/d; $P < 0.01$), whereas urinary N excretion did not differ between the diets ($P = 0.39$), leading to a decrease in the UN:FN ratio ($P = 0.03$) in cows fed BFTHT relative to those fed AHT. Overall results in the current study suggest that feeding BFTH in a lactation high-forage diet did not affect overall lactational performance, whereas it shifted routes of N excretion evidenced by the decreased UN:FN ratio compared with feeding AH. The positive impact on environment may be attributed to a functional effect of CT as well as a unique cell wall structure of BFTH.

Key Words: alfalfa hay, birdsfoot trefoil hay, nitrogen excretion

Table 1597.

Table 1. Plasma TSAA concentrations for cows fed different RP-Met products

Item	CON	SM1	SM2	MPN	ASM	SEM	*P*-value
TSAA, μ*M*	95.4[c]	137.9[a]	142.3[a]	107.1[b]	101.7[bc]	3.7	0.001
TSAA, % of total AA – TSAA	3.93[c]	6.01[a]	5.98[a]	4.45[b]	4.39[b]	0.11	0.001

[a-c] Means within rows differ at $P < 0.05$.

1597 Determination of relative methionine bioavailability in lactating cows fed Smartamine M, Mepron, and AminoShure M using the plasma-free AA dose–response method.
N. L. Whitehouse*[1], C. G. Schwab[2], S. M. Fredin[3], and A. F. Brito[1], [1]*University of New Hampshire, Durham,* [2]*Schwab Consulting, LLC, Boscobel, WI,* [3]*Adisseo, Inc., Alpharetta, GA*.

In vivo measurements of bioavailability of Met in rumen-protected Met (RP-Met) products are critical to determine their contribution to metabolizable Met supply. The objective of this experiment was to use the plasma free AA dose–response method to compare the bioavailability of Met in Smartamine M (Adisseo, Antony, France) from the new (SM1) and original (SM2) production plants along with 2 additional commercially available RP-Met products, Mepron (MPN; Evonik Ind., Kennesaw, GA) and AminoShure-M (ASM; Balchem Corp., New Hampton, NY). Ten multiparous lactating Holstein cows, fed Met-deficient diets, were used in a replicated 5 × 5 Latin square design with 7-d periods. Treatments included a negative control with no added RP-Met (CON) or 30 g of Met supplied by the 4 RP-Met products. Milk samples were collected and DMI measurements were made on d 5, 6, and 7. Blood samples were collected 2, 4, 6, and 8 h after the morning feeding (0500 h) on d 5, 6, and 7. Plasma was pooled by cow per day for AA analysis by HPLC. Data were analyzed using the MIXED procedure in SAS. Milk yield (46.0 kg/d; SEM = 1.0; $P = 0.60$), DMI (27.4 kg/d; SEM = 0.6; $P = 0.93$), and milk fat content (3.60%; SEM = 0.11; $P = 0.95$) were unaffected by treatments. Milk protein content was greatest ($P = 0.002$; SEM = 0.04) for cows fed SM1 (2.98%) and SM2 (3.00%), intermediate for those fed MPN (2.93%), and least for ASM (2.89%) and CON (2.87%). Plasma total sulfur AA (TSAA) concentrations (μ*M*) were greatest for cows fed SM1 and SM2 and intermediate for cows fed MPN and ASM compared with cows fed CON (Table 1). Plasma TSAA concentrations were expressed as a percent of total AA; TSAA were regressed on the 0- and 30-g Met treatments. Slopes for SM1, SM2, MPN, and ASM were 0.070 (SE = 0.004), 0.070 (SE = 0.004), 0.020 (SE = 0.004), and 0.015 (SE = 0.005), respectively. The bioavailability of Met (% of total Met), calculated as the slope ratio relative to SM1, were 100, 28, and 22% for SM2, MPN, and ASM, respectively. Based on the published bioavailability of Met in SM2 (80%), the calculated bioavailabilities of Met in SM1, MPN, and ASM were 80, 23, and 17%. There was no difference in Met bioavailability between SM1 and SM2. Bioavailability of Met in MPN and ASM are less than previous estimates compared with Smartamine M.

Key Words: bioavailability, methionine

1598 Impact of three rumen-protected lysine prototypes on dairy cow performance, milk composition, and milk casein.
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Differences in formulation of the protective matrix of lysine products may impact rumen degradation and intestinal availability. The objective was to determine the effect of different formulations of lysine products on milk, milk protein, and casein yields. The study was conducted as a replicated 5 × 5 Latin square design in which 10 lactating, multiparous Holstein cows were assigned to either a lysine-deficient control ration (–Con), lysine-sufficient ration (+Con), or the –Con supplemented with either 1 of 3 different lysine prototypes (Lys1, Lys2, and Lys3; Balchem Corporation, New Hampton, NY). Rations were balanced using AMTS version 4.1.4 assuming 50.0 kg/d milk, 3.70% fat, 3.00% protein, and 740 kg BW. The +Con ration contained 1.60% porcine blood meal and was formulated to have MP, MP methionine, and MP lysine balances of −16.2, +0.1, and +4.9 g/d, respectively. The –Con ration was identical to +Con except that porcine blood meal was reduced to 0.64% with additional soybean hulls being added in its place, and –Con was formulated to have MP, MP methionine, and MP lysine balances of −42.8, +0.1, and −14.5 g/d, respectively. The lysine prototypes were supplemented at 0.21% of ration DM and contained 38% lysine, which were predicted to increase the MP lysine balance to +0.3 g/d. Periods were 14 d, and milk samples were collected on Days 11 to 14 of each period. Data collected during the last 4 d of each period were averaged by cow and analyzed using the Glimmix procedure of SAS. The model included a covariate (data collected during the 2-wk standardization period), fixed effects of treatment and period, and random effects of cow and cow within block. There were no treatment effects on DMI, protein or casein percentage or yield, lactose percentage, milk urea nitrogen (MUN),

or somatic cell count (SCC) (Table 1). There was an effect of treatment on milk yield ($P = 0.02$) and fat yield ($P = 0.03$). Lys1 increased milk yield compared with all other treatments except +Con and Lys1 increased fat yield compared with Lys3 and +Con. The positive milk response for Lys1 compared with –Con suggests that the Lys1 prototype was effective in meeting the lysine deficit in the –Con ration.

Key Words: bovine, lysine, prototype

Table 1. Effect of lysine supplementation on production measures. NO Table provided for placement!

1599 Effects of soybean meal, Fermenten, or expeller soybean meal on milk performance and intake in lactating dairy cattle.

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The objective of this study was to evaluate effects of three different dietary sources of protein on intake, milk performance, and temporal changes in BW and condition score in lactating dairy cattle. Primiparous ($n = 48$) and multiparous ($n = 144$) cows were stratified by milk production and randomly allocated into 12 pens containing 4 primiparous and 12 multiparous cows each. Cattle ranged from 60 to 180 DIM and averaged 712 kg of BW at trial start. Diets consisted of (DM basis) 42% corn silage, 13% alfalfa forage, 20% grain corn, and 25% protein premix containing either soybean meal (Diet A), Fermenten (Diet B), or a expeller soybean meal (Diet C), at a 3.5% inclusion rate. All 3 diets provided a similar level (DM basis) of aNDFom (31%), CP (14.7%), starch (26.2%), and ME (70 Mcal ME/d) as predicted by the CNCPS. The trial consisted of a 2-wk adaptation/covariate period where all cows were fed diet C and covariate measurements were taken. Pens were then randomly allocated to treatments and weekly measurements of milk production, intake, BW, and condition score were taken for 10 wk. All data were analyzed using Proc Mixed in SAS with pen as the experimental unit. In the first 6 wk of the experimental period, an increase in DMI was observed for cows fed diet B compared with cows fed diet A and C (28.1 vs. 26.8 and 26.2 kg/d, respectively; $P < 0.01$). Cows fed diet B made more energy-corrected milk (45.6 kg/d) compared with cows fed diets A and C (44.0 kg/d for both A and C; $P < 0.01$). Milk protein and fat yield was also increased in cows fed diet B. All cows gained condition score over the duration of the experiment; however, cows fed diet A gained 0.03 BCS/wk less than cows fed diets B and C ($P < 0.01$). The results from this experiment demonstrate beneficial milk performance responses to Fermenten when fed with a source of rumen available true protein. Responses are consistent with a potential decrease in ruminal CP degradation as demonstrated by previous research in our lab. Results also demonstrate the value of rumen-degradable protein vs. rumen-protected protein when fed in nitrogen-efficient diets in high-producing dairy cattle.

Key Words: Fermenten, milk performance, nitrogen, rumen degradable protein

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1600 Effect of ruminal bypass lysine on amino acid status, performance, and carcass characteristics of steers fed corn product–based diets.

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Corn and corn coproducts are the predominant sources of protein for feedlot cattle today, making up nearly 100% of diets in the Midwest. However, corn protein is a poor source of lysine, and current NRC models predict that a 45% corn, 30% DDGS, and 20% corn silage diet with 5% mineral supplement is deficient in lysine, despite the fact that the CP content of the diet (15%) exceeds requirements. Therefore, 84 steers were allotted by BW (367 ± 5.6 kg) and breed composition to 3 treatments to determine the effect of ruminal bypass lysine on blood AA, performance, and carcass characteristics. Treatments included a control with no added lysine or urea (Con), a diet that contained 0.5% Lys (AjiPro-L; Ajinomoto Inc., Chicago, IL), and a diet that contained 0.5% urea (urea). The lysine treatment was formulated to deliver 50 g/d of AjiPro-L (10 g/d of lysine). Twenty-eight steers were fed each diet and steers were housed in pens of seven (4 pens/treatment) that were blocked by BW (heavy and light). Steers were implanted with Revalor-XS at feedlot entry and were fed 300 mg of Optaflexx daily during the last 42 d of the study. Steers were slaughtered at a common BW (622 ± 13.8 kg). Data were analyzed as a randomized complete block design using the MIXED procedure of SAS. The model included the random effects of block and pen and the fixed effects of supplement and day as well as the supplement × day interaction. Total plasma AA did not differ among treatments at slaughter ($P = 0.93$); however, tryptophan tended ($P = 0.10$) to be greater (95.9, 87.8, and 103.4 μg/mL for Con, Lys, and urea, respectively) and PUN was ($P = 0.05$) greater (12.4, 12.7, 14.4 mg/dL for Con, Lys, and urea, respectively) for steers fed urea. There was no difference in DMI ($P \geq 0.62$), BW ($P \geq 0.91$), gain ($P \geq 0.73$), or G:F ($P \geq 0.75$) at any time point during the study. Treatment had no effect on HCW ($P = 0.50$), LM area ($P = 0.80$), marbling ($P = 0.93$), or any other carcass parameter ($P \geq 0.43$). In conclusion, it appears that an all corn/corn product diet provides a sufficient amounts of lysine to finishing feedlot cattle and supplemental bypass lysine may not be needed.

Key Words: beef feedlot, bypass lysine, growth

1601 Determining ruminal lysine degradability of a bypass soybean meal product and an encapsulated lysine source. J. M. Prestegaard*[1], A. L. Kenny[1], M. M. Masiero[1], and M. S. Kerley[2], *[1]University of Missouri, Columbia, [2]Division of Animal Sciences, University of Missouri, Columbia*.

A single-flow, continuous culture system was used to evaluate microbial efficiency (MOEFF), CP digestibility, VFA concentration, NH_3 concentration, OM digestibility, and lysine digestibility of a bypass soybean meal product and an encapsulated lysine source. Inoculated fermenters were randomly assigned to 1 of 3 treatments in 2 consecutive replicates (n = 24): a lysine-deficient basal diet (CON) consisting of corn, soybean meal, and corn silage; a lysine-sufficient diet (RP-SBM) containing rumen-protected soybean meal in replacement of soybean meal in the basal diet; and a lysine-sufficient diet (RP-LYS) consisting of CON supplemented with rumen-protected lysine. All treatments were balanced for similar amounts of rumen degradable protein to supply sufficient peptides and NH_3 based on microbial requirements. Fermenters were individually fed at 0800 and 1700 h for 7 d, consisting of a 4-d acclimation period to stabilize the microbial population and a 3-d sampling period. Volatile fatty acid and ammonia concentrations were analyzed in samples taken 0 and 4 h after morning feeding. Effluent was collected, composited, and frozen on the final 3 d of each replicate. Fermenter contents were collected and frozen on the final day of each replicate for bacteria analysis. No differences were observed for OM digestibility, apparent and true CP digestibility, NH_3, acetate, or propionate. In replicate 1, butyrate (mM) was greater (P = 0.01) for CON (13.63) relative to RP-SBM (9.30) or RP-LYS (9.00); however, no differences were observed in replicate 2. For both replicates, MOEFF (g effluent bacterial N/kg OM truly digested) tended to be greater (P = 0.08) in RP-LYS (21.32) than RP-SBM (17.62) and CON (17.49). Dietary lysine (g) was measured to be 0.33, 0.3,4 and 0.43 for CON, RP-SBM, and RP-LYS, respectively. Bypass dietary lysine (g) was lesser (P < 0.01) in RP-LYS (0.06) relative to RP-SBM (0.13) and CON (0.11). Lysine digestibility (%) was greater (P < 0.001) for RP-LYS (85.84) relative to RP-SBM (60.15) or CON (65.73). However, total effluent lysine (g) was statistically similar (P = 0.11) for CON (0.33), RP-SBM (0.36), and RP-LYS (0.33). Bacterial lysine in effluent (g) tended to be higher (P = 0.09) in RPLYS (0.27) relative to RP-SBM (0.23) and CON (0.22). Although dietary lysine in RP-LYS was degraded to greater extent by rumen microbes than in RP-SBM or CON, it appears the rumen microbial population compensated for lysine loss.

Key Words: continuous culture, lysine, rumen fermentation

1602 Effects of rumen-protected lysine and methionine on milk yield and milk composition in lactating Holstein cows fed two different levels of crude protein. A. Ostrensky[1], G. Negro[2], A. M. D. Santos[1], A. Anater[1], D. R. Ribeiro[1], L. F. Greco[3], M. N. Pereira[4], and R. D. Almeida*[2], *[1]Pontifícia Universidade Católica do Paraná, Curitiba, Brazil, [2]Universidade Federal do Paraná, Curitiba, Brazil, [3]Kemin South America, Indaiatuba, Brazil, [4]Universidade Federal de Lavras, Lavras, Brazil*.

Experimental objectives were to evaluate the effects of rumen-protected lysine and rumen-protected methionine (RPLM) supplementation on milk yield and composition of dairy cows. Holstein cows (n = 35) were housed in a free-stall barn and milked twice daily, received bST injections every 10 d, and were paired blocked based on milk yield, days in milk, and lactation order. The treatments consisted on four groups: 1) lower CP without RPLM supplementation (LPXX), formulated to 15.8% CP, 6.63% Lys as percent of MP, and 1.82% Met as percent of MP; 2) lower CP with RPLM supplementation (LPAA), formulated to 15.9% CP, 6.90% Lys as percent of MP, and 2.31% Met as percent of MP; 3) higher CP without RPLM supplementation (HPXX), formulated to 17.4% CP, 6.56% Lys as percent of MP, and 1.80% Met as percent of MP; and 4) higher CP with RPLM supplementation (HPAA), formulated to 17.5% CP, 6.92% Lys as percent of MP, and 2.32% Met as percent of MP. Experimental cows were fed simultaneously twice a day the same basal diet in a TMR and they were supplemented with soybean meal and/or RPLM (Lysipearl and Metipearl; Kemin, Brazil). The experimental design was a 4 × 4 Latin square with 28-d periods. Milk yield and composition were determined in the last 6 d of each period and analyzed using the mixed procedure of SAS containing the effects of milk yield in the covariate period, period, treatments (CP level, AA supplementation, and their interaction), and cow as a random effect. Milk yields were 39.26, 40.16, 39.72, and 40.25 kg/d for LPXX, LPAA, APXX, and APAA, respectively (P = 0.69 for CP level and P = 0.30 for AA supplementation). Cows fed higher CP diets showed higher (P = 0.002) protein content (3.34 ± 0.04%) than animals fed lower CP diets (3.29 ± 0.04%). The HPAA group had a tendency (P = 0.10) to produce more protein yield (1.335 ± 0.03 kg/d) than LPXX (1.283 ± 0.03 kg/d). There were no differences among treatments for all the other parameters: 3.5% fat-corrected milk, energy-corrected milk, milk energy output, fat, lactose, and total solids contents and yields. Increasing CP in the diet resulted in higher protein content in milk.

Key Words: amino acids, crude protein, metabolizable protein

Table 1604.

Table 1- Blood urea concentration and microbial protein syntheses of bulls fed with diet containing different levels of additives.

	Additives (mg/kg DM)						Contrast e P value			
	MON 30				VM	SEM	VM vs MON	L	Q	VM vs VM/ MON
Variables	0	15	25	34	34					
Blood urea (mg/KgPV)	3.23	3.23	2.70	2.87	3.06	0.15	0.41	0.14	0.06	0.39
Microbial protein (g/day)	1068	972	790	1141	862	85.05	0.12	0.39	0.61	0.04

1603 Immunometabolic gene expression in blood neutrophils (PMN) in Holstein dairy cows supplemented with rumen-protected methionine or rumen-protected choline during the peripartal period. P. Montagner[1], Z. Zhou*[1], D. N. Luchini[2], J. J. Loor[1], and M. Nunes Corrêa[3], *[1]University of Illinois, Urbana, [2]Adisseo S.A.S., Alpharetta, GA, [3]Federal University of Pelotas, Pelotas, Brazil*.

Objectives of this study were to evaluate mRNA expression of 30 genes related to neutrophil adhesion, chemotaxis and migration, oxidative stress, Toll-like receptor pathway, methionine cycle, and glutathione metabolism in response to rumen-protected methionine (MET) and choline (CHO) supplementation during the peripartal period. Forty multiparous Holstein cows were used in a randomized complete block design with 2 × 2 factorial arrangement of MET and CHO level (with or without). Treatments were control (CON), no MET or CHO; CON + MET (SMA); CON + CHO (REA); and CON + MET + CHO (MIX). From −21 d (close-up) to 30 d after calving, cows received the same diet (1.52 Mcal NE_L/kg DM) from close-up to calving. From calving to 30 d, cows were on the same diet (1.71 Mcal NE_L/kg DM) and continued to receive the same treatments through 30 d. MET supplementation was adjusted daily at a rate of 0.08% (DM basis) of diet and CHO was supplemented at 60 g/cow per day. Blood neutrophils were isolated on −10, 8, and 29 d relative to calving for quantitative PCR analysis. Data were analyzed as a factorial design with repeated measures using PROC MIXED in SAS. As expected, regardless of treatments, highest expression of proinflammatory genes (*TNFα* and *BPI*) ($P < 0.05$) were observed on 8 d, suggesting more pronounced inflammatory status compared with −10 and 29 d relative to parturition. The main effect of CHO toward greater ($P = 0.01$) expression of *cell adhesion molecule 1* (*CADM1*) and interactions of CHOL × day for PMN adhesion–related genes (*SELL*, *CXCR2*, and *ICAM1*) suggest activation of PMN in CHOL cows. In contrast, MET supplementation led to lower ($P = 0.02$) expression of *ITGAB2*, suggesting less activated status of PMN in MET cows. CHO cows also tend to have greater ($P = 0.06$) *IL10* compared with other treatments. Although *IL-10* was not changed by MET, main effect of MET was observed for lower *IRAK1*, suggesting a less pronounced inflammation in MET cows. Both *MPO* and *SOD2* were greater in MET cows whereas the main effect of CHO was not detected for *SOD2*; such changes likely were associated with reactive oxygen production in PMN. However, PMN functional study is required to confirm the proposed relationship. Overall, data indicate neutrophil gene network respond differently to peripartal supplementation with MET or CHO. Additional studies to examine the methionine and choline mechanism of action in PMN appear warranted.

Key Words: choline, methionine, transition cow

1604 Estimation of microbial protein and blood urea of confined bulls fed with diets containing virginiamycin and monensin sodium. F. R. Camilo*[1], A. M. Mobiglia[1], J. J. D. R. Fernandes[2], V. R. M. Couto[3], F. D. D. Resende[4], G. R. Siqueira[4], and R. K. Grizotto[5], *[1]CAPES Foundation, Ministry of Education of Brazil, Brasilia, Brazil, [2]UFG, Goiania, Brazil, [3]Universidade Federal de Goiás, Goiânia, Brazil, [4]APTA – Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [5]APTA – Agência Paulista de Tecnologia dos Agronegócios (São Paulo Agency of Agribusiness Technology), Colina, Brazil*.

The propose of this trial was to evaluate the effects of diets containing isolated and combined levels of virginiamycin (VM) and monensin sodium (MON) on microbial protein and blood urea of confined Nellore bulls. Fifteen Nellore bulls (536 kg of BW) with ruminal cannula were used in a randomized complete block design with five treatments in three replicates. The blocks were defined by initial BW. Treatments were defined by levels of VM and MON (mg/kg of DM) as follows: 30MON, 15VM+30MON, 25VM+30MON, 34VM+30MON, and 34VM. Animals were fed ad libitum twice daily with isonitrogenous and isoenergetic diets, with a 88:12 concentrate:roughage (sugarcane bagasse) ratio. The animals were kept in feedlot in individual pens for 28 d. The blood was

collected from the jugular vein before feeding and 2 and 3 h after feeding on the Days 0, 7, 14, 21, and 28. Spot sampling technique was realized on 28 d to estimate the daily excretion urinary of purine derivatives and then estimate microbial protein production. Data are shown in Table 1. There were effects ($P < 0.10$) on blood urea concentration between treatments and grams per day microbial protein for 34VM+30MON and 34VM treatments. The association of VM and MON resulted in greater microbial protein syntheses and effect quadratic in blood urea. In conclusion, the use of 34VM+30MON may increase of production of microbial protein, and blood urea resulted in lower concentration using 25VM+30MON on diet. Supported by Phibro/Minerva/FAPEG.

Key Words: additives, feedlot, virginiamycin

1605 Rumen fluid metabolomics analysis associated with feed efficiency on crossbred steers.

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The rumen plays a central role in the efficiency of digestion in ruminants. To identify potential differences in rumen function that lead to differences in feed efficiency, rumen metabolomic analysis by ultra-performance liquid chromatography/time-of-flight mass spectrometry and multivariate/univariate statistical analysis were used to identify differences in rumen metabolites. Individual feed intake and BW gain was measured on 144 crossbred steers for 105 d on a high-concentrate ration. Eight steers with the greatest ADG and 8 steers with the least ADG within 0.32 SD of the mean DMI were selected for the study. The DMI did not differ between ADG groups (10.10 ± 0.05 kg/d; $P = 0.41$); however, ADG was greater ($P < 0.01$) in the greatest ADG group (1.96 ± 0.02 kg/d) than the least ADG group (1.57 ± 0.02 kg/d). Rumen fluid was collected at slaughter. Metabolite identification was obtained through a mass-based bovine database search. Verification of the identities of selected metabolites was conducted by comparing tandem mass spectrometry fragmentation patterns with those from authentic compounds. Principal component analysis and *t* test on rumen fluid metabolic profile identified 90 metabolites ($P < 0.10$) that segregated with ADG group. These metabolites were primarily involved in linoleic and α-linolenic metabolism (impact value 1.0 and 0.75, respectively; $P < 0.05$); both pathways were downregulated in the greatest ADG group compared with least ADG group. Ruminal levels of four metabolites associated with ADG group were screened by receiver operating curve analysis to test their efficacy as biomarkers for ADG. Subsequently, a partial least square discriminate analysis was used to develop a predictive model to verify and optimize the exclusive biomarkers. The combination of pentadecanoic acid, eicosanoic acid, linoleic acid, and α-linolenic acid produced a good predictor of feed efficiency, AUC (95% CI) = 0.901 (0.67–1.0), representing 87.5% of sensitivity and 75% of specificity. All four metabolite levels decreased in greatest-ADG animals vs. least-ADG animals in the rumen fluid. As well, higher fold levels of small molecules in the rumen fluid were found in greatest ADG vs. least ADG ($P < 0.05$), such as folic acid (13%), malonyl-CoA (30%), pyroglutamic acid (57%), oleamide (13%), and alloxan (23%; glucose analog). This study indicates that metabolomics based on ruminal fluid can yield metabolites that can predict and classify feed efficiency. Furthermore, on the basis of the pathway analysis of biomarkers, ruminant fluid metabolomics profile give new insight into the physiology of feed efficiency. The USDA is an equal opportunity provider and employer.

Key Words: average daily gain, dry matter intake, ultra-performance liquid chromatography quadrupole time of flight tandem mass spectrometry

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1606 Enrichment of cattle rumen with bison rumen contents improves nitrogen digestion.

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This study investigated if the transfer of rumen contents from bison to cattle enhances cattle total tract fiber digestion. The experiment was a repeated measures design with two rumen transfers using 16 rumen cannulated Angus × Hereford cross beef heifers (461 ± 21 kg BW). Heifers were adapted to a barley straw diet (70/30% of DM, forage/concentrate) for 28 d before the experiment. After 46 d, 70% of rumen contents were removed from each heifer and replaced with mixed rumen contents collected after slaughter from 36 bison. This procedure was repeated 14 d later. Intake, chewing activity, apparent total tract digestion, ruminal passage rate, VFA, ammonia N, and protozoa counts were measured before the first transfer and 2 wk after the second transfer. The DMI increased ($P = 0.04$) from 1.39 to 1.50% of BW after the rumen transfers. Total chewing time did not change ($P = 0.74$; 13.9 h/d) but the chewing time per kilogram DM and NDF intake was reduced ($P < 0.001$) after rumen transfers. The DM, OM, NDF, and ADF digestibility were not affected ($P \geq 0.44$) by rumen transfers, but the total N digestibility was improved ($P < 0.001$; 68.3 vs. 70.4%). Microbial N flow (g/d) increased ($P = 0.03$); however, the efficiency of microbial N synthesis (g/kg of digested OM) was not improved ($P = 0.77$). No differences ($P > 0.14$) were observed for the ruminal rate of passage of fluids and solids. Ruminal ammonia N (m*M*) was not affected ($P = 0.77$) before feeding by rumen transfers but was greater ($P = 0.05$) 6 h after feeding. Total VFA (m*M*) and the proportion of butyrate

Table 1607.

Effects of nitrate and monensin on rumen fermentation parameters.

Daily means	0 NIT		1.25 NIT		2.5 NIT		SEM	*P*-value[1]		
	0 MON	4 MON	0 MON	4 MON	0 MON	4 MON		NIT	MON	NIT × MON
Total gas (L)	3.03	3.12	2.69	2.51	3.34	2.82	0.20	0.02	NS	NS
CH_4, mM/d	40.90	29.40	31.18	24.58	26.20	23.79	1.79	<0.01	<0.01	0.04
CO_2, mM/d	97.36	93.17	83.79	80.45	87.96	98.09	5.06	0.02	NS	NS
N_2O ($x10^{-4}$), mM/d	48	54	45	37	54	39	3.8	0.03	0.08	0.02
DMD, (g/100g DM)	69.26	69.12	69.31	69.13	68.85	69.13	1.36	NS	NS	NS
NH_3-N, (mg/dL)	23.50	22.0	17.28	18.33	15.72	15.73	1.28	<0.01	NS	NS
Protozoa, cell/mL ($x10^3$)	4.90	3.89	4.90	3.91	3.95	4.18	0.83	NS	NS	NS

[1] NS indicates P>0.10.

increased ($P < 0.001$); however, acetate and the C2:C3 ratio decreased ($P \leq 0.02$) before and 6 h after feeding as a result of rumen transfers. As a result of rumen transfer, total protozoa counts and the proportion of *Ostracodinium* increased ($P < 0.001$) whereas *Entodinium* decreased ($P < 0.001$) before and at 6 h after feeding. Overall, cattle rumen inoculation with bison rumen contents improved diet protein digestion; however, DM and NDF digestibility were not affected.

Key Words: bison, digestibility, rumen inoculum

1607 Effect of nitrate, monensin, and the combination of additives on rumen fermentation using a semicontinuous culture system. M. Capelari*[1], K. A. Johnson[2], B. Latack[1], J. Roth[1], and W . Powers[1], *[1]Michigan State University, East Lansing, [2]Washington State University, Pullman*.

A 37-d experiment was conducted to investigate the effect of nitrate (NIT) and monensin (MON) on rumen fermentation using a semicontinuous culture system. We hypothesized that the combination of additives would reduce CH_4 emissions beyond that of either additive alone, without affecting production parameters. Additives (0, 1.25, and 2.5% diet DM of NIT; 0 and 4 mg/L of MON) were tested alone and in combination (NIT+MON; 6 total treatments; 3 replicates/treatment). Buffer and water were added to eighteen 2.2-L vessels on d −8 (1.2 L of a 50:50 mixture). The first 7 d (d −7 to 0) served as a steady state phase. On d −7, rumen fluid was pooled from 5 nonadapted lactating cows fed a 50:50 forage to concentrate diet and filtered through 2 layers of cheesecloth, and 1 L was transferred to each vessel along with 30 g of solid rumen content and 20 g of a basal diet (50:50 forage to concentrate) in a 8 by 20 cm nylon bag (50 μm mesh size). On d −6, 20 g of the basal diet replaced the solid rumen content bag, and from this point onward, 2 bags, each containing 20 g of the treatment diet, were always present in the vessels for 48 h. Buffer was infused at a constant rate (70 mL/h) throughout the experiment with a peristaltic pump. Gas production was measured daily. Twice weekly, DM disappearance (DMD), pH, and ammonia nitrogen (NH_3–N) were measured. Treatment did not affect DMD (69.13 g/100 g DM; $P > 0.05$). Compared with the negative control treatment, addition of NIT reduced total gas production (2.84 vs. 3.03 L/d; $P = 0.02$), CH_4 production (28.65 vs. 40.9 m*M*/d; $P < 0.01$), and CO_2 production (87.57 vs. 97.36 m*M*/d; $P < 0.05$). Compared with the negative control, addition of MON reduced CH_4 production (29.4; $P < 0.01$). Further CH_4 reduction, compared with the negative control, was observed when NIT+MON was added (24.31 vs. 40.9 m*M*; $P = 0.04$). No treatment effects were observed for pH (7.1) or protozoa count (4.3×10^3). Addition of NIT reduced NH_3–N (16.65 vs. 23.5 mg/dL; $P < 0.01$). The combination of NIT+MON enhanced reduction of CH_4 production in a semicontinuous culture fed a 50:50 forage:concentrate diet, with no detriment to DMD.

Key Words: in vitro, methane, protozoa

1608 Metagenomic census of predominant *ureC* genes of ureolytic bacteria in the rumen of dairy cows.
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Rumen ureolytic bacteria elaborates urease to break down urea to ammonia for the synthesis of microbial protein, yet little is known about the diversity and distribution of rumen ureolytic microorganisms. The urease *ureC* gene has been chosen as the target gene for analysis of the urea-degrading microorganisms in various environments. This research investigated the predominant *ureC* genes of the ureolytic bacteria in the rumen of dairy cows using high-throughput sequencing. Six dairy cows with rumen fistulas were assigned to a two-period crossover trial. One group (Ctrl; $n = 3$) were fed the diet without urea and the other (Urea; $n = 3$) were fed rations plus 180 g urea/cow per day at three separate times. Rumen bacterial samples from liquid, solid, and wall fractions were collected for *ureC* gene amplification and sequencing using Miseq. Results showed that supplementation of urea did not change the rumen *ureC* gene abundance, whereas the wall-adherent bacteria (WAB) revealed a distinct ureolytic bacterial profile compared with solid-adherent bacteria (SAB) and liquid-associated bacteria (LAB). The *ureC* gene diversity and richness of rumen WAB was lower than that in the SAB and LAB ($P < 0.05$). The rumen predominant *ureC* gene operational taxonomic units (OTU) were gathered in clusters II, IV, and VI. Operational taxonomic units 5, 6, 15, 18, 12, 27, and 25 in the WAB; OTU 3, 4, and 1 in the LAB; and OTU 13, 19, and 21 in the SAB were predominant in each fraction, respectively. Most of the predominant OTU showed low similarity (72–91%) to the known rumen bacteria. The results suggested that the rumen of dairy cows harbors plenty of unidentified ureolytic bacteria. This survey contributes new data to existing *ureC* gene information relating to the ureolytic microbial community in ruminants and provides a basis for obtaining the regulation targets of ureolytic bacteria to mitigate urea hydrolysis in the rumen.

Key Words: diversity, rumen, *ureC* genes

1609 Rumen bacterial communities continue to shift five weeks after switching diets from conserved forage to pasture.
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Bacterial community structure is known to shift as a result of diet changes, but it is not known how long it takes for the bacterial populations to stabilize. The objective of this study was to characterize the weekly dynamics of rumen bacterial community composition of cows transitioning from an indoor diet, comprising conserved forage (CF), to a pasture. Five lactating Holstein dairy cows, maintained on a CF diet during the winter season, were switched to a pasture and followed for 5 wk. Individual rumen digesta samples were collected via esophageal intubation on wk −1, 1, 2, 3, 4, and 5 relative to the diet switch. Microbial DNA was extracted and the V1 to V3 region of the 16S rRNA gene was amplified. Sequence reads were obtained using Illumina MiSeq (version 3) and sequences were analyzed using MOTHUR (version 1.36.1). Bacterial densities ($\log_{10}$ 16S rRNA gene copies/mL rumen digesta) were quantified by real-time PCR. Data were analyzed using a repeated measures ANOVA in SAS (version 9.4). By wk 3 on pasture, bacterial densities in rumen digesta were higher when compared with CF (8.9 vs. 9.4, 9.4, and 9.5 $\log_{10}$ copies/mL for wk −1, 3, 4, and 5, respectively; $P < 0.01$). Bacteroidetes was the predominant phylum, accounting for 48 to 81% of total bacteria, followed by Firmicutes (16–47%) and TM7 (0–4%). *Prevotella* was the predominant genus of the Bacteroidetes phylum. By wk 5 on pasture, a higher abundance was observed of both bacteria of the phylum Bacteroidetes (75.3%) and *Prevotella* species (72.7%) when compared with CF (65.4 and 58.3% for Bacteroidetes and *Prevotella*, respectively; $P < 0.05$). The genus *Ruminococcus* was more abundant during wk 1 and 2 after the diet switch (3.4% for both weeks), when compared with 2.0% on wk −1 of CF ($P < 0.01$). Similarly, bacteria in the family Lachnospiraceae were more abundant during wk 1 and 2 (8.4 and 8.2%) and then became less abundant by wk 5 of cows grazing pasture (3.1%) when compared with wk −1 of cows on a CF diet (5.4%; $P < 0.05$). *Butyrivibrio* species were more abundant on wk 4 after the diet switch (3.6 vs. 1.7% for wk 4 of pasture and wk −1 of CF, respectively; $P < 0.05$) and then, on wk 5, returned to an abundance similar to CF (1.5%). In conclusion, rumen bacterial communities are highly dynamic after a diet switch and did not stabilize within 5 wk of cows grazing pasture.

Key Words: bacterial diversity, dairy cow, Illumina MiSeq

1610 Metabolome and microbiome associations after a grain and sugar challenge. H. M. Golder*[1,2], S. Denman[3], C. McSweeney[3], and I. J. Lean[1,2], *[1]Scibus, Camden, Australia, [2]University of Sydney, Camden, Australia, [3]CSIRO Animal, Food and Health Services, Queensland Bioscience Precinct, St. Lucia, Australia*.

Holstein heifers ($n = 40$) were allocated to 5 groups: 1) control (no additives), 2) virginiamycin (10 g/head·d; VM), 3) monensin (2.2 g/head·d) + tylosin (0.44 g/head·d; MT), 4) monensin (2.5 g/head·d) + yeast (Levucell SC Direct; 25 g/head·d; MY), and 5) sodium bicarbonate (200 g/head·d) + magnesium oxide (30 g/head·d; BUF). Heifers were fed twice daily a 62% forage:38% concentrate total mixed ration at 1.25% of BW DM/d for a 20-d adaptation period with their additive or additives. Fructose (0.1% of BW/d) was added to the ration for the last 10 d of adaptation. On d 21, heifers were challenged with a ration consisting of 1.0% of BW DM wheat and 0.2% of BW fructose plus their additive or additives. Stomach tube rumen samples were collected 3.6 h after consumption of the challenge ration and analyzed for pH; ammonia, d- and l-lactate, and VFA; and histamine concentrations and total bacteria. The 16S rRNA gene spanning the V4 region was PCR amplified and sequenced using an Illumina MiSeq platform. Sequence data was analyzed using the Quantitative Insights into Microbial Ecology software package (QIIME). Coinertia analysis, including Monte Carlo estimations (Ade4 package, R software) was conducted using operational taxonomic units (OTU) and rumen fermentation data from each group. A linear model was fitted to the OTU data and pairwise comparisons were performed to examine the significantly different OTU between groups ($q < 0.1$). Coinertial analysis explained 31.9% of the total variation in the associations among rumen fermentation products, bacterial community composition, and groups. Histamine and valerate concentrations explained the most variation in the microbiome. Contrasts between the control vs. BUF and control vs. MT groups showed these groups had the lowest number of significantly different OTU (14 and 23 OTU, respectively), indicating they may have similar microbiomes. The MLY vs. BUF had the highest number of significantly different OTU (826 OTU), suggesting their microbiomes had the greatest difference. New reference OTU14997 from the *Streptococcus* genus was more abundant in the control vs. MLY, VM vs. MLY, and BUF vs. MLY groups. New reference OTU20477 from the *Lactobacillus* genus was more abundant in the control vs. VM, MLY vs. VM, and BUF vs. VM groups. *Lactobacillus ruminis* was also more abundant in the MLY vs. VM and BUF vs. VM groups. *Lactobacillus mucosae* was more abundant in the BUF vs. VM group. The feed additives appeared to influence different microbial populations after the challenge.

Key Words: coinertia, feed additives, ruminal acidosis

1611 Ruminal dosing with *Megasphaera elsdenii* and strain persistence are associated with milk fat depression in Holstein cows. F. Cacite[1] and P. J. Weimer*[2], *[1]Federal Univ. of Mato Grosso, Cuiabá, Brazil, [2]USDA-ARS, Madison, WI*.

The objectives of this study were 1) to examine the effects of ruminal dosing of cows with the bacterium *Megasphaera elsdenii* (ME) on milk fat production and 2) to examine the persistence of the dosed species in the rumen. Nine cows (51–201 d in milk [DIM]) were divided into 3 groups balanced for DIM, milk production, and milk fat content and were fed the same TMR that contained corn silage, finely ground high-moisture corn, alfalfa haylage, corn oil, and monensin. The three treatments included ruminal dosing with pure cultures of one of two strains of ME (4257 and 5045, at an average of 1.9×10^{12} cells/dose) recently isolated from milk fat-depressed cows and a control dosed with sterile culture medium. To encourage persistence of ME, approximately 40% of the ruminal contents from each cow were removed just before dosing, and 108 g of sodium lactate was added for all treatments, on each of the 3 dosing days spaced 48 h apart. Milk production and composition were determined from 3x-daily milk samples collected from 8 d before first dosing to 21 d after first dosing, and ruminal fluid samples were collected for bacterial community analysis via 16 S rRNA metagenomics on the Illumina MiSeq platform. The dosing procedures resulted in a transient ruminal lactate concentration of up to 46 m*M* and a subsequent decrease in acetate:propionate ratio ($P < 0.0001$) as the lactate was metabolized. Both milk fat percentage and yield substantially varied by cow ($P < 0.001$) and were decreased ($P < 0.01$) during the week of dosing, when ME abundance was high. Data analysis of 112 ruminal samples using PROC REG of SAS revealed a negative correlation between ME relative abundance and milk fat percentage in cows dosed with ME strain 4257 ($r^2 = 0.46$, $P < 0.0001$) but not in cows dosed with strain 5045 ($r^2 = 0.056$, $P = 0.146$). Control cows dosed with lactate but not an ME inoculum displayed weak negative correlation between milk fat percentage and ME abundance ($r^2 = 0.183$, $P = 0.007$), suggesting that the native ME populations were also associated with reduced fat content. Similar results were observed for fat yield. Neither *Propionibacterium acnes* nor *Eubacterium pyruvativorans* were detected in even the most highly fat-depressed cows. The data confirm previous reports of a strong relationship between ME abundance and milk fat depression but suggest that the effect may be ME strain dependent.

Key Words: *Megasphaera*, milk fat, ruminal microbiome

1612 Potential for live yeast culture to enhance nitrate mitigation of methanogenesis in Jersey dairy cattle. R. A. Meller[1], J. M. Ashworth[1], A. M. Gehman[2], and J. L. Firkins*[1], [1]*The Ohio State University, Columbus,* [2]*Alltech, Inc., Nicholasville, KY.*

Concern over the environmental impact of dairy production has stimulated research to decrease enteric CH_4 production. One approach is feeding the electron acceptor NO_3 to be reduced by bacteria such as the selenomonads, thus outcompeting methanogens for aqueous H_2. We hypothesized that a live yeast culture (Yea-Sacc [YS]; *Saccharomyces cerevisiae*; Alltech, Inc.) would stimulate the reduction of NO_3 completely to NH_3 and thereby improve the ratio of CH_4 emission:energy-corrected milk production while decreasing blood methemoglobin concentration. Twelve lactating Jersey cows (8 multiparous and noncannulated and 4 primiparous and ruminally cannulated) were used in a replicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Cattle were fed diets either containing 1.5% NO_3 (from calcium nitrate) after an adjustment period or a control diet (containing urea isonitrogenous to NO_3) and were given a top-dress of ground corn without or with YS. All noncannulated cows were spot measured for CH_4 emission by mouth using GreenFeed (C-Lock Inc., Rapid City, SD). The main effect of NO_3 decreased ($P < 0.01$) methane 17% but decreased ($P < 0.01$) DMI by 10% (from 19.8 to 17.8 kg/d) such that the CH_4:DMI ratio tended ($P = 0.14$) to decrease by 8%. Milk and milk fat production were not affected, but NO_3 decreased ($P < 0.01$) milk protein from 758 to 689 g/d. Ruminal pH was decreased more after feeding diets without NO_3, and the acetate:propionate ratio was greater for cows fed NO_3, especially when combined with YS (interaction, $P = 0.01$). Others have noted lower palatability and lower consumption per meal, which is consistent with our observations. Methemoglobin was higher ($P = 0.01$) for cattle fed NO_3 than those fed urea but were still low (1.5 vs. 0.5% and only once exceeded 5%), documenting minimal risk for NO_2 accumulation at our feeding levels of NO_3. Although neither apparent OM nor NDF digestibilities were affected ($P > 0.15$), apparent N digestibility had an interaction ($P = 0.06$) such that, compared with those fed either diet without NO_3, N absorption was slightly higher for those fed NO_3 without YS but slightly lower for those fed NO_3 with YS. Under the conditions of this study, NO_3 did mitigate ruminal methanogenesis but was not particularly effective after considering that it depressed DMI and milk protein. Based on few interactions detected, YS had a minimal role in attenuating either of these responses.

Key Words: live yeast culture, methane, nitrate

1613 Inhibition of methanogenesis by nitrate, with or without defaunation, in continuous culture. B. A. Wenner*, B. K. Wagner, Z. Yu, N. St. Pierre, and J. L. Firkins, *The Ohio State University, Columbus*.

With regard to the focus of methane (CH_4) mitigation in ruminant production systems, nitrate (NO_3) serves as an alternative sink for aqueous hydrogen [H_2(aq)] accumulating in the rumen, producing ammonium via NO_3 reduction pathways and thereby decreasing CH_4 production. Defaunation has also been correlated in meta-analyses with decreased methanogenesis. We hypothesized defaunation might increase the CH_4 mitigation effect of NO_3 by removal of a symbiotic source of substrate to methanogens. In the present study, we applied a 2 × 2 factorial treatment arrangement in a 4 × 4 Latin square design to continuous culture fermenters ($n = 4$). Treatments were control ($-NO_3$) vs. nitrate ($+NO_3$; 1.5% of diet DM), factorialized with control (faunated [FAUN]) vs. defaunated (DEF). Fermenters were fed once daily (40 g DM; 50:50 forage:concentrate diet); four periods lasted 11 d with 3 d of sample collection. Buffer dilution and solids passage rate were maintained at 7.0 and 5.0%/h, respectively. There were no main effects of DEF or interaction of faunation status with addition of NO_3 ($P > 0.05$). The main effect of $+NO_3$ increased ($P < 0.05$) H_2(aq) compared with $-NO_3$ by 11.0 μM. The main effect of $+NO_3$ also decreased ($P < 0.05$) daily CH_4 production compared with $-NO_3$ by 8.17 mmol CH_4/d. Because there were no treatment effects on NDF digestibility ($P > 0.10$), the main effect of $+NO_3$ also decreased ($P < 0.05$) CH_4 production compared with $-NO_3$ by 1.43 mmol CH_4/g NDF digested. There were no effects of treatment ($P > 0.10$) on other nutrient digestibilities, N flow, or microbial N flow per gram of nutrient digested. These data support the existing literature that NO_3 incorporation in the diet can decrease the methanogenesis by dairy cattle. More importantly, methanogens are not necessarily inhibited by defaunation in a highly reduced environment. However, practical considerations such as nitrite toxicity and on-farm dietary adaptation to NO_3 should be considered before implementing this practice in U.S. dairy production systems.

Key Words: defaunation, methane, nitrate

1614 Does weaning age affect the development of ruminal and fecal microbiomes in dairy calves?
S. J. Meale[1], S. Li[2], P. Azevedo[2], H. Derakhshani[2], J. C. Plaizier[2], M. Steele*[3], and E. Khafipour[2], *[1]UMR Herbivores, INRA, Vetagro Sup, Saint-Genès-Champanelle, France, [2]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*.

Despite the advantages of feeding an elevated plane of nutrition to preweaned calves, this feeding strategy may increase a calf's susceptibility to depressed growth during weaning. We hypothesized that weaning at an earlier age would result in a more rapid shift in gut microbiota and consequently be the cause of this growth depression. Therefore, our study examined the effects of weaning age on ruminal and fecal microbiomes in Holstein calves fed an elevated plane of nutrition before weaning. Twenty female Holstein calves were randomly assigned at birth to be weaned at 6 (early [EW]) or 8 (late [LW]) wk. Milk replacer (150 g powder/L water) was offered at 1.2 kg/calf per day in 2 meals until a 1-wk step-down. Rumen fluid and feces were sampled at wk 5, 7, and 9, representing EW5, EW7, EW9, LW5, LW7, and LW9. Deoxyribonucleic acid was extracted, and the V4 region of the 16S rRNA bacterial gene was amplified and subjected to paired-end Illumina sequencing. The output paired-end reads were merged using the PANDASeq assembler, analyzed using QIIME, and aligned to the Greengenes database. Alpha-diversity of bacterial communities was calculated using different richness estimators. Differences in β-diversity of microbiota across treatments and age were tested using PERMANOVA. Alpha-diversity indices did not differ ($P > 0.05$) across weaning age × week in feces. However, differences ($P < 0.05$) between EW5 and EW7 calves were observed in the rumen for Shannon and inverse Simpson indices. Beta-diversity of both rumen and fecal microbiota differed ($P \leq 0.04$) between weaning age × week, indicating a more gradual shift in late-weaned calves toward a postweaned state, compared with an abrupt shift in early-weaned calves. Bacteroidetes was the dominant ruminal phyla in preweaned calves, decreasing in abundance ($P = 0.02$) after weaning, regardless of the age of weaning. A corresponding increase ($P \leq 0.09$) in Firmicutes at weaning resulted in it becoming the dominant ruminal phyla in postweaned calves. The opposite shift in dominance was observed in feces where Firmicutes was dominant before weaning and Bacteroidetes was dominant in postweaned calves. These two phyla accounted for an average 86% of total ruminal or fecal sequences regardless of age or treatment. These results indicate that late weaning at 8 wk facilitates a more gradual shift in microbiota toward a postweaned state compared with early weaning at wk 6. Hence, weaning later could reduce the adverse effects caused by feeding a high plane of nutrition before weaning.

Key Words: calves, feces, microbiome, rumen, 16S ribosomal ribonucleic acid gene sequencing, weaning

1615 Analysis methods differ in recovery of microbial glycogen. M. B. Hall*, *U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI.*

Microbial glycogen is an 1,4-,1,6-α-glucan produced from carbohydrates and stored within bacterial and protozoal cells. Enyzmatic analysis of glycogen in bacteria requires lysis of cells to make glycogen available to enzymatic attack. Lysis is typically performed with alkaline treatment. The objective of this study was to compare the detection of corn starch and of α-glucan in a fermentation pellet by 3 lysis methods from the research literature: 30% KOH boiled for 3 h (30%K), 0.2 *N* NaOH boiled 15 min (0.2N), and 0.31 *N* NaOH at room temperature for 15 min (0.31N). Fermentation pellets were prepared in an in vitro fermentation with mixed ruminal microbes in Goering and Van Soest medium, with 3 g/L of glucose, fermented for 2 h. Each fermentation vessel was quantitatively transferred into a centrifuge tube and centrifuged at 13,000 × *g* for 45 min at 5°C. Supernatants were discarded. Pellets were resuspended in 0.9% saline and recentrifuged. Supernatant was discarded and pellets were frozen at −20°C. As per individual protocols, 30%K and 0.2N were performed on undried pellets transferred into 50-mL beakers and 0.31N was performed on freeze-dried fermentation pellets. Samples were analyzed in duplicate in 2 analytical runs on 2 separate days in a randomized complete block design with fermentation pellet as the experimental unit. The statistical model for each substrate included method and fermentation run as a random variable. After incubation with alkali, all samples were neutralized with acid, and acetate buffer was added to bring the pH to 4.9 to 5.0. The 30%K and 0.2N samples received 0.1 mL of heat-stable α-amylase and 200 U of amyloglucosidase and were incubated for 2 h at 50°C. 0.31N received 0.25 mL Hazyme DCL enzyme preparation and was incubated for 16 h at 55°C. After bringing samples to volume with distilled water, samples were centrifuged to clarify and the supernatant was analyzed for glucose by a glucose oxidase–peroxidase assay. Alpha-glucan was expressed as glucose × 0.9. Recovery of corn starch was 96.7, 95.8, and 91.6% with 0.2N and 0.31N greater than 30%K, respectively ($P < 0.01$). Alpha-glucan in fermentation pellets was 29.6, 29.8, and 26.0 mg with 0.2N and 30%K greater than 0.31N, respectively ($P < 0.03$); 0.31N gave recoveries 87 to 88% of the other treatments. The pattern of starch recovery did not reflect that of microbial α-glucan recovery. With the alkaline lysis methods tested, a boiling treatment appears to be necessary for greatest microbial glycogen recovery.

Key Words: bacteria, glycogen, rumen, starch

Table 1616.

Measure	LoN-Glc	LoN-Lac	HiT-Lac	HiU-Lac
6 h Residual carbohydrate				
Glc or Lac, mg	8.28	31.0	18.9	34.3
Detected maxima				
Microbial N, mg	2.05	0.66	1.62	1.22
Glycogen, mg	18.5	0.77	1.30	1.22
Organic acid carbon, mg	19.6	16.3	19.5	11.9

1616 Utilization of lactose by mixed ruminal microbes is affected by nitrogen type and level and differs from utilization of glucose. M. B. Hall*, *U.S. Dairy Forage Research Center, USDA-ARS, Madison, WI*.

The objective of this study was to evaluate the effects of providing lactose (Lac) at differing nitrogen (N) levels and types and glucose (Glc) at a low N level on products formed and substrate utilized by mixed ruminal microbes. The 3 N treatments were applied via modification of Goering and Van Soest medium: LoN (60% of enzymic digest of casein removed; 300 mg N/L) and HiU or HiT with urea or an enzymic digest of casein, respectively, added to LoN to give 451 mg N/L. Glucose and Lac were added at 3 g/L (79.5 mg/fermentation vial). Two replicated in vitro fermentations with mixed ruminal microbes were performed. Inoculum donors were 2 ruminally cannulated cows individually provided with 200 g each of Lac and Glc per day via their diets for 14 d before the fermentations. Vials, the experimental units, were destructively sampled hourly from 0 through 6 h of fermentation. Data were analyzed as a randomized complete block design. Organic acid carbon is the sum of carbon in acetate, propionate, butyrate, valerate, and lactate. Detected maxima and endpoints were analyzed with the factors treatment and fermentation run (random variable) in the statistical model. Orthogonal contrasts of Glc vs. all Lac, Lac LoN vs. HiN, and Lac HiT vs. HiU were evaluated. Significance was declared at $P < 0.05$ and a tendency was declared at $0.05 < P < 0.10$. Glucose was utilized more rapidly than Lac, giving less residual Glc than Lac at 6 h ($P = 0.02$); HiT tended to have a lower value than HiU at 6 h ($P = 0.07$). Maximum detected glycogen was greater for Glc than for all Lac ($P < 0.01$), which did not differ from each other ($P > 0.66$). Maximum detected organic acid carbon values did not differ among treatments, except for a tendency for a greater amount with HiT than with HiU ($P = 0.06$). Maximum detected microbial N accumulation (a proxy for cell growth) was greater for Glc than for Lac ($P = 0.04$) and tended to be greater for Lac with HiN than with LoN ($P = 0.07$). Rumen microbes utilize Glc and Lac differently; N level and type alters utilization of Lac.

Key Words: fermentation, lactose, rumen

1617 Effect of dietary energy source and level on rumen bacteria community in lactating dairy cows. D. Bu*[1,2,3], S. Li[4], Z. Yu[5], S. Gao[1], L. Ma[1], X. Zhou[6], and J. Wang[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Sciences, Chinese Academy of Agricultural Sciences, Beijing, P. R. China, [2]CAAS-ICRAF Joint Lab on Agroforestry and Sustainable Animal Husbandry, World Agroforestry Centre, East and Central Asia, Beijing, P. R. China, [3]Hunan Co-Innovation Center of Animal Production Safety, CICAPS, Changsha, P. R. China, [4]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [5]The Ohio State University, Columbus, [6]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, P. R. China*.

Increased dietary energy level and degradation rate are beneficial to rumen microbial protein synthesis and milk production by dairy cattle. This study aimed to examine the effects of dietary energy source and level on rumen bacterial community in lactating dairy cows. Eight primiparous Chinese Holstein cows were used in a replicated 4 × 4 Latin square design. Cows were allocated to four treatments arranged in a 2 × 2 factorial design with energy levels (NEL, 1.52 vs. 1.72 Mcal/kg of DM, referred to as LE vs. HE) and energy sources (steam-flaked corn or ground corn, SFC vs. GC). All cows were fed twice daily ad libitum. Each experimental period consisted of 14 d for adaptation and 7 d for sample collection. Rumen fluid was collected in the morning 3 h after feeding via stomach tubing at d 17. Total DNA was extracted from each rumen sample, and the V4 hypervariable region of 16S rRNA gene was amplified and subjected to paired-end Illumina sequencing. After merging of paired-end sequencing reads, the low-quality sequences were removed and the quality-checked sequences were clustered into operational units (OTU) using the UPARSE pipeline. The resulting OTU were taxonomically classified using the RDP classifier implemented in QIIME. The bacterial communities were profiled using α diversity measurements, whereas the effects of both energy sources and levels were evaluated based on UniFrac distance using a

permutational ANOVA method. The differences in bacterial community structure were examined using DESeq2 in R. The LE and the GC treatments decreased bacterial richness as indicated by lowered number of species detected and estimates of both Chao1 and ACE ($P < 0.05$). The lower Shannon diversity index also suggests that LE and GC treatments decreased evenness of the rumen bacterial communities ($P < 0.05$). The composition of the bacterial communities was similar at the phylum level between two types of corn, but the high-energy diet altered bacterial communities by increasing Cyanobacteria while reducing Firmicutes and Proteobacteria ($P < 0.05$). At the genus level, the SFC diet had lower relative abundance of *Papillibacter* but higher relative abundance of *Mitsuokella* than the GC diet ($P < 0.05$). In contrast, dietary energy levels affected bacterial communities more extensively, with 51 genera being affected. The results indicate that increase in dietary energy level can affect rumen bacterial community to a greater extent than energy source when provided as steam-flaked vs. ground corn ($P < 0.05$)

Key Words: energy (source and level), metagenomics, rumen bacterial community

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1618 Effect of different microbial inoculants on fermentation characteristics of *Miscanthus* silage and their rumen fermentation and digestibility.

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The present study investigated the effect of starter culture of different microbial strains on *Miscanthus* silage quality and its in vitro and in vivo digestibility. *Pediococcus pentosaceus* NJ19, *Pichia anomala* NJ22, and *Saccharomyces cerevisiae* NJ50 were used as starter culture strains. A total of 4 experimental groups including the control (without inoculation) and three treatments (with inoculation) were used. Treatment NJ19 was inoculated at 10^7 cfu/g and treatments NJ22 and NJ50 were inoculated at 10^5 cfu/g of fresh weight. Silage quality was evaluated after 30 d of fermentation. Rumen fermentation patterns were determined using in vitro rumen simulated fermentation system. The effect of starter culture on palatability of *Miscanthus* silage and apparent nutrient digestibility were estimated using 4 rumen cannulated Hanwoo steers. An in vivo trial was performed based on a replicated 4 × 4 Latin square design. Regarding silage quality, DM in NJ19 and NJ50 was significantly lower than the control ($P < 0.05$). Significantly higher CP was found in NJ19 in comparison to other strains ($P < 0.05$). All treatments showed significantly elevated lactic acid production when compared with the control ($P < 0.05$). The highest production was recorded in the NJ19 treatment ($P < 0.05$). Acetic acid in NJ19 was significantly higher than in the other treatments ($P < 0.05$), and NJ22 was significantly lower than the others ($P < 0.05$). Significant difference in in vitro DM digestibility (IVDMD) was detected at 24 h of incubation. *Miscanthus* silage with NJ19 showed a significantly higher IVDMD ($P < 0.05$). Total VFA production in NJ19 was significantly higher than that in the other treatments ($P < 0.05$). Feed intake and apparent DM digestibility of *Miscanthus* silage with NJ19 were significantly higher than in the other treatments ($P < 0.05$). No significant differences among treatments were detected in OM, NDF, and ADF digestibility. These results indicate that inoculation with *P. pentosaceus* in *Miscanthus* silage can improve its ruminal fermentation, feed intake, and DM digestibility without negatively affecting the rumen environment.

Key Words: digestibility, microbial inoculant, *Miscanthus* silage, ruminal fermentation

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1619 The effects of varying undigested neutral detergent fiber and physically effective neutral detergent fiber content of fresh cow rations on dry matter intake, rumination, and milk yield in multiparous Holstein cows.

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The objective of this study was to evaluate the effects of varying levels of undigested NDF ($uNDF_{240}$; NDF remaining after 240 h of in vitro fermentation) and physically effective NDF (peNDF) content of fresh cow rations on DMI, rumination, and milk yield. Previously unpublished data from our lab indicated that cows fed higher $uNDF_{240}$ (approximately 10.7% DM) had higher DMI and improved health status compared with cows fed lower $uNDF_{240}$ (approximately 8.3% DM) in the postpartum period. Multiparous Holstein cows ($n = 56$) were fed a common prepartum ration beginning 28 d before expected parturition and randomly assigned at calving to one of two postpartum diets differing in content of $uNDF_{240}$ and peNDF (Table 1). Treatment diets, high fiber (HF; $n = 27$) and low fiber (LF; $n = 29$), were formulated for equivalent MP and starch, with higher fiber levels achieved through the addition of straw in the HF diet. At 29 d in milk (DIM), HF cows were switched to the LF diet and all cows were fed the LF diet through 42 DIM. Repeated measures data were analyzed with the MIXED procedure of SAS with model effects of treatment, time, and treatment × time. A treatment × time interaction ($P < 0.01$) was observed for DMI when expressed as a percent of BW, such that DMI for cows fed HF was lower in wk 3 (3.05% ± 0.07 vs. 3.35% ± 0.07; $P < 0.01$) and 4 (3.13% ± 0.06 vs. 3.50% ± 0.06; $P < 0.01$) postpartum. Despite this difference in intake, total daily rumination was not different between treatments (overall mean 543.4 ± 3.5 min/d; $P > 0.10$) at any time point. A treatment × time interaction for average weekly milk yield was observed ($P < 0.01$), such

that cows fed HF had lower milk production in wk 4 (46.4 ± 1.1 vs. 50.1 ± 1.0 kg/d; $P < 0.01$). However, differences in energy-corrected milk were not different (overall mean 47.8 ± 1.4 kg/d; $P > 0.10$). Increasing $uNDF_{240}$ and peNDF content of fresh cow rations may limit intake starting in wk 2 postpartum; however, differences in milk yield were not observed until wk 4 postpartum and limiting effects were alleviated after switching to the LF diet. We speculate that the LF diet may have contributed adequate $uNDF_{240}$ in this scenario, resulting in optimal DMI, whereas the additional $uNDF_{240}$ in the HF diet may have had limiting effects.

Key Words: physically effective neutral detergent fiber, undigested neutral detergent fiber, transition cow

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1620 Bacterial diversity in the feces of lambs fed purple prairie clover (*Dalea purpurea* Vent.) and alfalfa (*Medicago sativa*). Q. Huang[1,2], D. Holman[1], T. W. Alexander[3], T. Hu[2], L. Jin[1], Z. Xu[1], T. A. McAllister[4], S. Acharya[1], and Y. Wang*[1], *[1]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada, [2]College of Animal Science and Technology, Northwest A&F University, Yangling, P. R. China, [3]Lethbridge Research and Development Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [4]Lethbridge Research and Development Centre, AAFC, Lethbridge, AB, Canada*.

Our previous studies have shown that purple prairie clover (PPC) reduced the fecal shedding of *Escherichia coli* O157:H7 in lambs and generic *E. coli* in cattle, a response attributed to the presence of condensed tannins (CT). This study assessed the effect of PPC and PPC CT on the composition of the bacterial community in the feces of lambs using high-throughput 16S rRNA gene pyrosequencing. A total of 18 individually fed lambs were randomly divided into three groups and fed alfalfa (Alf), a 40:60 (DM basis; Mix) mixture of Alf and PPC, and Mix with polyethylene glycol (Mix-P) for 18 d. The Mix and Mix-P diets contained about 36 g CT/kg DM. Polyethylene glycol (PEG; MW6, 000) was sprayed onto the Mix-P diet to inactivate the biological activity of CT. Fecal samples were collected on Day 0, 13, and 18 through digital rectal retrieval. The samples were freeze-dried, DNA was extracted, and bacterial 16S rRNA gene amplicons were sequenced using the 454 pyrosequencing technology. Regardless of diet, bacterial communities were dominated by Firmicutes and Bacteroidetes, with a large proportion of OTU within these phyla remaining unclassified at the genus level after analysis. Diet had no effects on the fecal bacterial composition at the phylum level or on α-diversity metrics. Compared with the Alf diet, the Mix diet reduced the number of OTU associated with *Butyrivibrio* ($P = 0.01$), *Anaeroplasma* ($P = 0.02$), and unclassified bacteria within the families Peptococcaceae ($P = 0.03$), Christensenellaceae ($P = 0.01$), Erysipelotrichaceae ($P = 0.02$), S24-7 ($P = 0.02$), and Dehalobacteriaceae ($P = 0.03$). Similar reductions occurred within the orders RF39 ($P = 0.05$) and ML615J-28 ($P = 0.02$), but no difference was observed between Mix and Mix-P groups ($P > 0.05$). In contrast, a greater proportion of genus *Prevotella* ($P = 0.02$) was found in the Mix group compared with the Alf group. These results indicate that PPC CT up to 36 g/kg DM in the diet exert only minor effects on the composition of the fecal bacterial community of lambs.

Key Words: condensed tannins, 454 pyrosequencing, gut microbiota, purple prairie clover

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1621 Comparisons of microbial populations found in the rumen and in a dual-flow continuous culture fermentation system using high-throughput 16S amplicon sequencing. I. J. Salfer*, H. E. Larson, and M. D. Stern, *University of Minnesota, St. Paul*.

Dual-flow continuous culture fermenters are commonly used to study rumen fermentation in vitro. Previous research has shown that certain microbial populations are maintained within continuous culture at concentrations similar to in vivo values. The development of high-throughput genetic sequencing allows us to gain a global understanding of the microbial population in the rumen. The objective of this study was to use 16S amplicon sequencing to study phylogenetic differences and similarities between microbial communities found in the rumen of dairy cattle with those found in a dual-flow continuous culture fermentation system. Samples were collected from a rumen fluid, fermenter inoculum, and effluent collected directly from fermenters during 10 d of operation. Deoxyribonucleic acid (DNA) was extracted from samples, amplified to generate cDNA libraries, and sequenced using the Illumina MiSeq platform. Sequences were aligned using Mothur version 1.34.0 software and data were compared based on sample type (rumen vs. inocula vs. fermenter), inoculum donor, and day of fermenter operation. Redundancy analysis (RDA) was performed to determine correlations between fermentation measurements based on microbial community. Community differences were assessed using UniFrac metrics, analysis of molecular variance (AMOVA), and analysis of similarity (ANOSIM) based on Bray–Curtis dissimilarity matrices. Differences in taxonomic composition of different sample types were analyzed for kingdom phylum, class, order, and family taxonomic levels. Functional inferences were made by matching taxonomic data to KEGG orthology terms using PICRUSt software and analyzed by sample type. Results showed that UniFrac, AMOVA, and ANOSIM metrics were different ($P < 0.05$) between fermenters and rumen and inoculum samples. The microbial community within fermenters appeared to stabilize by Day 7 of fermenter operation. Bacteroidetes and Firmicutes made up the two most abundant phyla in rumen, inoculum, and fermenters and did not differ ($P > 0.10$) between sample types. Proteobacteria, Tenericutes, Spirochaetes, and Verrucomicrobia were found in dissimilar abundances ($P <$

0.05) between different sample types. Prevotellaceae was the most abundant family in all three sample types and did not vary ($P > 0.10$) between rumen, inoculum, and fermenter samples. PICRUSt predictions showed that AA metabolism, membrane transport, energy metabolism, and cellular processes and signaling were affected ($P < 0.05$) by sample type but that metabolism of carbohydrates, cofactors and vitamins, and lipids were not ($P > 0.10$). The overall microbial community differs between natural rumens and fermenters, but the concentrations of several prominent taxa are maintained.

Key Words: continuous culture, rumen, 16S sequencing

1622 Evaluation of in vitro and in situ starch digestibility assays. S. E. Schuling*, D. Schimek, and B. Vander Wal, *Hubbard Feeds Inc., Mankato, MN*.

The objective of this experiment was to evaluate commercial in vitro and in situ starch digestibility assays to estimate ruminal starch digestibility (RSD) and rate of ruminal starch degradation (kd). Twelve commercial dairy herds located in Wisconsin, Pennsylvania, and Missouri were used (4 free-stall and 8 tie-stall housing). Fecal samples were collected from 5 high- and 5 low-producing cows from each herd, and samples of total mixed rations (TMR) were collected after feed delivery from each pen ($n = 8$) or directly in front of each cow ($n = 80$). Corn silage (CS; $n = 13$) and corn (dry, $n = 9$, and high-moisture, $n = 7$) samples were also collected from each farm. Feed samples were thoroughly mixed and split for analysis. Fecal and TMR samples were sent to Rock River lab for starch analysis. Total tract starch digestibility (TTSD) was calculated from TMR and fecal starch content. The following equation was used to estimate RSD from TTSD: $y = 82.224 + (0.185 \times \text{ruminal})$, in which y = TTSD (Ferraretto et al., 2013). Samples of TMR, corn, and CS were sent to Rock River for 7-h in situ starch digestibility and to Dairyland lab for analysis of nutrient composition and 7-h in vitro starch digestibility. All herds tested milk through Dairy Herd Improvement Association and individual milk yield, milk fat, and milk protein content data were collected from test day closest to day of sample collection. The REG procedure of SAS was used to determine the relationship between in situ, in vitro, and in vivo RSD. In situ starch digestibility was related to in vivo RSD ($R^2 = 0.19$, $P < 0.002$). There was no relationship between in vitro and in vivo RSD ($R^2 = 0.01$, $P = 0.45$). The Cornell Net Carbohydrate and Protein System (CNCPS) uses ruminal starch kd to predict microbial protein production. Actual milk yield was related to model-predicted milk yield using model default kd for RSD ($R^2 = 0.69$, $P < 0.0001$). Ruminal starch kd was calculated for CS and corn using in situ data and entered into the CNCPS model (version 6.5; AMTS, LLC). This relationship was improved when measured in situ starch kd was entered for corn and CS ($R^2 = 0.76$, $P < 0.0001$). In conclusion, in situ starch digestibility at 7 h is a good approach for estimating RSD in vivo and using kd from this method improves milk yield predictions from the CNCPS model.

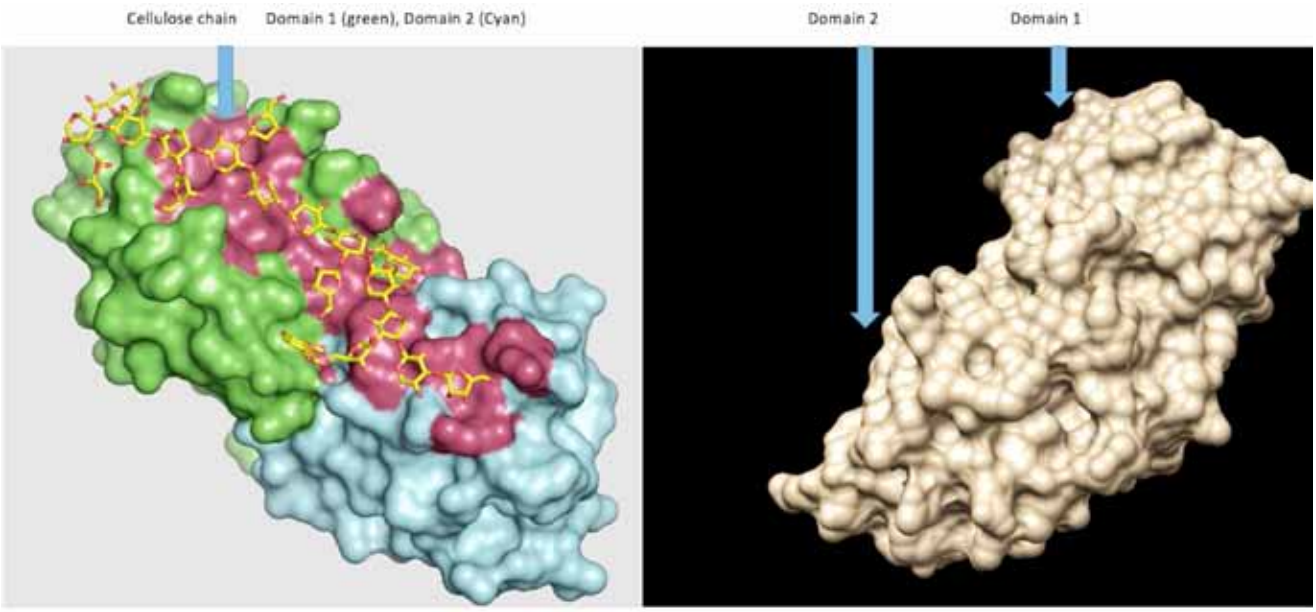
Key Words: in situ, in vitro, ruminal starch digestibility

1623 Effect of rumen acidosis and short-term feed restriction on messenger ribonucleic acid expression of genes relating to gut barrier function and immune response in Holstein steers. K. M. Wood*[1,2], R. L. A. Pederzolli[1], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]University of Guelph, Guelph, ON, Canada*.

The objective of this study was to identify whether ruminal acidosis (ACID) or feed restriction (FR) affect genes influencing barrier function (claudin [CLDN], occludin [OCLN], tight-junction protein-1 [ZO-1], and tight-junction protein-2 [ZO-2]) and immune response (toll-like receptor-2 [TLR2], toll-like receptor-4 [TLR4], and Fc fragment of IgA receptor [FCAR]). Twenty-one Holstein steers were randomly blocked and assigned to 1 of 3 treatments: control (CON), ACID, and FR. Steers were fed a common diet with a 50:50 F:C ratio once daily at 0800 h for a 5-d baseline period followed by a challenge period. Rumen acidosis was induced by restricting feed to 25% DMI for 1 d and then offering pelleted barley (30% DMI:BW) the following day. Steers on the FR treatment were restricted to 25% DMI for 5 d. Steers were killed and tissues were collected from the rumen (RUM), jejunum (JEJ), and distal colon (DC) for measurement of mRNA expression using real-time PCR. Relative fold change was calculated by the ΔΔCt method, using pairs of endogenous controls (glyceraldehyde 3-phosphate dehydrogenase, large ribosomal protein P0, or β-actin) and then normalized to the mean of the CON. Data were analyzed as a randomized complete block design using treatment as a fixed effect and block as a random effect. In the rumen, CLDN and OCLN were increased in FR over others ($P \leq 0.02$) and TLR4 was increased by 1.62- and 1.98-fold over CON ($P \leq 0.05$) for ACID and FR, respectively. In the JEJ, expression of CLDN was greater in ACID than in CON and FR ($P = 0.01$) but both ACID and FR had greater expression of OCDN ($P < 0.01$), ZO1 ($P = 0.01$), and ZO2 ($P < 0.01$) than CON. In addition, there was greater mRNA expression for FCAR in FR steers ($P \leq 0.007$) than in ACID and CON steers and greater TLR4 in FR than in CON ($P = 0.04$). In the DC, genes relating to barrier function (CLDN, OCLN, and ZO2) were greater for FR than for CON ($P \leq 0.04$). These data demonstrate that mRNA expression of genes relating to barrier function and immune response in the gastrointestinal tract are differentially affected by nutritional stressors. Nutritional challenges affect the expression of genes related to barrier function in immune response in the gastrointestinal tract. This may have implications in identifying how cattle adapt to nutritional challenges and to identify strategies to improve gut barrier function.

Key Words: acidosis, cattle, gut barrier function

Fig 1625.



1624 Use of fecal starch as an indicator of starch digestibility and starter intake in preweaned dairy calves. T. S. Dennis*, W. Hu, F. X. Suarez-Mena, T. M. Hill, J. D. Quigley, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH.*

Fecal starch (FS) has been used as a tool to evaluate starch digestibility in lactating dairy cows and feedlot steers. Some on-farm advisors are also using FS in a similar way to evaluate solid feed digestibility in preweaned dairy calves. Our objective was to evaluate the relationship of FS with starter intake and starch digestibility in preweaned dairy calves. Male Holstein calves initially 43 ± 2.9 kg BW from a single farm (N = 35) were fed different amounts of milk replacer ranging from 0.66 to 1.1 kg DM daily (27% CP and 17% fat) and weaned by 7 wk of age. Starters contained 37% whole corn, 20% whole oats, 35% protein pellet, and 3% molasses and contained 43% starch (first set) and 38% starch (second set). Fecal grab samples were taken from calves at 3 (n = 20), 6 (n = 20), and 8 wk (n = 35) of age. Twelve fecal samples per calf were taken via rectal palpation over a 5-d period each week, frozen daily, combined on an equal wet-weight basis, and subsampled for analysis. Chromic oxide was used as an external digestibility marker at 3 and 6 wk, whereas AIA was used as an internal marker at 8 wk. Milk replacer and starter intakes (offered and refused) were recorded daily during collection. Linear regression analysis of starch digestibility (%) and dry feed intake (kg/d) vs. fecal starch (%) were determined using PROC REG of SAS. At 3 wk of age, starch digestibility increased ($y = 0.69x + 40.80$; $R^2 = 0.53$, $P < 0.01$) and starter intake decreased ($y = -0.01x + 1.32$; $R^2 = 0.20$, $P = 0.05$) with increasing FS. At 6 wk of age, starch digestibility ($P = 0.11$) and starter intake ($P = 0.96$) were not related to FS. At 8 wk of age after calves were weaned, starch digestibility decreased as FS increased ($y = -0.62x + 99.7$; $R^2 = 0.86$, $P < 0.01$), whereas FS and starter intake were not related ($P = 0.17$), a relationship in contrast to the previously observed result in calves still consuming milk replacer. In the current study, results suggest that FS was not a good estimate of starch digestion or dry feed intake in the preweaned calf but has promise for evaluating starch digestibility in calves after weaning.

Key Words: dairy calf, digestion, fecal starch

1625 Expression and purification of a novel bacterial expansin from *Bacillus subtilis* that synergistically degrades cellulose with fibrolytic enzymes. A. A. P. Cervantes*[1], I. Muhammad[2], C. F. Gonzalez[3], D. Vyas[1], and A. T. Adesogan[1], *[1]Dep. of Animal Sciences, IFAS, University of Florida, Gainesville, [2]University of Florida, Gainesville, [3]University of Florida, Gainesville.*

Expansin-like proteins are a recently discovered group of proteins that can change the mechanical properties of plant cell walls. Many can synergistically improve cellulose degradation by fibrolytic enzymes. This study aimed to express and purify a novel bacterial expansin-like protein from *Bacillus subtillis*. Primers were constructed based on the Expansin-Yoaj protein sequence (accession number: WP_015383820.1) and tested using genomic DNA from *Bacillus subtillis* strain, UD1022. The plasmid p15TV-LdtR was used as template and transformed in *E. coli* DH5-α. Standard methods were used for chromosomal DNA isolation, restriction enzyme digestion, ligation, transformation, and agarose gel electrophoresis. The His-tagged fusion proteins in the plasmid were overexpressed in *E. coli* BL21-Star (DE3) cells. Then the cells were lysed

using a French Press and purified with a metal chelate affinity-column charged with Ni^{2+}. The remaining fraction was dialyzed, then protein concentration and molecular weight were determined. Protein identity was confirmed by sequencing and using Phyre[2] software. To examine the protein activity and synergism with cellulase, we examined if the expansin protein increased hydrolysis of carboxymethylcellulose (10 mg/ml) by *Trichoderma reesei* β 1- 4 endoglucanase EC (3.2.1.4) beyond the increase caused by the endoglucanase alone. The experiment had 5 (treatments: Control, enzyme, enzyme + expansin-like protein at doses of 100, 200, and 300 mg/ml) × 5 (incubation durations: 0,12, 24, 36, and 48 h) factorial treatment structure with 3 replicates per treatment combination. Additionally, all expansin doses were incubated by triplicate without cellulase for 48 h. Data were analyzed using the Generalized Linear Model of R. Protein concentration ranged from 0.130 to 0.345 mg/ml with an average molecular weight of 27 kDa. The Phyre[2] software revealed a two domain structure with polar residues typical in similar non-hydrolytic proteins. Synergistic increases in cellulose hydrolysis of 6 to 10% were detected ($P < 0.05$) by adding 100 but not 200 mg/ml of expansin-like protein. Whereas, adding 300 mg/ml of expansin-like protein decreased cellulose hydrolysis. Synergistic effects were more evident at 12 and 24 h (5 to 15%; $P < 0.05$) than at 36 and 48 h. On the other hand, using expansin alone did not exhibit hydrolytic activity after 48 h regardless of the dose. The newly expressed non-hydrolytic expansin-like protein synergistically increased cellulose hydrolysis by cellulase.

Key Words: expansin, synergistic effects, fibrolytic enzymes

1626 Annual rhythms of milk, fat, and protein production in U.S. dairy cattle. I. J. Salfer*, C. D. Dechow, and K. J. Harvatine, *Penn State University, State College.*

An annual pattern of milk composition has been well appreciated in dairy cattle with highest milk fat and protein observed during the winter and lowest in the summer. However, the rhythm has not been well quantified. The cosine function is commonly used to model repeating daily and seasonal rhythms and allows determination of the amplitude (mean to peak), phase (time at peak), and period (time between peaks) of the rhythm. The objective of this study was to use cosine analysis to characterize the annual rhythm of milk, fat, and protein production using both national milk production and herd-level data. First, 10 yr of monthly average milk butterfat and protein concentration by milk market were obtained from the USDA Agricultural Marketing service database. We first determined if the data fit a cosine function with a 12 mo period using the linear form of the cosine function by random regression in PROC Mixed. A zero amplitude test was used to determine significance of the rhythm. Fat and protein concentration fit a cosine function with a 12 mo period in all milk markets. There was an interaction between milk marketing order and milk fat and protein concentration ($P < 0.01$). The phase (time at peak) ranged from October 6 to January 6 for fat and from November 21 to December 12 for protein. The amplitude of the rhythm ranged from 0.07 to 0.14% for fat production and from 0.08 to 0.12% for protein production. The amplitude of milk fat rhythm generally was lower in southern markets and higher in northern markets. Second, the annual rhythm of milk yield and milk fat and protein yield and concentration were analyzed in monthly test day data from 1684 cows from 11 tie-stall herds in Pennsylvania. Milk, fat, and protein yield and fat and protein concentration followed yearly annual rhythms. Milk and protein yield were highest in May, fat yield and concentration were highest in February, and protein concentration was highest in November. There was an interaction of herd with the rhythm of milk yield, fat yield, and fat concentration. In conclusion, there is an annual rhythm of milk yield and milk fat and protein yield and concentration that fits a cosine function and varies by geographical location and herd.

Key Words: annual rhythms, milk synthesis, yearly pattern

1627 Molecular physiology of rumen papillae following an acidosis challenge. C. E. Kent-Dennis*, J. A. Pasternak, and G. B. Penner, *University of Saskatchewan, Saskatoon, Canada.*

The objective of this experiment was to evaluate the effect of ruminal acidosis on transcript abundance and localization of proteins regulated by local inflammation in the ruminal epithelium. Seven ruminally cannulated beef cows were used in a crossover design with two periods and two treatments (acidosis or control). Heifers were fed a baseline TMR with 50:50 forage to concentrate ratio and DMI was recorded daily. The acidosis induction consisted of feed restriction (25% of DMI for 1 d) followed by a grain challenge (30% of baseline DMI) and provision of the full TMR. Ruminal pH was monitored using indwelling probes and ruminal papillae biopsies were collected on d 2 and 6 following the induction of acidosis for RNA extraction and immuno-histofluorescence. Prostaglandin-endoperoxide synthase (PTGS1) and PTGS2 facilitate prostaglandin synthesis and were selected as targets because expression is thought to be regulated by inflammation. Gene expression was measured by quantitative real-time PCR, normalized to the geometric mean of three housekeeping genes within period. Immuno-histofluorescence of toll-like receptor (TLR)-9 and TLR-4 were used to evaluate localization in a subset of samples. Statistical analysis was performed using the MIXED procedure of SAS 9.4, with treatment and period as fixed effects. A pH threshold of 5.8 was used to define the occurrence of ruminal acidosis. During the day of the grain challenge, ruminal pH for acidosis cows was below pH 5.8 for 543 min, whereas pH of controls did not fall below the threshold at any time ($P = 0.02$). Minimum and mean pH were less on the

challenge day (min: 5.4 vs. 6.2 ± 0.17 and mean: 5.9 vs. 6.6 ± 0.14, respectively; $P < 0.01$) for acidosis than control cows. Two days after acidosis induction, transcriptional abundance of PTGS1 and PTGS2 in ruminal papillae were decreased by 1.37 ($P = 0.02$) and 2.08 ($P < 0.01$) fold, respectively, relative to controls. When evaluated at d 6, no differences were observed. TLR-9 was not ubiquitously expressed, but rather was concentrated in small areas within regions of the ruminal epithelium. TLR4 was intracellularly expressed in the stratum basale, stratum spinosum, and stratum granulosum regardless of treatment. The results of this study suggest a potential acute anti-inflammatory response following acidosis, which was also tightly regulated. However, the downregulation of PTGS2 was unexpected; related transcripts are being studied to elucidate these effects.

Key Words: acidosis, inflammation, rumen papillae

1628 Endocannabinoid and lipid metabolism gene network expression in adipose tissue of peripartal cows with low or high body condition score at calving. A. S. Alharthi*[1], Z. Zhou[1], D. N. Luchini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*Adisseo S.A.S., Alpharetta, GA.*

Our previous research revealed a strong inflammatory response within adipose tissue during the transition into lactation. Whether this localized effect is a result of oxidative stress induced by lipolysis and fatty acid oxidation or via the production of endocannabinoids remains to be determined. The objective of this study was to investigate the expression of genes composing the endocannabinoid signaling system and lipid metabolism in adipose tissue during the transition period in dairy cows. Twenty multiparous Holstein cows were retrospectively divided by prepartum body condition score (BCS) into two groups (10 cows/group): BCS $\leq$ 3.25 (LoBCS) and BCS $\geq$ 3.75 (HiBCS). Adipose tissue was biopsied at d −10, 7, and 20 relative to parturition. Tissue RNA was used to evaluate 17 target genes via quantitative real time RT-PCR. Data were log2 transformed and analyzed by the MIXED procedure of SAS. Among the endocannabinoid-related genes, a BCS × day was observed for *NAPEPLD*, *CNR2*, and *FAAH*. Expression of *NAPEPLD* and *CNR2* was greater at d 7 in LoBCS than HiBCS cows, while *FAAH* was upregulated at d 7 and 20 LoBCS than HiBCS cows. Expression of monoglyceride lipase (*MGLL*), which inactivates 2-Arachidonoylglycerol, was overall greater ($P < 0.05$) across time in LoBCS than HiBCS. In addition, LoBCS than HiBCS cows had a strong tendency ($P = 0.06$) for greater overall expression of *POMC* across time. Regarding the genes related with lipid metabolism, a BCS × day ($P = 0.04$) was observed for the mitochondrial enzyme *SOD2*, important for clearing reactive-oxygen species that cause cellular stress and inflammation, because of greater expression at d 7 in LoBCS than HiBCS. Similarly, a strong tendency ($P = 0.07$) for a BCS × day was observed for *LIPE* due to greater expression at d 7 and 20 in LoBCS than HiBCS. Among genes associated with lipolysis, LoBCS compared with HiBCS cows had overall greater expression of *ABDH5* ($P = 0.04$) and *ATGL* ($P = 0.02$), indicating a greater state of basal lipolysis over time. Although no BCS effect was detected for *CPT1A*, its expression increased sevenfold on d 20 versus −10, indicating a robust capacity of adipose for fatty acid oxidation. Overall, data indicated that cows with prepartum BCS below 3.25 experienced greater alterations in lipid metabolism and endocannabinoid signaling. A potential linkage between those pathways and risk of disorders postpartum remains to be determined.

Key Words: body condition score, endocannabinoid, lipid mobilization

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1629 Endocannabinoid network and proopiomelanocortin gene expression in peripartal bovine liver in response to rumen-protected methionine supplementation. A. S. Alharthi*[1], Z. Zhou[1], D. N. Luchini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*Adisseo S.A.S., Alpharetta, GA.*

Results from our previous work revealed a beneficial effect of rumen-protected Met (MET) supplementation during the transition period on postpartal immune function, inflammation, and cow performance. Endocannabinoids (EC; 2-Arachidonoylglycerol, oleoylethanolamide, and anandamide) are produced on stimulation of EC receptors expressed in central nervous system and peripheral tissues. These compounds have orexigenic, anorexigenic or pro- and anti-inflammatory properties. Because MET-fed cows had a better immune and liver function postpartum, we sought to determine any changes in the EC gene network and the hormone precursor proopiomelanocortin (POMC). Twenty-two multiparous Holstein cows were fed experimental treatments consisting of a basal control diet (CON; $n = 11$) and CON plus Met (Smartamine M, Adisseo NA) (MET; $n = 11$). All cows received the same far-off diet from −50 to −22 d before expected calving, close-up diet from −21 d to expected calving, and lactation diet from calving through 30 d in milk (DIM). MET supplementation was adjusted daily from −21 d to 30 DIM at a rate of 0.08% (DM basis) of diet DM. The liver was biopsied at −10, 7, 20, and 30 d relative to parturition. RNA was extracted and used for quantitative real-time RT-PCR. Expression of each target gene was normalized by the geometric mean of three internal control genes. Data were log2 transformed and analyzed using the MIXED procedure of SAS. A strong tendency for a treatment × day effect was observed for the EC receptor *CNR2* ($P = 0.06$), the lipase *MGLL* ($P = 0.08$), the amidase *NAAA* ($P = 0.08$) and *POMC* ($P = 0.07$). These results were associated with greater expression of *MGLL* and *POMC*in MET compared with control cows on d 7, while the expression of *NAAA* was greater in MET compared with control cows on d −10 and 7. In contrast, the interaction for *CRN2* was associated

with lower expression in MET compared with control cows on d −10. There was an overall greater ($P < 0.05$) expression of the fatty acid amide hydrolase *FAAH* and the EC-synthesizing enzyme *NAPEPLD* in MET compared with control cows. Overall, results indicate that alterations in the hepatic EC signaling network in response to MET might be involved in the positive effect on performance and liver function. Additional studies to investigate the mechanism of action of MET on the hepatic endocannabinoid system appear warranted.

Key Words: endocannabinoid, liver, methionine, transition period

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1630 Substrate utilization by *Megasphaera elsdenii* strain NCIMB 41125. A. M. Mobiglia*[1], F. R. Camilo[1], and J. S. Drouillard[2], [1]*CAPES Foundation, Ministry of Education of Brazil, Brasilia, Brazil,* [2]*Kansas State University, Manhattan.*

Megasphaera elsdenii (ME) is a key lactate-utilizer in grain-fed cattle, but less is known of its competitiveness in the rumen when administered as a probiotic before feeding grains. Our objective was to evaluate capacity for ME to utilize a wide range of alternative substrates, including glucose, fructose, galactose, arabinose, xylose, maltose, sucrose, lactose, trehalose, raffinose, fructo-oligosaccaride (FOS), potato starch, soy protein, and succinate. A basal medium (NC) was prepared with yeast extract, soy peptone, minerals, vitamins, and cysteine, and used alone or amended with sodium lactate or one of the above carbon sources. Lactate medium was adjusted to pH 5.6 and all other media were adjusted to pH 6.0. Hungate tubes containing sterile media were inoculated with 2% of a fresh culture containing approximately 9.6×10^8 CFU/mL ME strain NCIMB 41125 and incubated at 39ºC for 12 h. Changes in VFA concentrations were measured by gas chromatography using a capillary column (DB-WAX; J&W Columns) and flame ionization detector. Optical density (OD), measured as absorbance at $\lambda = 600$ nm, and pH were quantified, and cultures were enumerated on agar plates to determine viable cell counts. The study was a randomized complete block with individual cell culture as the experimental unit. Data were analyzed as mixed models with substrate as the fixed effect and block as a random effect. OD readings of cultures with arabinose, galactose, lactose, trehalose, and potato starch were comparable ($P > 0.05$) to NC, indicating limited capacity for metabolism of these carbon sources. Growth was greater with fructose compared to other substrates ($P < 0.05$), followed by glucose, lactate, and maltose, all of which were greater than NC ($P < 0.05$). Growth in media with FOS, raffinose, xylose, sucrose, and soy protein were marginally greater than NC ($P < 0.05$), while succinate inhibited growth ($P < 0.05$). Changes in culture pH and VFA concentrations were consistent with changes in OD measurements. Viable cell counts were lowest ($P < 0.05$) for succinate (6.8 versus 7.9 log CFU/mL for succinate and NC, respectively), again indicating an inhibitory effect of succinate on ME. Cultures with fructose, maltose, and glucose all had low terminal pH (4.31, 4.82, and 4.85, respectively), which may have adversely affected viable cell counts (8.15, 8.27, and 8.84 log CFU/mL, respectively). This study provides evidence for metabolism of a broad range of carbon sources by *Megasphaera elsdenii* strain NCIMB 41125.

Key Words: *Megasphaera elsdenii,* NCIMB 41125, substrates

1631 16S rRNA Bacterial sequences suggest dietary intervention can be used to change microbial community structure to reduce methane emission in Holstein dairy cattle. W. Tom*, J. V. Judy, P. J. Kononoff, and S. C. Fernando, *University of Nebraska-Lincoln, Lincoln.*

The rumen microbiome plays a critical role in host nutrient acquisition, and diet has been shown to alter the composition and function of the rumen microbiome. Most microbes in in the rumen resist in vitro culturing, remaining largely uncharacterized. Recent advances in next generation sequencing (NGS) methodologies provide an excellent opportunity to better understand changes in the structure of the rumen microbiome, which may lead to novel strategies to increase animal productivity and reduce livestock greenhouse gas emissions. This study utilizes high throughput sequencing of the 16S rRNA gene to compare bacterial community structure and abundance under different dietary conditions to evaluate the effect of the rumen microbial community on methane production in Holstein dairy cows. The experiment follows a randomized row by column design (8 x 4). Eight different Holstein cows were fed four different diets; reduced fat distillers grain (RFDDGS) mix, corn oil grain mix, calcium sulfate grain mix, and a standard corn and soybean meal control. Each diet was fed for 28 d and methane emissions were measured using indirect calorimetry (headboxes). Additionally, rumen samples were collected on Day 28 via esophageal tubing for microbial community analysis. Before receiving the first treatment diet, all cows were maintained on the same common diet to reduce animal to animal variation. DNA sequencing was performed using the Illumina MiSeq™ platform. Comparisons of rumen 16S rRNA bacterial communities show a significant difference in microbiome composition both by animal and by diet (PERMANOVA, $p < 0.001$). Pairwise comparison of all diets was performed using a Wilcoxon rank-sum test revealing significant differences between corn oil and RFDDGS ($p < 0.001$), calcium sulfate and RFDDGS ($p < 0.001$), corn oil and control ($p < 0.001$), and calcium sulfate and control ($p < 0.01$). Upon examining differences in operational taxonomic unit (OTU) abundances we identified multiple OTUs showing log fold changes between diets, supporting that bacterial community composition differs based on diet. This data suggests that dietary intervention can be used to mitigate methane emission by

controlling the microbial population within the rumen.

Key Words: bacterial community, microbiome, next generation sequencing, 16S rRNA

1632 Inulin as prebiotic for *Lactobacillus salivarius* and *Enterococcus faecium* with probiotic potential in ruminants.

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Milk production in Mexico is deficient and there are diarrhea problems in nursing calves. Lactic acid bacteria (LAB) are found in the digestive tract and show an antagonistic effect against enteric pathogens. Addition of prebiotics such as inulin to diets of calves might control gastrointestinal flora. Therefore, the aim of this research was to evaluate the influence of inulin on in vitro growth performance of *Lactobacillus casei* (*Lc*), *Lactobacillus salivarius* (*Ls*), and *Enterococcus faecium* (*Ef*). In vitro incubations were performed at 37°C, replacing the MRS glucose for inulin. The experimental design was complete randomized and treatments (T) were: T1 = MRS-glucose + Ls; T2 = MRS-glucose + Ef; T3 = MRS-glucose + Lc; T4 = MRS-inulin + Ls; T5 = MRS-inulin + Ef; T6 = MRS-inulin + Lc; T7 = MRS-inulin + Ls + Ef; T8 = MRS-inulin + Ls + Lc; T9 = MRS-inulin + Ef + Lc; and T10 = MRS-inulin + Ls + Ef + Lc. Variables were growth curve, pH, lactic acid production, ammonium, strains resistance to hydrochloric acid and bile salts, and antagonism against *Escherichia coli* and *Salmonella typhimurium*. Data were statistically analyzed with PROC GLM of SAS, and Tukey test ($P < 0.05$) was used to compare treatments means. Analysis of results showed a positive effect of inulin on the growth of strains, higher absorbance readings in MRS-inulin as compared to MRS-glucose (2.35^{d}, 2.28^{d}, 2.30^{d}, 2.83^{abc}, 2.67^{c}, 2.64^{c}, 2.75^{abc}, 2.93^{a}, 2.72^{bc}, and 2.88^{ab}, from T1 to T10, respectively; $P < 0.05$) and higher bacterial count at the end of the growth curve (10.98^{d}, 10.76^{d}, 11.29^{d}, 13.11^{c}, 13.63^{b}, 13.77^{a}, 12.93^{c}, 12.74^{c}, 12.43^{c}, and 12.92^{c} Log_{10} UFC mL^{-1} from T1 to T10, respectively; $P < 0.05$), whereas no changes were found for the other variables. We conclude that LAB *Ls* and *Ef* fermented inulin with a positive effect on strains growth, without affecting their probiotic potential.

Key Words: *Enterococcus faecium*, inulin, *Lactobacillus salivarius*

1633 Moisture content influences ensiling characteristics, in situ disappearance, and in vitro digestion characteristics of reconstituted corn grain.

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Grain processing is a key factor influencing efficiency of feed utilization in feedlot cattle. Reconstitution of corn grain followed by ensiling modifies structural characteristics of grain, thereby improving starch availability and animal performance. The objective of this experiment was to evaluate changes in ensiling characteristics of corn grain reconstituted to different moisture levels, and to determine impact on in situ and in vitro digestion. Corn grain was ground to 4000 µ and subsequently mixed with water to final moisture concentrations of 27, 30, 33, and 36%. Grains were packed into 12 concrete silos (2-m dia. x 2-m height), each containing approximately 2650 kg of grain (3 silos per moisture level). Grains were allowed to ensile for 90 d, then sampled by drilling two 3-cm cores to a depth of 60 cm, which were composited to form one sample for each silo. Ensiled grains and a dry-rolled corn control (DRC) were characterized with respect to pH, moisture content, 16-hour in situ disappearance, and in vitro fermentation by mixed ruminal microbes. Grain pH was determined after steeping 25 g of grain in 100 mL deionized water for 1 h at room temperature. For in vitro fermentations, 3 g of grain (DM basis) were added to 250-mL screw-top bottles, mixed with 140 mL of artificial saliva and 10 mL of strained ruminal fluid, flushed with nitrogen, capped with Ankom gas pressure monitors, and placed into a shaking incubator at 39ºC for 16 h. Terminal pH was measured for each culture, and samples of supernatant were mixed 4:1 with 25% w/v metaphosphoric acid solution for determination of VFA profiles by gas chromatography using a flame ionization detector. In situ dry matter disappearance (ISDMD) of grains was measured over a 16-h ruminal incubation. The pH of ensiled grains was 6.3, 4.42, 4.23, and 4.15 for 27, 30, 33, and 36% moisture, respectively (linear and quadratic effects, $P < 0.01$). ISDMD were 36, 46, 43, 47, and 57% for DRC and ensiled grains with 27, 30, 33, and 36% moisture, respectively (linear, $P < 0.01$), in vitro gas production amounts were 89, 161, 163, 221, and 284 mL, respectively (linear, $P < 0.01$), and total VFA concentrations of cultures were 41, 58, 69, 86, and 100 mM, respectively (linear, $P < 0.01$). Moisture content of reconstituted, ensiled grain has a large impact on in situ and in vitro fermentation characteristics.

Key Words: corn, reconstitution, starch

1634 On the way to optimize the two stage Tilley and Terry technique for a more accurate in vitro assessment of rumen modifiers. A. Russouw[*1], E. Raffrenato[1], F. Chaucheyras-Durand[2], and E. Chevaux[2], [1]*Department of Animal Sciences, Stellenbosch University, Stellenbosch, South Africa,* [2]*Lallemand SAS, Blagnac, France.*

In vitro techniques using rumen inocula are routinely used to estimate NDF rumen and total tract digestibility values. By controlling the micro-environment of the test flask, the technique does not represent the dynamic environment of the rumen, often resulting in higher digestibility values when compared to in vivo values. Furthermore, because of the stability of the system, testing rumen modifiers in vitro may result in biased conclusions. Among the possible parameters, our objective was to assess the effects of using different buffers, NDF levels and doses of a live yeast assumed to stimulate fiber digestion, on rumen NDF and total tract OM in vitro digestibility (NDFd and TTOMd) using a modified Tilley and Terry procedure. Three buffers (Kansas State-KS; McDougall-MD; Goering and Van Soest-GV), two forages (wheat straw-WS, 83% NDF; oat hay-OH, 60% NDF) and 4 doses of yeast (0, 10^5, 10^6, 10^7 cfu/ml) were tested. Residual NDF of the fermented samples were obtained at 12, 24, and 48 h. The fermented samples followed also 48 h acid pepsin treatment for OMd estimation. NDF rate of digestion (kd) was calculated using a first order decay model and estimated iNDF using the 240 h fermentation residual. Data were analyzed according to a randomized complete block design with a factorial arrangement of treatments. The main tested effects were buffer, NDF level, and yeast dose. Run was considered random effect and response variables were NDFd and kd. The buffers resulted in different NDFd and kd ($P < 0.01$) with the KS resulting in the lowest and MD in the highest NDFd and TTOMd, for both WS and OH. Yeast interacted with both NDF level and buffer ($P < 0.01$), resulting in more effective action (higher kd) with higher NDF and GV and KS buffers. The most effective yeast dose was the 10^6 cfu/ml, when compared to the others across NDF levels and buffers, increasing kd on average 0.025 to 0.035 and 0.038 to 0.044 h^{-1} for WS and OH, respectively. Therefore, all parameters tested affected conclusions on the effectiveness of the rumen modifier tested.

Key Words: buffers, live yeast, NDF digestibility, Tilley and Terry

1635 Effect of feeding different flaxseed-based products on the rumen microbial community of dairy cows evaluated by high-throughput DNA sequencing. E. Castillo-Lopez[*1], J. Moats[1], N. D. Aluthge[2], H. A. Ramirez Ramirez[3], T. A. McAllister[4], C. L. Anderson[2], D. A. Christensen[1], T. Mutsvangwa[1], H. Lee-Rangel[5], G. B. Penner[1], and S. C. Fernando[2], [1]*University of Saskatchewan, Saskatoon, Canada,* [2]*University of Nebraska, Lincoln,* [3]*Iowa State University, Ames,* [4]*Lethbridge Research and Development Centre, AAFC, Lethbridge, Canada, Lethbridge, Canada,* [5]*Universidad Autonoma de San Luis Potosi, San Luis Potosi, Mexico.*

Four ruminally-cannulated lactating Holstein cows (mean and SD, 116.5 ± 17.5 DIM; 712.7 ± 92.3 kg BW) were used in a 4 × 4 Latin square with 28-d experimental periods to evaluate the effect of feeding flaxseed-based products on the rumen microbial population. Treatments (DM basis) were: 1) CONT, a control diet containing 51.9% of a barley-based concentrate, 20.0% alfalfa hay, and 28.2% barley silage; 2) FLAX, inclusion of 11.4% of a non-extruded flaxseed-based product which contained 55% flaxseed, 37% field peas, and 6.8% dehydrated alfalfa; 3) EF, inclusion of 11.4% of an extruded flaxseed-based product which contained 55% flaxseed, 37% field peas, and 6.8% dehydrated alfalfa; and 4) EFT, inclusion of 11.4% of an extruded flaxseed-based product which contained 55% flaxseed, 37% high-tannin faba beans (*Vicia faba*), and 6.8% dehydrated alfalfa. The flaxseed-based products used in FLAX, EF, and EFT were included (3 kg/d) by partially replacing 3 kg/d of the barley-based concentrate. At the end of each period, samples of ruminal contents were collected and DNA was extracted from samples. The V3 hypervariable region of the 16S rRNA bacterial gene was amplified and sequenced. Sequenced reads were subjected to phylogenetic classification using the pipelines UPARSE and QIIME. Data for the abundance of bacterial taxa were analyzed using the MIXED procedure of SAS. Major bacterial phyla were not affected ($P \geq 0.34$) by diet and included *Bacteroidetes* (48.8 ± 3.66%), *Firmicutes* (46.0 ± 3.92%), and *Proteobacteria* (1.3 ± 0.30%). Major bacterial families were similar ($P \geq 0.71$) across diets and were represented by *Prevotellaceae* (20.2 ± 2.82%) and *Veillonellaceae* (16.3 ± 6.19%). In addition, major genera remained unaffected ($P \geq 0.38$) and included *Prevotella* (19.3 ± 2.47%) and *Succiniclasticum* (14.5 ± 6.12%). However, compared to CONT, there were shifts in some bacterial families and genera for EF and EFT. The biohydrogenating bacteria, *Clostridium*, decreased ($P < 0.01$) resulting in 0.4, 0.1, 0.1, and 0.2 ± 0.05% for CONT, FLAX, EF, and EFT, respectively. Flaxseed extrusion and high-tannin faba beans did not affect predominant bacterial taxa; however, there were shifts in less abundant taxa including a decrease in

the biohydrogenating genus *Clostridium*.

Key Words: biohydrogenation, extruded flaxseed, rumen microbiome, tannin

1636 Effects of inoculum source and ammoniation on in vitro gas production kinetics of barley straw.

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A batch culture was conducted to assess the effects of inoculum source and ammoniation on in vitro gas production (GP) and DM digestion (DMD) kinetics of barley straw (BS). The experiment was a 2 × 2 × 2 factorial with low- vs. high-fiber digesting rumen inoculum; ammoniated vs. untreated BS; and with and without the replacement of forage with concentrate. All substrates were ground through a 2-mm screen. Inoculum was collected from two low- and two high-fiber digesting beef heifers as defined by the rate of digestion (0.021 to 0.026/h) and effective degradability (ED) of DM of BS. For the concentrate treatment (BSC), 30% BS was replaced by an equal amount of concentrate. Additional vials containing only concentrate were used to correct for its contribution to GP. The GP was recorded at 3, 6, 9, 12, 24, 36, 48, and 72 h and DMD was measured after 6, 12, 24, 48, and 72 h. The experiment was repeated three times on different days. Data were fitted to exponential models: $GP = b(1-e^{-c(t-L)})$ and $DMD = a+b(1-e^{-c\,(t-L)})$. The GP parameters were not affected by inoculum source, but lag time decreased ($P < 0.01$) with ammoniation (0.6 h) vs. untreated (1.5 h) or with BSC (0.7 h) vs. BS (1.4 h). Initial GP (ml/g OM) increased ($P < 0.01$) with ammoniation (8.1) vs. untreated (7.1) or with BSC (8.2) vs. BS (7.0). For DMD, the high- vs. low-fiber digesting inoculum decreased ($P < 0.01$) the soluble fraction, lag time and ED of DM without affecting the potentially digestible fraction or rate of disappearance of the potentially digestible fraction. Ammoniation improved ($P < 0.01$) DMD kinetics (soluble, 11 vs. 15%; potentially digestible, 50 vs. 59%; rate, 5.4 vs. 6.2%/h; lag time, 2.8 vs. 2.0 h) and ED (30 vs. 36%) of BS. The BSC compared with BS had greater ($P < 0.01$) ED (36 vs. 31%) without altering other DMD parameters. Although both inoculum source (soluble, $P < 0.05$; lag time, $P < 0.01$; and ED, $P < 0.10$) and BSC (potential digestible fraction, lag time, and ED; $P < 0.01$) exhibited an interaction with ammoniation, kinetic parameters tended to be improved by ammoniation. These results suggest that inoculum from high-fiber digesting cattle did not improve in vitro GP or DMD of BS. In addition, the study confirmed that ammoniation improved the ruminal digestion of BS.

Key Words: ammoniated straw, batch culture, inoculum source

1637 Feeding ground flaxseed to lactating dairy cows decreases the ruminal proportion of *Archaea*, but does not change the major species of cellulolytic bacteria.

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The objective of this study was to investigate the impact of incremental amounts of ground flaxseed (GFX) on ruminal microbiota of lactating Jersey cows. Twelve lactating organically-certified Jersey cows (76 ± 23 DIM and 431 ± 25 kg of BW), part of a larger feeding trial, were used in a replicated 4 × 4 Latin square design with 21-d periods (14 d for diet adaptation and 7 d for sample collection). Cows were randomly assigned to 1 of 4 treatments (DM basis) consisted of 55% mixed-mostly grass silage, 8% mixed-mostly grass hay, 2% roasted soybean and: 1) 0% GFX, 6% soybean meal (SBM), and 27% corn meal (CM), 2) 5% GFX, 4.8% SBM, and 23.2% CM, 3) 10% GFX, 3.5% SBM, and 19.5% CM, and 4) 15% GFX, 2% SBM, and 16% CM. Ruminal fluid was sampled using an esophageal tube 7 h after the morning feeding on d 17 to 19 of each experimental period, pooled, and frozen at −80°C until analysis. After DNA extraction, the 16S rRNA gene V4 variable region PCR primers 515/806 were used. Following amplification, PCR products were pooled in equal proportions based on their molecular weight and DNA concentration, purified using calibrated Ampure XP beads, and then used to prepare the DNA library for Illumina TruSeq DNA analysis (Mr. DNA Molecular Research Laboratory, Shallowater, TX). Sequencing was performed on a MiSeq and data were processed using a proprietary analysis pipeline. Final operational taxonomical units were classified using BLASTn against a curated database derived from GreenGenes, RDPII, and NCBI. Orthogonal polynomial contrasts were used to test linear and quadratic effects. Results are shown in Table 1. The ruminal proportion of archaea responded quadratically to feeding GFX. Specifically, the proportion of *Methanobrevibacter* sp. and *Methanosphaera* sp. responded quadratically, whereas that of *Methanomicrobium* sp. decreased linearly with the greatest level of GFX resulting in the lowest values. Quadratic effects were also observed for *Fibrobacter* sp. and *Prevotella* sp. with feeding GFX. Whereas the 3 major ruminal cellulolytic species (*Fibrobacter succinogenes*, *Ruminococcus albus*, and *Ruminococcus flavefasciens*) were not affected by GFX supplementation, the ruminal proportion of *Prevotella ruminicola* and *Prevotella briantii* responded quadratically

Table 1637.

Table 1. Effect of ground flaxseed (GFX) on ruminal microbiota.

	Diets (% GFX)					$P < 0.05$	
% of total	0%	5%	10%	15%	SEM	Linear	Quadratic
Archaea	5.70	4.17	4.39	3.20	0.66	<0.01	0.01
Methanobrevibacter sp.	5.49	3.99	4.21	3.04	0.67	<0.01	0.02
Methanomicrobium sp.	0.06	0.05	0.05	0.04	0.01	0.04	0.15
Methanosphaera sp.	0.14	0.12	0.12	0.11	0.01	0.04	0.04
Butyrivibrio fibrisolvens	0.14	0.15	0.13	0.14	0.02	0.82	0.62
Prevotella sp.	11.3	12.7	14.1	17.7	0.87	<0.001	<0.001
Prevotella ruminicola	0.10	0.14	0.16	0.25	0.03	<0.001	<0.01
Prevotella bryantii	0.01	0.02	0.02	0.03	0.004	<0.001	<0.001
Fibrobacter sp.	2.10	2.11	2.02	1.77	0.14	<0.01	<0.01
Fibrobacter succinogenes	0.21	0.22	0.21	0.27	0.08	0.31	0.37
Ruminococcus sp.	5.86	5.68	5.26	4.64	0.21	<0.001	<0.001
Ruminococcus flavefaciens	0.46	0.45	0.44	0.46	0.03	0.76	0.78
Ruminococcus albus	0.02	0.03	0.03	0.03	0.03	0.43	0.48

with greatest values found when feeding 15% GFX. Overall, feeding incremental amounts of GFX to lactating dairy cows decreased the ruminal proportion of methanogens, but did not affect the 3 major species of ruminal cellulolytic bacteria.

Key Words: dairy cows, ground flaxseed, ruminal microbiota

1638 Data acquisition settings of the Ankom RF system and inocula donors affect in vitro gas production.

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In vitro gas production (IVGP) provides information about the fermentation of feeds. The Ankom RF is a gas-release system that electronically acquires gas pressures. Objectives were to determine the effects of valve-opening pressure (OP) and release time (RT) on IVGP and evaluate the effects of inocula donor on IVGP of selected substrates. Settings for OP were 1, 3, or 8 psi and for RT were 250 or 500 msec. Blended inocula (strained ruminal fluid and ruminal solids blended with media) were composited from 3 steers fed high-NDF (40.3% DM; HF) or high-starch (28.3% DM; HS) diets. Data acquisition terminated early in run 4, and only IVGP for 3, 4.5, 6, 9, 12, 24, and 36 h were evaluated. Duplicate substrates and triplicate blanks were fermented for each OP and RT combination in two runs each with HF or HS inoculum. For each time, the statistical model included order of inoculation, donor (D), substrate (S), D*S, OP, and RT, with module within run as the experimental unit. Blank IVGP increased until 12–18h, then decreased linearly with a leak rate of −0.35 mL/h. Blank subtraction corrected for leakage resulting in plateau-shaped curves and differentiated lag responses for all S. Donor HF generated higher blank IVGP (4.4 mL at 9 h) than HS, which indicated more fermentable matter in HF inoculum. Blank IVGP decreased with increasing order of inoculation. Across S, IVGP differed ($p < .01$) among OP after 3 h (22.9, 0.5, and −23.7 mL/g, for 1, 3, and 8 psi, respectively). For 3 to 24 h, IVGP was higher ($p < .01$) for 500 than 250 msec RT (maximum difference of 38.1 mL/g at 9 h). Numerical derivatives of cumulative curves showed spikes when valves opened. Lower OP and shorter RT resulted in more valve openings, and also obtained lower headspace pressures. Donor HF generated lower IVGP than HS across all S, which was significant ($p < .006$) after 6 h. Up to 18 h, there was a D*S interaction ($p < .036$) with HF generating more IVGP for stover while HS was greater for corn starch. There was little difference in IVGP between HF and HS for solka floc or HMC. Results indicate that blank correction was necessary and IVGP was greater for OP of 1 psi and RT of 500 msec. Data acquisition settings may affect fermentation or create artifacts in measurements. Settings and donors should be

optimized to meet experimental objectives.

Key Words: Ankom RF, gas production, inoculum donor

1639 Effect of duration of in vitro incubation on disappearance of NDF and starch from chopped corn plants versus their resulting corn silages.

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The corn silage fermentation process and its duration can alter the extent of in vitro digestion of NDF and starch. The objective of this study was to determine whether extending in vitro incubation time will enlarge or dispel differences between fermented and unfermented corn plants in extent of in vitro digestion. Ten corn silages were prepared from Pioneer non -BMR hybrids grown at a single location and harvested on a single date at an average of 36% DM. Disappearance of NDF and starch from the unfermented chopped corn plants and from the kernel processed corn silages produced from these plants fermented for 4 mo was measured after various in vitro incubation time intervals at a commercial laboratory. Despite differences among samples in NDF and starch content, no differences among these silages for in vitro NDF digestibility or 7 h starch digestion were detected. At the longest incubation times tested, unfermented plants and corn silages had similar digestibility. But at shorter incubation times, extent of digestion of NDF and starch for the corn silages was related curvilinearly ($P < 0.05$) to those for unfermented plants. In vitro disappearance of NDF was 9, 12, 11, 10, 9, and 3% points lower for corn silages than for chopped corn plants at in vitro incubation times of 6, 12, 24, 30, 40, and 240 h. In vitro starch disappearance was 5, 9, 12, 5, 0, and 0% points greater for corn silages than for chopped corn plants at in vitro incubation times of 2, 4, 7, 12, 24, and 72 h. The correlation between unfermented plants and their silages in both NDF and starch disappearance within an incubation time interval proved weak (R2 = 0.00 to 0.36). In vitro disappearance of starch from these corn silages was not correlated with kernel processing score. Based on the typical in vitro fermentation times used commercially, corn silage fermentation for 4 mo increased in vitro digestion of starch but decreased in vitro digestion of NDF. The difference between unfermented corn plants and corn silages at various in vitro fermentation times implies that improvements in ruminal starch digestion from corn silage allowed to ferment for several months should be greatest with shorter ruminal residence times (7 h or less). However, adverse effects on NDF digestion may partially counterbalance the energy benefit from increased ruminal starch digestibility associated with longer fermentation times.

Key Words: corn silage, NDF, starch

1640 Rumen protozoal communities are dynamic after a dietary switch from conserved forage to pasture.

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Rumen protozoa shift in response to dietary factors, however, little is known about the stabilization of rumen protozoa populations after a diet change. The objective of this study was to characterize the weekly shift in rumen protozoal communities during the transition from a conserved forage (CF) to pasture. Individual rumen digesta samples were obtained from five lactating Holstein cows on weeks −1, 1, 2, 3, 4, and 5 relative to the diet switch. DNA was extracted from rumen digesta and the V3-V4 region of the 18S rRNA gene was amplified using PCR. Sequence reads were produced with the Illumina Miseq (v.3) platform and bioinformatics were performed using the MOTHUR program (v. 1.36.1). Real-time PCR was used to assess protozoal densities (cells/mL digesta). The PROC MIXED procedure of SAS (v. 9.4) was used to analyze data using a repeated measures ANOVA. On week 5 of pasture, protozoal densities were higher than CF (4.97 vs. 3.48 cells/mL digesta, respectively; $P < 0.01$). The genera *Entodinium* ranged from 2–79% abundance, *Dasytricha* from 3–71%, *Eudiplodinium* from 1–51%, *Isotricha* from 1–35%, and *Ostracodinium* from 1–17%. The genus *Isotricha* was most abundant on week 1 after the diet switch ($P < 0.05$). The abundance of protozoa belonging to the genus *Dasytricha* was higher than the CF diet by week 5 on pasture ($P < 0.05$), while protozoa of the genus *Eudiplodinium* tended to be lower after week 5 when compared to CF. In conclusion, protozoal populations were highly dynamic across weeks and within animals.

Key Words: diversity, Illumina MiSeq, protozoa densities

1641 Effects of *Bacillus subitilis* supplementation on milk production and rumen fermentation of dairy cows.

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The objective of this study was to assess the effect on milk performance and rumen fermentation of *Bacillus subtilis* C-3102 (Calsporin®; Asahi Calpis Wellness Co., Ltd., Japan). Three hundred and seventy-five lactating cows (132 primiparous, 243 multiparous; BW = 621 ± 76 kg; DIM = 145 ± 93, yield = 42.1 ± 8,1 kg/d) were randomly allocated to 3 treatments and fed a common TMR containing 15.4% CP, 39.7% NDF and 1.57 Mcal of NEl/kg. Treatments consisted of no supplementation (T0), 1.5 x 10^5 CFU/g (T1), and 3 x 10^5 CFU/g (T2) supplementation with *B. subitilis* C-3102. Calsporin® was supplemented individually during milking using a precision feeding system. At each milking, cows received either 100 g of barley (T0), or 100–150 g of barley containing Calsporin®

Table 1640.

	Diet						SE	*P* value
	Conserved Forage	Pasture						
Taxa	week -1	week 1	week 2	week 3	week 4	week 5		
Dasytricha	25.02	23.44	6.35	36.06	26.54	52.38	9.08	0.15
Eudiplodinium	18.12	16.57	30.96	21.68	9.49	4.56	4.82	0.07
Entodinium	14.93	10.61	31.61	14.77	27.06	12.80	7.16	0.52
Isotricha	5.70	21.93	3.31	3.70	10.28	9.41	3.27	0.23
Ostracodinium	9.54	3.70	3.04	3.24	5.10	1.89	1.59	0.01
Diplodinium	0.65	1.09	1.58	1.26	1.24	0.20	0.37	0.90
Epidinium	1.15	0.95	1.48	1.64	1.70	0.03	0.43	0.57
Un-Ophryoscolecidae	13.58	11.06	16.70	11.13	12.33	5.25	3.37	0.30
Un-Entodiniomorphida	2.48	1.29	0.78	1.29	0.81	1.51	1.35	0.09
Un-Trichostomatia	1.70	3.97	1.80	2.93	1.87	5.19	0.58	0.03
<1% abundance	6.03	5.09	2.39	2.30	3.57	6.79	0.90	0.01

Un = unclassified; *P*-values compare the CF diet with the average of pasture weeks 4 and 5.

to supplement either 0.3 (T1) or 0.6 g/cow/day (T2) for 105 d. Cows are milked 3 times a day. Milk production was recorded daily. Thirty cows (10 from each treatment) were sampled for rumen contents at 42 and 84 d using an esophageal tube after the morning milking. Rumen pH and VFA concentrations determined. Data were analyzed using a mixed-effects model with week as a repeated measure. Cow was the experimental unit (n = 125). Primiparous cows on T2 produced more ($P <$ 0.01) milk after wk 6 of study (35.6 ± 0.82 kg/d) than primiparous cows on T1 and T0 (34.2 ± 0.82 kg/d), whereas multiparous cows on both T1 and T2 (38.5 ± 0.82 kg/d) produced ($P <$ 0.05) more milk than multiparous cows on T0 (36.1 kg/d) after 3 wk of study. Changes in rumen fermentation profile were minor. Rumen molar proportions of propionate decreased (P < 0.05) at 84 d compared with d 42 in T1 and T2 (from 26.8 to 25.2 ± 0.48%) compared with T0, which remained constant (24.8 ± 0.48%). Molar proportions of rumen butyrate decreased ($P < 0.05$) between 42 and 84 d in T0 (from 11.5 to 9.9 ± 0.43%) compared with in T1 and T2, which remained constant (10.5 ± 0.43%). The supplementation of Calsporin® seems to exert a positive effect on milking persistency of dairy cows, with a positive response already obtained 1.5 x 10^5 CFU of *B. subtilis*/g. About 3 and 6 wk of exposure to treatments are needed for a milk response to become evident in multiparous and primiparous cows, respectively.

Key Words: probiotic, rumen, yield

1642 Effect of *Enterococcus fecalis* SROD5 supplementation on microbial communities and quantities of in vitro rumen fermentation.

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Enterococcus fecalis is one of the beneficial microorganisms, which produces fumarate reductase that converts fumarate to succinate and reduces methane production in vitro. Hence, this study was conducted to determine the effect of *E. fecalis* SROD5 supplementation on archaeal diversity and microbial population. Fresh culture of *E. fecalis* SROD5 (7.5 × 10^8 cfu/ml) at different inclusion rates (0, 0.1%, 0.5%, and 1.0%) were investigated using in vitro rumen fermentation. Ruminal samples were collected from cannulated Holstein Friesian cow and 40:60 rice straw to concentrate ratio were used as substrate at 1 g dry matter (DM) per 100 ml buffered rumen fluid. Samples from in vitro fermentation of 12 h incubation were used for determination of microbial community and quantity. Pyrosequencing of archaeal 16S rRNA gene showed that the number of operational taxonomic units (OTU) was highest in supplementation of 0.1% *E. fecalis* SROD5 (39). Shannon-Weaver index were comparable among control and treatments while Chao 1 was higher in 0.1% and 0.5% supplementation of *E. fecalis* SROD5 with 52 and 54, respectively. Meanwhile, alignment of archaeal reads showed that almost all retrieved from in vitro rumen fermenta samples fell into the phylum *Euryarchaeota*, which predominantly affiliated with family *Methanobacteriaceae* (97% to 99%) followed by *Methanomicrobiaceae*, and *Methanosarcinaceae*. Abundance of *Methanobrevibacter* was higher in non-supplementation of *E. fecalis* SROD5 with 96.54%. Higher abundance of *Methanomicrobium* was observed in 0.1% *E. fecalis* SROD5 supplementation while higher abundance of *Methanosphaera* and unclassified *Methanobacteriaceae* as well as the presence of *Methanimicrococcus* were observed in 0.5% *E. fecalis* SROD5. Supplementation of 0.1% *E. fecalis* had the highest quantities of total bacteria (2.59 × 10^8 copies/ml), total fungi (1.03 × 10^4 copies/ml), *Fibrobacter succinogenes* (1.62 × 10^5copies/ml), and *Ruminococcus flavefaciens* (1.51 × 10^3 copies/ml) while the highest methanogen quantity was observed in non-supplementation of *E. faecium* with 2.74 × 10^1 copies/ml). Addition of *E. fecalis* SROD5 changed the archaeal communities of in vitro rumen fermenta. Supplementation of 0.1% *E. fecalis* SROD5 increased microbial

population and decreased methanogen quantity.

Key Words: *Enterococcus fecalis* SROD5, in vitro, pyrosequencing

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1643 Effects of dietary neutral detergent fiber and starch ratio on rumen epithelial cell morphological structure and gene expression in dairy cows.

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Dietary neutral detergent fiber (NDF):starch ratio has been considered a potential indicator to reflect carbohydrate composition in diet formulation and could affect the composition and content of VFA in rumen of dairy cow. Rumen epithelial papilla as small bumps of the rumen mucosal epithelium could broaden the surface of the rumen, which was beneficial for improving the absorption ability of nutrients, especially for VFA. This study was designed to investigate the effect of dietary NDF:starch ratio on rumen epithelial cell morphological structure and gene expression. Eight primiparous dairy cows including 4 rumen cannulated animals were assigned to 4 total mixed rations with NDF:starch ratios of 0.86, 1.18, 1.63, and 2.34 from T1 to T4 in a replicated 4 × 4 Latin square design. The duration of each period was 21 d including a 14 d adaptation period and a 7 d sampling period. Rumen epithelial papilla was collected from rumen cannulated cows. Morphological structure of rumen epithelial papilla was detected and several genes related to the absorption and metabolism of VFA and growth of rumen epithelial papilla cell were analyzed with quantitative real-time PCR, including NHE1, NHE3, NHE4, MCT1, MCT2, MCT4, Na/KATPase, HMGCS, ACSS1, ACSS2, ACSS3, HMGCL, ACAT1, IGFBP3, IGFBP5, and IGFBP6. The results showed that the thickness of stratum spinosum and basale was linearly increased with increasing of dietary NDF:starch ratio (39.58^{a}, 42.84^{a}, 43.24^{a}, and 54.22^{b} mm for T1 to T4, $P = 0.02$), which indicated that surface of the rumen wall could be broadened and the absorption capability of VFA could be improved with the increasing dietary NDF: starch ratio. Expression of HMGCS as the limited enzyme in synthesis of ketone body metabolized by VFA was linearly downregulated ($P = 0.02$), while the expression of MCT2 positively correlated with the absorption capability of VFA was linearly upregulated with the dietary NDF:starch ratio increasing ($P < 0.01$). As dietary NDF:starch ratio increased, expression of IGFBP5 related to the growth of rumen epithelial papilla was downregulated ($P < 0.01$), while IGFBP6 expression was upregulated ($P < 0.01$), which were regulated by the short-chain fatty acids (SCFA) part of VFA. Dietary NDF:starch ratio significantly improved the thickness of stratum spinosum and basale of rumen epithelial papilla and regulated genes expression of VFA absorption and metabolism and growth of rumen epithelial cell, which may be indicative of an activated response of VFA absorption improvement with dietary NDF:starch ratio increasing.

Key Words: dairy cow, NDF: starch ratio, rumen epithelial cell morphological, gene expression

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1644 Rumen disappearance of capsaicin and dihydrocapsaicin in lactating dairy cows.

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The objective of this study was to assess rumen disappearance rate and escape of the two main active compounds of *Capsicum* oleoresin, capsaicin (CAP), and dihydrocapsaicin (DHC), in lactating dairy cows. The study involved 4 early- to late-lactation Holstein cows (24 ± 2.9 kg/d DMI; 38 ± 5.2 kg/d milk yield; 624 ± 28 kg BW) and consisted of 3, 10-d experimental periods. *Capsicum* oleoresin (CO) was administered into the rumen of the cows at 3 pulse-doses: 250, 500, and 1000 mg/cow. All cows received 250 mg CO in period 1500 mg in period 2, and 1000 mg in period 3. Chromium-EDTA was used as a rumen fluid phase passage rate marker. On day one of each experimental period, CO and Cr-EDTA solutions were administered intraruminally in each cow through the rumen cannula at the time of feeding (cows were fed once daily around 8 a.m.). Rumen fluid samples were collected at 0 (background), 0.5, 1, 2, 6, 12, and 24 h post-CO administration and analyzed for Cr, CAP, and DHC. Concentration data were fitted to a single exponential decay model using the NLIN procedure of SAS. The rate of degradation of CAP or DHC was found as: $k_{Cr} \div k_{CAP}$ or $k_{DHC} \times 100$, where k_{Cr} is the slope of decline in Cr concentration in ruminal fluid (on average 0.25 ± 0.06 h^{-1}) and k_{CAP} or k_{DHC} are slopes of decline in CAP and DHC concentrations. Rumen disappearance rates of CAP were 1.34 ± 0.711, 0.91 ± 0.248, and 1.50 ± 0.309 h^{-1} for 250, 500, and 1000 mg CO, respectively. Rumen disappearance rates of DHC were 2.22 ± 1.018, 1.82 ± 0.336, and 1.62 ± 0.372 h^{-1}, respectively. Rumen escape of CAP was estimated at 15.4, 32.6, and 17.6%, respectively, and that of DHC was 31.7, 19.3, and 16.1%, respectively. Average concentration of DHC in fecal samples was 35.6 ± 6.05 ng/g with the 1000 mg dose, whereas capsaicin was not detected in feces. CAP and DHC concentrations were 361 ± 52.6 and 203 ± 27.9 ng/mL in milk, respectively, with the 1000 mg dose, and the compounds were not detected in milk from non-treated cows. In this study, rumen escape of CAP and DHC in lactating dairy cows was

between 15.4 and 32.6%, depending on dose.

Key Words: capsaicin, dihydrocapsaicin, rumen disappearance

1645 WS Effects of capsaicin source on blood capsaicin, glucose and insulin concentrations, rumen fermentation and nitrogen balance of sheep.

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This study evaluated the bioavailability of ruminally-protected capsaicin, and potential effects on rumen microbial fermentation, diet digestibility, and N retention of sheep. Twenty-one wether lambs (36.1 ± 1.0 kg BW) were used in 2 experimental periods (19 d each) based on BW (9 and 12 lambs in period 1 and 2, respectively). From d 1 to 7 of each period, lambs were adapted to indoor individual pens, and then moved to metabolism crates from d 8 to 19. Lambs were fed twice daily alfalfa hay and 1 of 3 supplements containing no capsaicin (CON), unprotected capsaicin (DCAP), or ruminally-protected capsaicin (RPCAP). On d 14 and 19, blood samples were collected at 0, 0.5, 1, 2, 4, 8, and 12 h, and on d 19 rumen fluid samples were collected 4 h after supplement delivery. Feces and urine were collected once daily for 5 d. The experiment was a randomized complete block, and the model included treatment, h, and treatment × h. Capsaicin was not detected in serum of lambs, and no treatment × h interactions ($P \geq 0.06$) occurred for plasma glucose or insulin on d 14 or 19. Total VFA concentrations were lowest for DCAP, intermediate for RPCAP, and greatest for CON ($P = 0.05$). Acetate proportions (mol/100 mol) tended to be lower ($P = 0.06$) for DCAP than CON and RPCAP. Fecal excretions of DM, OM, NDF, and ADF were lower ($P < 0.01$), and DM, OM, NDF, and ADF digestibility (% of intake) were greater ($P < 0.01$) for lambs fed DCAP than CON and RPCAP. Nitrogen intake, fecal and urinary N, N digestibility, and N retention were not affected ($P \geq 0.15$) by treatments. Greater differences in rumen VFA concentrations between DCAP and CON than RPCAP and CON suggest that shifts in microbial fermentation were greater when capsaicin was not ruminally-protected in a prill. Undetectable capsaicin in serum of lambs receiving capsaicin, and minimal effects of RPCAP on N balance indicates the concentration of capsaicin provided may not have entered systemic circulation. This could be due to potential microbial breakdown, inability to be absorbed, or rapid post-absorptive metabolism. Further work is warranted to develop a source of absorbable capsaicin that will withstand degradation in the rumen to allow an increase in blood capsaicin to serve as a potential anti-inflammatory supplement in ruminants.

Key Words: capsaicin, ruminally-protected, sheep

Fig 1646.

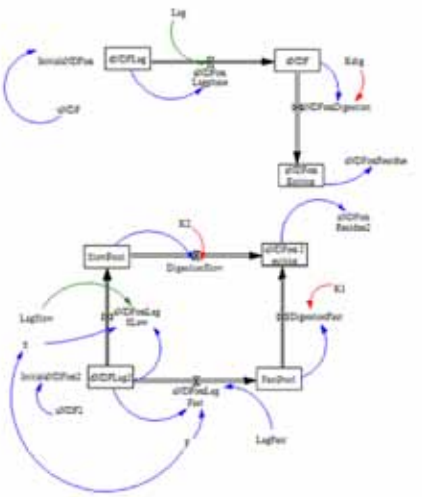

Figure 1. Multi compartment model describing in-vitro aNDFom digestion.

1646 Describing aNDFom in vitro digestion with a multi-compartment model and evaluation of predictions in the CNCPS v7.0 model.

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Models such as the CNCPS rely on having accurate values for digestion rate to aid in predicting metabolizable energy and protein yield from the rumen and subsequent milk yield and total tract digestibility. In vitro aNDFom digestion displays a sigmoidal shape, which is the result of a two-step process: the lag phase, where bacteria attach to substrate and establish digestion and the digestion phase where substrate is being degraded. In previous mechanistic models, the lag phase was discrete, meaning that aNDFom digestion could occur only after the lag phase was over. In other statistical models aNDFom digestion has been described with a multi-compartment system using γ functions. Such models can describe the sigmoidal shape of aNDFom digestion but the estimated rate of digestion were probabilistic and not deterministic. The objective of this study was to develop a mechanistic model that describes the sigmoidal behavior of in vitro aNDFom digestion, using differential equations to provide deterministic values of digestion rates. The proposed are multi-compartments models (Fig. 1), one describing aNDFom in plant by-products, where the digestible aNDFom fraction (dNDF) is unique; and the other describing aNDFom digestion in forages, where dNDF is further fractionated into fast and slow digesting pools. In both feed types a fraction remains un-digested over time (uNDF). In these models, the lag phase is a rate, the life-time of the dNDF fractions is consistent with a γ distribution, and the behavior of the system is sigmoidal. The model was fitted to 36 conserved forages, 32 fresh forages; and 15 plant by-products analyzed in-vitro. The quality of fit was evaluated with overall slope (1.03), intercept (0.01), R^2 (0.98), and an

RMSE (0.02) of the regressions of observed versus predicted. Further, the relevance of the model predictions were assessed by evaluating the RMSE of CNCPS predictions of ME allowable milk and aNDFom TTD, using information from a lactating cattle study where treatment diets were formulated to quantify the effects of aNDFom source and digestibility. Parameters of aNDFom digestion were calculated for each ingredient of the diets, and used as inputs for CNCPSv7.0. The experimental design was a 3 x 3 Latin square with 21 d adjustment and 5 d sampling periods this was used to develop the RMSE calculations. The RMSE of predictions among the three treatments were 0.8 Kg for ME allowable milk and 4% for aNDFom total tract digestibility.

Key Words: aNDFom, modeling, multi compartments model

1647 WS mammalian hormones associated with stress impact microbial fermentation of rumen fluid in vitro. L. L. Rath*, K. L. Samuelson, A. L. Salazar, F. A. Lopez, E. J. Scholljegerdes, and C. A. Loest, *New Mexico State University, Las Cruces.*

Mammalian stress hormones may negatively impact bacteria found in the digestive tract, which could be harmful to animals undergoing stress such as newly received cattle. This study evaluated the effects of epinephrine, norepinephrine, and cortisol on rumen microbial fermentation and gas production in vitro. Treatments included no stress hormone (CON), epinephrine (EPI), norepinephrine (NOR), cortisol (CORT), and a combination of EPI, NOR, and CORT (ALL). Catecholamine treatments were added to fermentation flasks at 1.125 ng/mL, and the cortisol treatment was added at 1.15 ng/mL of rumen fluid. At initiation of the study, rumen fluid was collected from two ruminally-cannulated cows, homogenized with McDougal's artificial saliva, and inoculated with one of 5 treatments for 5 consecutive periods. The rumen microbial fermentation products ammonia (NH_3) and volatile fatty acids (VFA) were sampled at h 0, 2, 4, 6, 8, and 12 during each of the first 4 periods to produce a total of 120 in vitro fermentation samples. The pH was also measured at each collection time. Gas production was measured during the final period at h 0, 0.25, 0.5, 0.75, 1, 1.5, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, and 12 from 24 fermentation flasks in which the 5 treatments were present in 4 replicates allowing for 4 blanks. Neither pH, NH_3, nor total VFA concentration were different ($P \geq 0.40$) among treatments. Molar percentages of acetate and isovalerate in rumen fluid were lower ($P < 0.01$) for EPI and NOR than CON, CORT, and ALL. Conversely, molar percentages of butyrate in rumen fluid were greater ($P = 0.03$) for EPI and NOR than CON, and intermediate for CORT and ALL. A treatment × hour interaction ($P < 0.01$) was observed for gas production from 8 h of incubation to the culmination of this experiment, indicating that microbial fermentation is altered by treatments.

Key Words: catecholamine, cortisol, fermentation

1648 RNA sequencing reveals differential expression of genes associated with an altered morphology of rumen papillae in lactating dairy cows fed diets with various forage sources. B. Wang[1], D. M. Wang[1], M. Liu[1], X. B. Wang[1], L. L. Guan[*2], and J. X. Liu[1], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Rumen epithelial wall plays an important role in nutrient absorption and animal health. However, whether forage quality affects rumen epithelial morphology is unclear. The current study was conducted to elucidate the effects of forage quality on rumen epithelial morphology and the potential underlying molecular mechanisms by determining the transcriptome of the rumen epithelium. To achieve these goals, eighteen mid-lactation dairy cows were fed three diets containing different forage sources, including alfalfa hay ($n = 6$, AH), corn stover ($n = 6$, CS), and rice straw ($n = 6$, RS), for 14 wk. The particle size of each diet, ruminal volatile fatty acids, and rumen epithelium thickness were determined, and RNA-sequencing was conducted. The dietary effect on gene expression was investigated by characterizing differential expressed genes through pair-wise comparisons (AH vs. CS, AH vs. RS, CS vs. RS). The concentration of volatile fatty acids in the rumen was greater in AH than in either CS or RS ($P < 0.05$). The thickness of the rumen papillae was greater in RS-fed cows than in cows fed AH or CS ($P < 0.05$), whereas the thickness of the papillary epithelium was reduced in CS-fed cows compared with those fed AH or RS ($P < 0.05$). In total, 37, 47, and 30 differentially expressed genes were identified from pair-wise comparisons between AH vs. CS, AH vs. RS, and RS vs. CS, respectively. Functional analysis revealed these genes involved in ion binding, proliferation and apoptotic processes, and regulation of cellular growth involving extracellular matrix proteins. Our results suggest that forages with different particle sizes and nutrients values affected rumen epithelium morphology by impacting ion binding, cell growth, and cell proliferation/apoptosis. Our findings provide insight into fundamental understanding on the effects of the dietary particle size and nutrient composition on rumen function that are needed for better management of dairy cow feeding.

Key Words: forage particle size, RNA sequencing, rumen epithelial morphology

1649 Effect of ruminal inoculum from bison or cattle on in vitro gas production, feed digestibility, and responses to exogenous enzyme supplementation.

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The objective of this study was to evaluate the effects of increasing the proportion of inoculum from bison vs. cattle with and without feed enzyme (FE) supplementation on in vitro fermentation of barley straw (BS), alfalfa hay (AH), and wheat dried distillers grain with solubles (DG). Two batch culture runs were conducted for each substrate examined. Barley straw and AH were ground through a 1-mm screen and DG was incubated as-is. In run 1, inocula were prepared by combining rumen fluid (vol/vol) of cattle fed a diet containing 70% BS and 30% concentrate (DM basis) and bison rumen fluid (unknown diet) at ratios of 100:0, 67:33, 33:67, and 0:100, respectively. The substrates were incubated for 96 h to determine gas production (GP) kinetics with gas pressure recording at 3, 6, 9, 12, 24, 36, 48, 72, and 96 h. Additionally, DM disappearance (DMD) was determined in run 2. Each run was a completely randomized design without or with FE addition at a rate of 2.0 μL/g substrate DM. The FE was a xylanase–glucanase commercial blend. Asymptotic GP (ml/g DM) of BS (254) and AH (263) was not affected, whereas that of DG responded quadratically (244, 240, 238, and 260; $P < 0.04$) with increasing bison inoculum. Rate of GP (%/h) also responded quadratically for BS (1.6, 1.6, 1.2, and 1.7%/h; $P < 0.01$) and AH (3.0, 3.0, 2.7, and 3.0%/h; $P < 0.03$) with increasing bison inoculum. Lag time of GP linearly ($P < 0.01$) decreased for BS (0.58, 0.93, 0.22, and 0.07 h), AH (0.63, 0.61, 0.29, and 0 h) and DG (0.21, 0.64, 0.11, and 0 h) with increasing bison inoculum. A quadratic ($P < 0.02$) response of DMD (31, 36, 35, and 34%) of BS to increasing bison inoculum was observed, whereas DMD of AH (55, 54, 51, and 51%) and DG (59, 58, 56, and 56%) linearly ($P < 0.01$) decreased. Addition of FE improved ($P < 0.05$) DMD of DG. Compared to cattle inoculum, bison inoculum did not enhance in vitro GP or DMD of the substrates examined. However, the mixture of cattle and bison rumen inocula did appear to synergistically reduce the lag time of GP and improve the DMD of BS. It suggests that the cattle rumen inoculum may lack certain enzymes that were present in the bison inoculum to digest BS, and that these enzymes were not provided by the FE examined.

Key Words: gas production, in vitro digestion, rumen inocula

1650 Ruminal fermentation from Nellore steers supplemented with additives in the rainy season.

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This trial aimed to evaluate the ruminal parameters (pH, ammonia-N and the VFA production) from animals fed supplements with monensin (MON), virginiamycin (VM) or both associated, in the rainy season. Twelve steers cannulated in the rumen (518.42 ± 55.40 kg) were housed in 12 paddocks (one animal on each paddock) of Brachiaria cv. 'Xaraés' and supplemented daily in 0.3% of BW. The diets were: supplement without additives (SUP), with MON (SUPM- 80 mg/kg), with VM (SUPV- 150 mg/kg) and supplement with MON and VM (SUPMV- 80 and 150 mg/kg, respectively). There were four experimental periods of 28 d (27 d for adaptation and 1 d for sampling). Animals were housed continuously in the paddocks with animals used in a trial for performance evaluating. Ruminal pH, ammonia-N, and VFA were measured on samples taken over a 12 h on Day 28 of each experimental period. Ruminal content was obtained at 0, 2, 4, 6, 8, 10, and 12 h after the period of feeding (1000 am). Data were analyzed as a completely randomly design with three replicates by treatment on each period, using the MIXED procedure of SAS. The pH, ammonia-N and VFA were analyzed as a repeated measure. The means of least squares were generated and compared ($P < 0.05$) by Tukey test. The ruminal pH from animals supplemented with additives were greater than animals supplemented without additives ($P < 0.01$), already for the concentrations of ammonia was not significant effect ($P = 0.09$). The acetate ($P < 0.01$) and propionate concentrations ($P < 0.01$) were lower in animals supplement with additives than animals supplemented without additives. However, the A:P ratio did not change ($P = 0.13$) with the inclusions of additives in supplements. The inclusion of MON, VM or both associated in supplements to fed steers on pasture in the rainy season increases the ruminal pH, decreases the acetate and propionate concentrations without affect the A:P ratio.

Key Words: monensin, pasture, propionate, ruminal pH, virginiamycin

1651 The micro gas test: A small scale in vitro system for high throughput analysis. K. Elberg[1], P. Steuer[*2], U. Habermann[2], J. Lenz[2], M. Nelles[1,3], and K. H. Südekum[4], *[1]Department of Waste Management and Material Flow, University of Rostock, Rostock, Germany, [2]Senzyme GmbH, Troisdorf, Germany, [3]German Biomass Research Center GmbH, Leibzig, Germany, [4]Institute of Animal Science, University of Bonn, Bonn, Germany.*

The evaluation of ruminal degradability of feeds and feed additives requires the knowledge of characteristic (kinetic) parameters. These parameters are mainly obtained using in vitro gas production methods. These include measurements at constant pressure (e.g., Hoheneheim gas test (HGT)), measurements at constant volume with accumulating pressure and measurements at constant volume with regular venting. To facilitate automated high throughput measurements, a small-scale system, based on pressure measurement with interval venting was developed and validated. The micro gas test [MGT] represents a cheap and versatile in vitro batch method which reduces the required inoculum volume as well as the personnel effort and space requirements significantly. The MGT is conducted in 20 mL gas chromatography vials that serve as reactors for gas production. Samples (e.g., feedstuffs) and reagents (e.g., feed additives) are accurately weighed into the vials and subsequently closed with a gas-tight sealing. The regulation of CO_2 atmospheric condition is realized through previous gas application. The ruminal fluid solution, which serves as inoculum, is prepared according to the HGT standard procedure. Incubation is performed in a heating chamber at 39°C and starts with dispensing 5 mL inoculum through a cannula into the sealed vial. Simultaneously the pressure is released through a second cannula to atmospheric pressure. For 24 and 48 h, respectively, relative pressure increase in the headspace above the sample is recorded at predefined intervals and subsequently vented. Measurements can be performed manually with manometers or automatically with adjusted autosampling systems. For the validation of the MGT a total of 14 feedstuffs, including a hay and a concentrate standard, were simultaneously incubated in the HGT and the MGT system. The same substrate-inoculum-ratio was applied for further comparison of kinetic parameters. The dried and ground (< 1 mm) feedstuffs covered a wide range of chemical compositions and digestibilities. The HGT method was prepared according to standard procedure. Compared to HGT the MGT resulted in lower ($P < 0.05$) maximum gas productions for all feedstuffs except lignocellulose. The differences were congruent to former findings on system comparisons between HGT and methods with constant volume and pressure release. However, a strong relationship between the HGT and MGT 24 h gas production could be observed. The regression analysis of mean values of both methods resulted in the equation: y = 0.87x + 1.62 with an R^2 of 0.99.

Key Words: automation, Hohenheim gas test, pressure measurement

1652 Rumen protozoal community structures are not altered in lactating dairy cows offered alternative forage crops during short-term grazing experiments. L. M. Cersosimo[*1], R. Tacoma[1], S. Greenwood[1], K. Juntwait[2], A. F. Brito[2], and J. Kraft[1], *[1]University of Vermont, Burlington, [2]University of New Hampshire, Durham.*

The objective of this study was to compare the rumen protozoal community structures and VFA in cows grazing pasture strip-tilled with alternative forage crops (AFC) or traditional grass-legume pasture mix. The study consisted of two, 21-d experiments, spring (SPR) and summer (SUM). Sixteen lactating Jersey cows (SPR: 85 ± 46 DIM; SUM: 143 ± 58 DIM) were split into two groups with eight cows assigned to the AFC (treatment, TRT) and eight cows assigned to traditional mixed grasses-legumes (control, CON). Pasture comprised 40% of the diet (DM basis), while a TMR comprised 60%. SPR AFC (2.4% of total DM) included barley, hairy vetch, rye, triticale, and wheat, and SUM AFC (10.0% of total DM) included buckwheat, oats, and chickling vetch. Milk samples were collected for four consecutive milkings (d 19–21). Individual whole rumen digesta samples (500 mL) were collected on d 20 and 21 of each experiment. Ruminal VFA samples were analyzed by GLC. Microbial DNA was extracted and the V3-V4 regions of the protozoal 18S rRNA gene were amplified via PCR. The program MOTHUR was used to perform bioinformatics analyses. A student's *t* test (JMP Pro 12) compared the LSM between groups and the PROC CORR model in SAS (v.9.4) performed Pearson correlations between rumen protozoal genera, animal performance, and VFA. Yields of milk, milk fat, and milk protein (kg/d) in SPR were: CON, 22.5; 1.08; 0.80 and TRT, 23.4; 1.15; 0.85 and in SUM: CON, 17.3; 0.74; 0.59 and TRT, 18.9; 0.92; 0.70, respectively. Total VFA (m*M*), and molar proportions of acetate (70.8%), propionate (16.0%), and butyrate (1.93%) did not differ in either experiment. The SUM TRT group had a lower ($P < 0.01$) isobutyrate proportion (0.80%) than the SUM CON group (0.98%). Abundance of protozoal taxa did not differ between groups in either experiment. The protozoal genera *Eudiplodinium* (CON: 43.0%; TRT: 49.3%) and *Entodinium* (CON: 48.1%; TRT: 37.1%) were most abundant in SPR and SUM, respectively. The protozoal genus *Diplodinium* (SPR: 6.48%; SUM: 3.28%) was positively correlated ($P < 0.001$) with milk production ($r = 0.69$), milk fat ($r = 0.64$), protein yields ($r = 0.61$), and ruminal propionate ($r = 0.38$; $P = 0.04$). The protozoal genus *Entodinium* was negatively correlated with milk yield ($r = -0.48$; $P < 0.01$). In conclusion, the rumen protozoal community structures and predominant VFA were not altered in AFC-fed cows, yet the genus *Diplodinium* was positively

correlated to animal performance and VFA.

Key Words: ciliates, *Diplodinium,* organic

1653 Metabolomics analysis reveals effect of corn silage levels on ruminal metabolic profiles in Holstein heifers.

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Controlling DMI could be one of the strategies to reduce feed cost and to increase efficiency in dairy heifer growth, whereas the metabolic mechanisms involved in control feeding have not been well examined. The objective of this study was to determine the effect of differing forage-to-concentrate ratios on the ruminal metabolite profiles in heifers under restricted feeding. Twenty-four Holstein heifers (8–10 mo and 253 ± 29 kg of BW) with similar body condition were randomly assigned into four groups and fed diets containing 20% (F20), 40% (F40), 60% (F60), and 80% (F80) of corn silage. All diets were isonitrogenous and isocaloric and provided equal amount of nutrients, and allowed for 800 g/d of ADG. The amount of feed offered was adjusted weekly based on BW. Total tract apparent digestibility of nutrients was determined with acid-insoluble ash as an internal digestibility marker with the TMR and fecal samples. Rumen fluid was sampled from each cow through a stomach tube 4 h after morning feeding at d 30 and analyzed using gas chromatography-time-of-flight/mass spectrometry. The digestibilities of DM (80.9% for F20, 79.4% for F40, 77.2% for F60, and 73.1% for F80, $P < 0.001$) and OM (84.3%, 82.3%, 80.1%, and 76.1%, respectively, $P < 0.001$) decreased linearly with increased corn silage. In total, 247 metabolites were identified from all four groups. The principal component analysis of the relative concentration of mutual metabolites revealed four separated metabolite profile clusters of four groups. The clusters derived from the F40, F60, and F80 partly overlapped with each other, whereas the cluster from the F20 was separated from the other three groups. When the mutual metabolites were used for pathway analysis, the impact values of the pathway were 0.32, 0.23 and 0.21 for pyruvate metabolism, citrate cycle and lysine degradation, respectively. These three pathways may play important roles in improvement of nutrition degradation and utilization. These indicated that lower forage level could promote rumen fermentation and provide more available nutrition for heifers.

Key Words: corn silage levels, heifers, metabolomics

1654 Response of rumen microbiota to diets containing different corn silage levels in Holstein heifers.

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Ruminants have evolved through a close symbiotic relationship with a vast ensemble of ruminal microbiota, which give important metabolic capabilities on the host. The objective of the present study was to evaluate effects of dietary corn silage levels on the changes in the microbiota of the rumen in Holstein heifers. Twenty-four half-sib Holstein heifers (8 to 10 mo of age) were blocked by BW and age in a randomized complete block design in equal numbers and assigned randomly to one of the four diets containing corn silage levels at 20, 40, 60, or 80% of DM. All diets were provided as TMR and calculated to meet the nutrition requirement of 800 g/d of ADG. The rumen contents were collected by the oral stomach tube method. Total genomic DNA of ruminal microorganism was extracted from the whole ruminal contents containing solid and liquid fractions. The V3-V4 region of the bacteria 16S rRNA gene (primers 336F and 806R), ITS1 region of the internal transcribed spacer region of fungi (primers ITS1-F and ITS2), and the partial 18S rRNA gene of protozoa (primers P-SSU-316F and GIC758R) were amplified by PCR. Paired-end sequencing was performed to sequence all libraries on an Illumina Miseq platform according to the standard protocols. For bacteria, a total of 1,544,372 valid reads and 202,189 OTUs were obtained by pyrosequencing. At the OTU level, a significant difference was found in the bacterial communities among all the treatment groups (AMOVA, $P < 0.05$), except that between the 40% and 60% forage groups (AMOVA, $P = 0.23$). The total number of valid reads and OTUs obtained for protozoa were 1,302,936 and 15,279. At the OTU level, a significant difference was found in the protozoal communities between the 20% and 60% forage groups (AMOVA, $P < 0.05$), between the 20% and 80% forage groups (AMOVA, $P < 0.05$), and between the 40% and 80% forage groups (AMOVA, $P < 0.05$). For anaerobic fungi, a total of 1,231,562 valid reads and 33,427 OTUs were obtained. At the OTU level, no significant difference was found in the fungal communities among all the treatment groups. This study demonstrated that the bacterial and protozoa communities in the rumen of Holstein heifers were altered at the OTU level by the dietary forage levels.

Key Words: forage level, heifer, ruminal microbe

1655 Effect of acetate addition and headspace gas composition on in vitro production of volatile fatty acids and gases. L. M. Judd* and R. A. Kohn, *The University of Maryland, College Park.*

The development of in vitro methods to accurately estimate gas production and volatile fatty acid (VFA) profile in rumen fermentation would enable isolation of fermentation effects from animal interactions. This experiment compared 4 headspace gas combinations with or without addition of 50 mM sodium acetate. Gas headspace treatments were: 1) CO_2 (100%), 2) CO_2–CH_4 (50/50), 3) CO_2–H_2 (95/5), and 4) CO_2–CH_4–H_2 (47.5/47.5/5). Each treatment was replicated in 4 tubes with repeated measures of VFA and gas volume taken at 0, 4, 16, 24, and 48 h. Timothy hay (0.1 g) was added to 20-mL tubes, and 0.5 mL sodium acetate solution or buffered medium were added to each tube. Tubes were equilibrated with each gas mixture before adding 9.5 mL rumen fluid. Tubes were incubated at 39°C while shaking with 20-mL syringes attached to collect and measure produced gases. Butyrate production at 4 h was affected ($P < 0.05$) by gas composition, and was: 2.96, 3.09, 2.33, and 1.44 (mM; SE ± 0.437) for treatments 1–4. Propionate production at 48 h was affected ($P < 0.05$) by gas composition, and was: 8.71, 8.97, 10.60, and 7.12 (mM; SE ± 0.789) for treatments 1–4. Gas production at 4 h was 1.08, 2.70, 0.98, and 1.43 (ml, SE ± 0.327) for treatments 1–4. Lower starting concentration of CO_2 in headspace gas may have caused CO_2 efflux from the buffer. There was a trend ($P < 0.1$) for an effect of the gas mix at 24 h on the acetate: butyrate (A:B) ratio of produced VFA. A:B ratios of produced gases were: 2.95, 2.77, 2.87, and 2.18 (mM; SE ± 0.208) for treatments 1–4. In contrast to expectation, there was a trend ($P < 0.08$) for greater acetate production with acetate addition (10.71 mM) than without (7.11 mM, SE ± 1.413). Initial gas composition of in vitro procedures can affect gas production and VFA profiles with higher percentage of CH_4 and H_2in headspace (more reduced conditions) favoring propionate and butyrate over acetate and gas production.

Key words: fermentation, gas profile, in vitro, volatile fatty acids

1656 Predicting the time course of ruminal pH from continuous reticular pH measurements. D. J. Seymour*[1], K. M. Wood[2,3], J. P. Cant[1], and G. B. Penner[2], *[1]Department of Animal Biosciences, University of Guelph, Guelph, Canada, [2]Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada, [3]University of Saskatchewan, Saskatoon, Canada.*

While the ability to continuously measure ruminal pH has been developed, its use is limited by its on-farm practicality. Being able to predict ruminal pH with an orally bolus-dosed reticular pH probe would add increased functionality to existing technology and aid in the diagnosis of SARA. The objective of this study was to develop a model to predict the time course of ruminal pH from continuous reticular pH measurements. pH was recorded every 5 min for 15 d in both the reticulum and rumen of 4 Hereford crossbred heifers (291 ± 8kg BW) as the proportion of concentration in the diet increased every 3 d from 50 to 60, 70, 80, and 88%. Visual inspection of pH time series data revealed that fluctuations in ruminal pH were smaller and lagged behind those of reticular pH. Fitting a polynomial distributed lag model to predict ruminal pH from reticular pH produced residuals that were serially correlated. Because residuals are not available for prediction of ruminal pH with only a reticular pH probe, a novel approach to autocorrelation correction was sought. Based on the hypothesis that over- and underprediction of ruminal pH is related to similar errors in reticular pH, a penalized cubic spline function was fit to time series of reticular pH to generate a smoothed predicted reticular pH curve with residuals. Ruminal pH was then estimated from predictions and residuals of the reticular spline function using the MIXED procedure of SAS. As an alternative, ruminal pH was predicted directly from reticular pH using an unobserved components model (UCM). The predictive ability of both methods was evaluated using 10-fold cross validation. The unobserved components model was able to fit the data better compared to the alternative model (RMSE = 0.26414 vs. 0.47120) though with a higher AICc score (−10356 vs. −21021); this can be resolved by log-transforming the data before analysis. The UCM also had a smaller average error in ruminal pH prediction compared to the alternative model (0.22 pH vs. 0.35 pH) with fewer model parameters (5 vs. 11). The low error is sufficient to predict ruminal pH from continuous reticular pH measurements, allowing for a more cost-effective diagnosis of SARA in near real-time using existing reticular pH probes.

Key Words: SARA, ruminal pH, unobserved components model

1657 Changes in milk production efficiency and ruminal bacterial community composition following near-total exchange of ruminal contents between high- and low-efficiency Holstein cows. P. J. Weimer*[1], M. S. Cox[2], T. Vieira de Paula[3], M. Lin[4], and G. Suen[2], *[1]USDA-ARS, Madison, WI, [2]University of Wisconsin-Madison, Madison, [3]Federal Univ. of Mato Grosso, Cuiabá, Brazil, [4]Yangzhou University, Yangzhou, China.*

The objectives of this study were to determine if milk production efficiency (MPE) could be altered by near-total exchange of ruminal contents between high- and low-MPE cows and to characterize ruminal bacterial community composition (BCC) before exchange and over time post-exchange. Three pairs of ruminally cannulated, third-lactation cows were selected whose MPE (energy corrected milk per unit dry matter

intake [ECM/DMI]) at similar levels of ECM differed over their first two lactations when fed the same total mixed ration. At 79–279 DIM, ~95% of ruminal contents were manually exchanged between cows within each pair. Ruminal pH, and concentrations and proportions of VFA, along with BCC (as determined by 16S rRNA gene sequencing on an Illumina MiSeq) were assessed immediately before and after the exchange, and just before feeding on days −8, −7, −5, −4, −1, 1, 2, 3, 7, 10, 14, 21, 28, 35, 42, and 56, relative to the day of exchange. Where ruminal pH or mol fraction of individual VFA differed ($p < 0.01$) between cows before exchange, they returned to the recipient cow's profile within 1 d. For all 3 low-MPE (LE) cows, MPE increased over 7 d post-exchange but declined thereafter. Two of the 3 high-MPE (HE) cows displayed sharp drops in MPE following introduction of the ruminal contents from the corresponding LE cow, but one surprisingly displayed a transient increase in MPE. For all 6 cows, both liquid- and solids-associated BCC were dissimilar between individuals within a pair before contents exchange. Immediately following exchange, BCC in all three pairs for both phases were more similar to that of the received inoculum than to pre-exchange BCC for that individual. For 5 of 6 cows, the solids-associated community returned within 5–7 d to higher similarity to the pre-exchange community of that host than to the donor community. Individual variability before the exchange was greater in liquids than in solids, as was the variability in the response of their bacterial communities to the exchange. One pair showed rapid return to pre-exchange BCC within 2 d, while the other two pairs took 7–10 d to become more similar to the pre-exchange host than the donor, and continued to change until reaching similarity to the pre-exchange community by 5–7 wk post-exchange. The data suggest a role for the ruminal bacterial community as a variable in MPE.

Key Words: milk production efficiency, ruminal contents exchange, ruminal microbiome

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1658 Synergism of cattle and bison inoculum on ruminal fermentation and bacterial communities in an artificial rumen (Rusitec) fed barley straw.

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This study evaluated the effect of increasing the proportion of bison relative to cattle inoculum on fermentation and microbial populations within an artificial rumen (Rusitec) fed barley straw. The experiment was a completely randomized design with four treatments (0, 33, 67, and 100% of bison inoculum replacing cattle inoculum) replicated in two Rusitec apparatuses with 8 fermenters each ($n = 4$/treatment). The experiment lasted 15 d with 8 d of adaptation and 7 d of sampling. Fermenters were fed a diet of 70% barley straw and 30% concentrate (DM basis). True digestibility of DM (DMD) was determined after 48 h of incubation from d 13 to 15, and daily NH_3 and VFA production were measured on d 9 to 12. Protozoa counts were determined at d 9, 11, 13, and 15 and particle-associated bacteria (PAB) from d 13 to 15. Selected bacterial populations in the PAB were measured using real-time polymerase chain reaction (qPCR). Data were analyzed using the MIXED procedure of SAS. Individual fermenter was considered the experimental unit and day of sampling as a repeated measure. Increasing the proportion of bison inoculum had a quadratic effect ($P < 0.05$) on straw, concentrate and total DMD (50.3, 52.0, 52.8, and 50.3% DMD, respectively), and on straw and total NDF disappearance (NDFD). Increasing bison inoculum linearly increased concentrate NDFD, total and concentrate N digestibility, as well as total daily VFA and acetate production. A quadratic response ($P < 0.05$) was observed for daily ammonia-N, propionate, and butyrate production. Increasing the proportion of bison inoculum linearly increased ($P < 0.05$) total protozoa numbers and had a quadratic effect ($P < 0.05$) on *Fibrobacter succinogenes*, linearly increased ($P < 0.10$) *Ruminococcus flavefaciens* and decreased ($P < 0.05$) *Ruminococcus albus* 16S rRNA copy numbers. Overall, bison inoculum more readily degraded feed protein than cattle inoculum, with a mixture of inoculums synergistically increasing the DMD and NDFD of barley straw. Direct inoculation of rumen contents across ruminant species may be a means of increasing ruminal fiber digestion.

Key Words: bison, rumen inoculum, Rusitec

1659 Effect of peNDF on milk production and composition in goats fed with NNFS replacing alfalfa hay.

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The aim of this work was to evaluate the effect of physically effective neutral detergent fiber (peNDF) in diets with non-forage fiber sources (NFFS) replacing alfalfa hay on milk production and milk composition in dairy goats. The experiment was designed as 4 x 4 Latin square with 8 Alpine goats at final stage lactation. Goats were offered 1 of 4 diets with different peNDF, 2 diets with alfalfa hay (peNDF = 17.3 and 24.1%), and 2 diets with NFFS replacing alfalfa hay (peNDF = 22.3 and 26.8%). The peNDF contents were determined from the sum of the proportion of dietary DM retained either on the 2 or on the 3 sieves of the Penn State Particle Separator multiplied by the neutral detergent fiber concentration of the diet. Each period consisted of 11-d of adaptation stage and 3-d of experimental measurements. Subsequently, diets were exchanged during the other 3 periods. During the experimental days, milk production was recorded and milk fat,

Table 1659.

Table. Milk production and composition affected by peNDF of diets with NFFS replacing alfalfa hay

	peNDF					
peNDF	17.3%	24.1%	22.3%*	26.8%*	SE	P
Milk production (l/d)	1.26[b]	1.39[a]	1.21[b]	1.25[b]	0.16	0.043
Fat (%)	3.10[b]	3.22[b]	4.05[a]	4.41[a]	0.57	0.001
SNF (%)	8.63[a]	8.48[a]	8.53[a]	8.49[a]	0.17	0.397
Protein (%)	3.26[a]	3.20[a]	3.23[a]	3.21[a]	0.06	0.353

[a],[b] Between lines, means with the same letter are not significantly different

*Diets with NFFS replacing alfalfa hay

nonfat solids, and protein were determined using an infrared analyzer. Data were analyzed using GLM procedure of SAS. According to our results, milk production was higher in the diet that contained more alfalfa hay ($P = 0.043$) and milk fat was higher in both rations with NFFS ($P = 0.001$). There was no effect on milk nonfat solids ($P = 0.39$) and protein ($P = 0.353$). In conclusion, the substitution of NDF from alfalfa with NDF from NFFS modified the peNDF in rations without reduced milk production and milk fat in goats.

Key Words: dairy goats, milk production, peNDF

1660 Effects of conventional dietary adaptation over periods of 6, 9, 14, and 21 d on rumen morphometrics of Nellore cattle. D. D. Estevam[1], I. C. Pereira[1], A. L. Rigueiro[2], F. T. Pereira[2], C. L. Martins[1], M. D. Arrigoni[1], and D. D. Millen[*2], *[1]São Paulo State University (UNESP), Botucatu, Brazil, [2]São Paulo State University (UNESP), Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to determine the effects of adaptation periods of 6, 9, 14, and 21 d on rumen morphometrics, and cell death and proliferation of rumen epithelium of feedlot Nellore cattle. The experiment was designed as a completely randomized block, replicated 6 times, in which 96 20-mo-old yearling Nellore bulls (391.1 ± 30.9 kg) were fed in 24 pens (4 animals/pen) according to the different adaptation periods adopted: 6, 9, 14, and 21 d. Each of the adaptation diets containing 70.0%, 75.0%, and 80.5% concentrate were fed for 2-d, 3-d and 7-d to cattle adapted for 6-d, 9-d and 21-d, respectively. The adaptation diets containing 70.0%, 75.0%, and 80.5% concentrate were fed for 4-d, 5-d and 5-d, respectively, to cattle adapted for 14-d. The finishing diet contained: 71.5% cracked corn grain, 14.0% sugarcane bagasse, 10.5% peanut meal, 2.5% supplement, 1.0% urea, and 0.5% limestone (DM basis). After adaptation one animal per pen was slaughtered ($n = 24$) for rumen epithelium evaluations. The remaining 72 animals were harvested after 88-d on feeding. At harvest, a 1-cm^2 fragment of each rumen was collected from cranial sac. The number of papillae per cm^2 of rumen wall (NOP) was determined, as well as the mean papillae area (MPA). The rumen wall absorptive surface area in cm^2 (ASA) was calculated as follows: 1 + (NOP*MPA)–(NOP*0.002). The papillae area expressed as % of ASA was calculated as follows: (NOP*MPA/ASA)*100. The cell proliferation index (CPI) and cell death index (CDI), both expressed as % of cells proliferating or dying in the rumen epithelium, were determined by PCNA and TUNEL immunohistochemistry techniques, respectively. Orthogonal contrasts were used to evaluate linear, quadratic, and cubic relationship between adaptation periods and the dependent variable. As the adaptation period lasted longer, ASA in cm^2 was affected ($P = 0.03$) cubically (6-d = 37.7; 9-d = 32.5; 14-d = 40.9; 21-d = 39.6). An interaction was observed between adaptation periods and harvesting dates for papillae area ($P = 0.04$), CPI ($P = 0.003$), and CDI ($P = 0.02$), where cattle adapted in 14-d showed larger papillae area (6-d = 97.0%; 9-d = 96.0%; 14-d = 97.5%; 21-d = 96.8%), and smaller CPI (6-d = 58.0%; 9-d = 58.5%; 14-d = 44.8%; 21-d = 53.3%) and CDI (6-d = 62.8%; 9-d = 60.0%; 14-d = 50.4%; 21-d = 57.1%) at the end of adaptation period, but no differences were detected ($P > 0.10$) at the end of finishing period. Yearling Nellore bulls should be adapted in 14 d, because it promoted better rumen epithelium development by the end of adaptation period.

Key Words: adaptation, Nellore, rumen

1661 Pantothenic acid does not affect the concentration of biotin in plasma of Holstein bull calves. G. Ferreira*, C. L. Teets, A. N. Bladen, and A. Geiger, *Virginia Polytechnic Institute and State University, Blacksburg.*

Pantothenic acid interferes with biotin absorption in non-ruminant species. The objective of this study was to determine whether pantothenic acid affects the concentration of biotin in the blood of young calves. Weaned bull calves ($n = 16$) were fed ad libitum a pelleted starter including no B-vitamins and hay for 2 wk before the beginning and until the end of the experiment. Water was available ad libitum at all times. Two weeks after weaning, calves were blocked by age and randomly assigned to 4 treatments according to a randomized complete block design. Treatments consisted of administering, for 14 d, a daily gelatin capsule containing no B-vitamins (CON), 10 mg of biotin (Rovimix Biotin; BIO), 240 mg of pantothenic acid (Rovimix Calpan; PAN), and 10 mg biotin + 240 mg pantothenic acid (BIO+PAN). Expeller soybean meal was used as a carrier of the vitamins in the capsules.

Blood samples were collected by venipuncture of the jugular vein at Days 0 and 14. Concentrations of avidin-binding substances (ABS) in plasma (1:20 dilution) were determined by a single-step competitive enzyme-binding assay (Ridascreen Biotin kit; R-Biopharm GmbH, Darmstadt, Germany). Statistical analysis was performed using the MIXED procedure of SAS as for a randomized complete block design with repeated measures. The statistical model included the effects of treatment (fixed, df = 3), block (random, df = 3), treatment by block interaction (random, df = 9), time (fixed, df = 1), treatment by time interaction (fixed, df = 3), and the random residual error. The concentrations of ABS in plasma were similar for all treatments ($P > 0.24$) and did not change after dosing vitamins over time (3.47 and 3.07 ng/mL for Days 0 and 14, respectively; SEM = 0.7 ng/mL; $P > 0.63$). Plasma concentrations of ABS were substantially higher than those previously reported for lactating dairy cows (0.7–2.1 ng/mL). Based on these data, and contrary to our expectations, pantothenic acid did not affect the absorption of biotin in young calves.

Key Words: biotin, calves, pantothenic acid

1662 Short-term feeding of a tocopherol mix (α-, β-, γ-, and δ) alters the daily pattern of tocopherol isoforms present in milk and blood in lactating dairy cows.

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Fed over several weeks, diets supplemented with α-tocopherol will increase α-tocopherol concentrations in blood and milk. With new attention being paid to other non-α isoforms of vitamin E, how short-term supplementation of other tocopherol isoforms affects subsequent milk and blood concentrations is poorly understood. The objective of this study was to determine the daily pattern of change in the concentrations of 4 isoforms (α-, β-, γ-, and δ) of tocopherol in blood and milk of cattle supplemented with a tocopherol mixture. Four healthy, multiparous Holstein cows (DIM: 179 ± 17 d) were fed a vegetable-derived oil (Tmix) enriched with γ- and δ-isoforms of Vitamin E (9% α-, 1% β-, 62% γ-, and 24% δ-tocopherol) for 7 consecutive days (~620 g Tmix/cow·d^{-1}). Composite milk (~25mL) and whole blood (~15mL) samples were collected daily before the morning feeding. Tocopherol isoform concentrations were determined by high pressure liquid chromatography. Data were analyzed in a complete randomized design with repeated measures. Significance was declared at $P \leq 0.05$. Gamma and α-tocopherols in blood increased by d 1 and d 2, respectively, after feeding with peak concentrations achieved by d 5 (3.6 ± 0.2 μg/mL and 14.1 ± 0.5μg/mL, respectively) when compared to d 0 (0.59 ± 0.2μg/mL and 10.0 ± 0.5μg/mL, respectively). In milk, γ- and α-tocopherol concentrations were elevated by d 2 (0.26 ± 0.04 mcg/g) and d 3 (0.72 ± 0.05mcg/g), respectively, compared to d 0 (0.06 ± 0.04mcg/g and 0.52 ± 0.05mcg/g, respectively). The data illustrate that ~5 d of Tmix feeding at the level used may be sufficient to reach a higher stabilized range of concentrations of the two measurable isoforms in milk and blood in the lactating Holstein. The data establish that this experimental design is adequate toward further refinement of experiments that will be valuable toward characterizing the kinetics and biological value of α- and γ-tocopherols. Additional sampling at the gut level may be informative in determining the fate of other isoforms.

Key Words: concentration, cow, tocopherol

1663 Effect of rumen protected vitamin B complex on metabolic parameters, milk production, and d 15 conceptus and endometrium outcomes.

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The aim of this project was to determine the effects of a rumen-protected vitamin B complex supplementation (VIT B) compared with a control diet containing no supplement (CON) on: milk production and components, concentrations of BHBA, haptoglobin and progesterone in plasma, ovarian dynamics, and Day 15 conceptus and endometrial outcomes. Fifty-one multiparous Holstein cows from the herd at the UBC Dairy Education and Research Centre were enrolled into the study 3 wk before parturition and were randomly assigned to one of the two treatments. Blood samples (2/week), weekly milk samples, and daily feed intake were collected. Cows were enrolled onto a double-ovsynch protocol at 33 ± 3 days post-partum and inseminated by timed artificial insemination (AI). Ovarian structures were monitored and measured using *per rectum* ultra-sonography. The uterus was flushed on Day 15 post-AI for conceptus collection and endometrial samples were collected at the same time. Data were analyzed by ANOVA using the GLM procedure of SAS. Overall, 42 cows were flushed and 13 embryos were collected (recovery rate = 31%). Vitamin B supplementation had no affect on the size of the embryo ($P = 0.49$), ovulatory follicle size ($P = 0.51$), or CL size at embryo collection ($P = 0.51$). However, cows with third or higher parity had significantly larger embryos compared to second parity cows (9.39 ± 1.44 vs. 1.73 ± 1.76, $P < 0.05$). Milk production ($P = 0.90$), milk fat ($P = 0.86$), and protein ($P = 0.37$) values were also similar between the two groups. BHBA levels between the two groups were identical ($P = 0.94$). To understand the effect of vitamin B complex supplementation on fertility at a molecular levels, transcripts related to embryo development

(WNT, AXIN, FZD), immune system (CXCL, IL, MX), adhesion (MYH, MMP), and genes involved in the regulation of vitamin B molecules (FOLR1, TCII) are being analyzed from the endometrial biopsies. In conclusion, strategic dietary vitamin B supplementation during the transition and early lactation did not affect major outcomes of production and reproduction in lactating dairy cows. Benefits of vitamin B in fertility might potentially be linked to endometrial and conceptus gene expression; however, no major differences were observed in production or metabolic parameters.

Key Words: conceptus, cows, dairy, endometrium, gene expression, milk production, nutrition, reproduction, rumen protected, Vitamin B complex

RUMINANT NUTRITION: WESTERN SECTION

1664 WS Effect of crude protein supplementation on performance of cow-calf pairs and replacement heifers grazing late growing season forage.

L. Canterbury*, P. Ebert, D. G. Lust, and E. A. Bailey, *Department of Agricultural Sciences, West Texas A&M University, Canyon.*

Concurrent experiments were conducted to evaluate the effect of protein supplementation to beef cattle grazing warm-season shortgrass forage during the late growing season. Cattle in all experiments grazed adjacent shortgrass pastures dominated by Buffalograss (*Buchloe dactyloides*) and Blue Grama (*Bouteloua gracilis*). Stocking rates ($\geq$ 2.3 ha/animal) were maintained such that forage availability was not limiting throughout the experiment. Precipitation in the area during the experiment was 176% of normal. For all Exp., treatments consisted of a supplemented group (1.32 kg per head of a 39% CP range cube fed 3 times a week) and a non-supplemented control group. Supplemented animals were fed a daily average of 0.22 kg of CP. In Exp. 1, 45 multiparous cow-calf pairs (initial BW 646 ± 13 kg) were individually weighed and body condition scored every 14 d. Forage clippings were taken simultaneously with BW measurements. Cow measurements and forage clippings began July 6 and concluded September 28. Cow final BW (P = 0.24) and ADG (P = 0.38) were not affected by treatment. There was no difference (P = 0.97) in cow final BCS regardless of treatment. Calf ADG (P = 0.54) and weaning weight (P = 0.45) were not affected by treatment. In Exp. 2, 26 primiparous cows (initial BW 546 ± 12 kg) were supplemented and measurements obtained in the same manner as Exp.1. Cow final BW (P = 0.39) and final BCS (P = 0.81) did not differ between treatments. Cow ADG (P = 0.07) tended to be greater when supplemented with 0.22 kg CP per day. Calf ADG (P = 0.50) and weaning weight (P = 0.11) did not differ between treatments. In Exp. 3, 25 replacement heifers (initial BW 412 ± 9 kg) were observed for BW and forage clippings were obtained every 14 d. Heifer final BW (P = 0.17) was not different between treatments. Heifer ADG (P = 0.02) was greater for supplemented heifers. Supplementing protein to cattle grazing late season medium quality forage is advantageous for increasing ADG in replacement heifers and potentially beneficial to improve condition in lactating primiparous cows. Repeating this experiment under varied precipitation patterns, as is normal for short-grass regions, would be beneficial to further examine the impact of late growing season protein supplementation on cow-calf pair/replacement heifer performance.

Key Words: beef cows, forage quality, supplementation

1665 WS Effect of corn-based supplementation on gas emissions, performance, and energetic losses of steers grazing wheat pasture.

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Thirteen Angus-cross steers (initial BW = 436 + 24 kg) were used in a crossover design to evaluate the effects of corn supplementation on gas emissions, performance, and energetic losses of steers grazing wheat pasture. Steers were allowed ad libitum access to wheat pasture (1.2 steers/ha), and were individually supplemented one of two treatments daily for two 30 d periods. Treatments included either 0.2 kg of pelleted wheat middlings (CON), or a dry-rolled corn supplement fed at 0.5% of BW plus 0.2 kg of pelleted wheat middlings (SUPP). After initial 30 d period, treatments were alternated and steers were supplemented an additional 30 d. Fecal output was determined with titanium dioxide (TiO_2) as an external marker. Beginning on d 14 of each period 15 g of TiO_2 was added to each steers supplement. In vitro analysis of wheat forage was determined to estimate DM digestibility of the wheat forage for each 30 d period. Forage intake was calculated using the determined fecal output and estimated forage digestibility. Ruminal CH_4 and CO_2 fluxes were measured using a GreenFeed (C-Lock Inc., Rapid City, SD) system. Urine energy loss was assumed to be 1.4% of GE intake. Oxygen production was estimated from CO_2 production, assuming a respiratory quotient of 1.05. Forage intake as percent of BW did not differ (P = 0.15) between CON (3.22%) and SUPP (3.61%). Average daily gain for CON and the SUPP averaged 1.4 kg and 1.3 kg, respectively, and was not influenced (P = 0.54) by supplementation. There were no differences ($P \geq 0.63$) among treatments for OM digestibility (CON: 84.9%; SUPP: 84.6%) and NDF digestibility (CON: 82.5%; SUPP: 83.1%). Carbon dioxide excreted (CON: 9.8 kg/d; SUPP: 10.5 kg/d) tended to be less (P = 0.08) for CON. No differences (P = 0.43) were observed in CH_4 emissions among CON and the SUPP supplement (334 and 351 g CH_4/d,

respectively). Corn supplementation decreased ($P = 0.02$) CH_4 g/kg of DMI by 20.5%. Methane as percent of GE intake was decreased ($P = 0.02$) by 21.6% when steers consumed the SUPP compared to CON. Heat production as a percent of GE intake decreased ($P = 0.03$) when steers consumed the SUPP. Under the conditions of this experiment, cereal grain supplementation reduced CH_4 emissions.

Key Words: energetic losses, methane, wheat pasture

1666 WS Effects of rumen protected arginine supplementation to cows during early or late gestation on progeny glucose tolerance.

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Our hypothesis was calves gestated by dams supplemented rumen protected arginine during early or late gestation would have improved glucose tolerance. To test this hypothesis, a two yr study was conducted. Dams were randomly assigned to one of three treatments; 1) grazing native range plus dried distillers grain (Control), or grazing native range plus dried distillers grain and Arg fed to provide 180 mg L-Arg/kg BW either during 2) early gestation (EARG) or 3) late gestation (LARG). In yr 1, 16 yearling calves (heifers $n = 8$, steers $n = 8$) and in yr 2, 24 (heifers $n = 10$, steers $n = 14$) yearling calves underwent a glucose tolerance test (GTT). On the days of the GTT, cattle were fed at 0600 h and indwelling jugular catheters were inserted at 0700 h. A 50% dextrose solution was injected at 0.5 mL/kg BW via the jugular catheter and subsequent 6 mL blood samples were collected at −5, −2, 0, 3, 6, 9, 12, 15, 20, 40, 60, 80, 100, and 120 min relative to the dextrose infusion. Glucose half-lives were estimated by regressing the logarithmically transformed glucose concentrations over time and area under the curve was determined using the trapezoidal summation method. Glucose area under the curve (AUC) did not differ ($P = 0.13$) between treatment groups; however, overall glucose concentration (conc.) tended ($P = 0.06$) to be lower for calves of arginine supplemented dams when compared with non-supplemented dams. There were no differences between treatment groups in reference to insulin AUC ($P = 0.57$), insulin half-life ($P = 0.85$), or overall insulin concentration ($P = 0.47$). In conclusion, rumen protected arginine supplementation to cows during varying times in gestation tends to affect overall glucose concentration in progeny during a glucose tolerance test; however, does not affect glucose or insulin AUC, half-life, or overall insulin concentration.

Key Words: arginine, glucose AUC, glucose half-life

1667 WS Effects of administering Ralgro to Holstein calves during the hutch period on growth performance.

K. L. McCarthy*[1], E. J. Scholljegerdes[1], J. A. Gould[2], and W. T. Nichols[3], *[1]New Mexico State University, Las Cruces, [2]Reynolds Creek Calf Ranch, Melba, ID, [3]Merck Animal Health, DeSoto, KS.*

We hypothesized that early administration of a Ralgro implant to 1 d old Holstein calves will improve growth performance. One thousand two hundred and forty-eight 1 d old Holstein steer calves (initial BW 41.2 ± 0.2 kg) were utilized in a completely randomized block designed experiment with truck load serving as the block (6 loads). On d 0, calves were individually weighed, tagged with an electronic identification tag, and vaccinated with Vision CD-T with Spur during initial processing. Calves were randomly assigned within block to receive one of two treatments: 1) growth implant containing 36 mg Zeranol ($n = 584$) or no growth implant ($n = 598$). Calves were individually housed in wood hutches and provided ad libitum access to grain starter (17.2% CP, 4% fat and NEm 0.49 Mcal/kg and NEg 0.34 Mcal/kg) and water. In addition, calves were offered two 1.9-L bottles of milk replacer two times daily (25.5% CP and 22.5% fat, DM basis). Implanted calves had greater DMI ($P < 0.01$) compared to non-implanted calves over the 92-d period. Likewise, ADG was greater ($P < 0.01$) when calves were implanted at 1 d of age versus non-implanted calves. However, due to the increase in DMI and ADG for calves receiving implants, G:F tended to differ ($P = 0.08$) between treatments. Overall, implanting calves with 36 mg of Zeranol did not appear to have any adverse effects on intake or feed efficiency in 1 d old calves during the hutch phase and improved ADG by 6%.

Key Words: calf, growth, hutch, implants, Zeranol

1668 WS Effects of protein concentration and degradability on performance and carcass characteristics of finishing heifers receiving 0 or 400 mg ractopamine hydrochloride.

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This study evaluated if excess protein decreases performance and carcass quality of finishing cattle fed diets with or without ractopamine hydrochloride (RH). Heifers were assigned to 48 pens in a randomized complete block design and pens of cattle were randomly assigned to 3 protein and 2 RH (0 vs. 400 mg/day) treatments. Protein treatments were steam-flaked corn-based diets containing 13.9% CP, 8.8% RDP, and 5.0% RUP (CON), 20.9% CP, 13.4% RDP, 6.1% RUP (High RDP), or 20.9% CP, 9.1% RDP, 10.4% RUP (High RUP). Cattle were weighed at initiation of RH and at shipping. No RH × CP

interactions ($P \geq 0.11$) occurred for performance or carcass traits. Excess CP did not affect ($P \geq 0.12$) final BW or ADG. Carcass-adjusted final BW and ADG tended to be greater ($P = 0.06$) for cattle receiving High RDP than High RUP and CON. Water intake, DMI, G:F, and carcass-adjusted G:F were not different ($P \geq 0.12$) among CP treatments. Hot carcass weight tended to be greater ($P = 0.06$) for cattle receiving High RDP than High RUP and CON. Dressing percentage was lower ($P < 0.01$) for cattle fed High RUP than High RDP and CON. Marbling score, 12th rib fat depth, LM area, and yield grade were not different ($P \geq 0.16$) among CP treatments. Heifers receiving High RUP tended to have lower ($P = 0.10$) KPH than CON. Percentage choice tended to be greater ($P = 0.09$) for heifers receiving High RDP vs. High RUP. Water and DMI were not different ($P \geq 0.36$) for RH vs. no RH. Cattle receiving RH had greater ($P < 0.01$) final BW, ADG, carcass-adjusted final BW, and carcass-adjusted ADG, and lower ($P < 0.01$) G:F and carcass-adjusted G:F compared with no RH. Hot carcass weights were greater ($P < 0.01$) and dressing percentage tended to be greater ($P = 0.09$) for cattle receiving RH, while marbling score was not affected ($P = 0.11$) by RH. Twelfth-rib fat depth tended to be lower ($P = 0.08$), and KPH was lower ($P = 0.02$) for RH vs. no RH. The LM area was greater ($P = 0.03$) for cattle receiving RH vs. no RH. Excess CP does not negatively impact performance or carcass traits of finishing cattle, and no interactions between CP and RH suggest that CP requirements are not affected by RH.

Key Words: cattle, protein, ractopamine hydrochloride

1669 WS Evaluation of *Eragrostis tef* (Zucc.) as a forage option for grazing beef cattle in the Southern High Plains. D. Sugg[*1,2], [1]*Texas Tech University, Lubbock,* [2]*Angelo State University, San Angelo, TX.*

To assess the potential of *Erogrostis tef* to provide a late summer supply of forage for livestock production in the Southern High Plains, four 2.66 ha paddocks equipped with subsurface drip irrigation were seeded with *Eragrostis tef* ('Tiffany' teff) at a rate of 3.72 kg/ha. Each paddock was stocked with commercial beef steers ($n = 5$; 289 ± 30.38 kg initial shrunk BW) at 51 d post-seeding resulting in an initial forage allowance of 202 kg DM/100 kg BW. Weekly samples of whole plant and canopy structure were obtained to describe DM, OM, and fiber concentrations. Appropriate sample height of canopy for the purposes of estimating selection quality was determined at the most proximal grazing site to each quadrat toss by recognition of a tiller with at least one leaf possessing the flat defoliation pattern characteristic of an ungulate bite. Biweekly samples included analysis of CP and IVTD. Leaf percentage of entire plant was quantified at 21 d intervals. Available DM and OM peaked at Day 28 and was lowest at Day 56 ($P < 0.01$). Whole plant and canopy DM ($P < 0.01$), OM ($P < 0.01$), NDF ($P < 0.01$), ADF ($P < 0.01$), and CP ($P < 0.01$) differed by day. Only in vitro true digestibility was not affected by maturation of either whole plant ($P = 0.12$) or canopy structure ($P = 0.61$). Leaf proportion of whole plant structure aligned with times of peak forage mass availability ($P < 0.01$). Teff grass stocked at a moderate rate with growing beef calves achieved adequate production with minimal inputs forage with minimal inputs to provide a quality forage base for approximately 2 mo of grazing in the Southern High Plains.

Key Words: digestibility, forage quality, grazing, teff, water

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1670 WS Salivary cortisol concentrations affect rumen microbial fermentation and nutrient digestibility in vitro. K. L. Samuelson[*1], A. L. Salazar[1], L. L. Rath[1], J. B. Alford[1], E. R. Oosthuysen[1], S. L. Ivey[1], D. M. Hallford[2], and C. A. Loest[1], [1]*New Mexico State University, Las Cruces,* [2]*Animal and Range Science Dep., New Mexico State University, Las Cruces.*

This study investigated effects of cortisol on fermentation and digestibility of nutrients by rumen microorganisms. Four dual-flow continuous culture fermentor (2700 mL) systems were used in a 4 × 4 Latin square design with 4 periods and 4 treatments. Each experimental period consisted of 13 d, which allowed 7 d for microbial adaptation, 3 d for cortisol treatment application, and a 3 d post-treatment period. Treatments consisted of 0, 3, 6, or 9 ng/mL of cortisol mixed into artificial saliva and continuously infused at a rate of 1.55 ± 0.05 mL/min. For the 3 d treatment period and the 3 d post-treatment period samples were collected at 0, 3, 6, 9, 12, 24, 36, 48, 60, and 72 h and were analyzed VFA, and NH_3. During the 3-d sampling period effluent was composited for analysis of OM, NDF, and CP digestibility. During cortisol treatment, cortisol × h ($P \leq 0.01$) was observed for acetate and valerate, total VFA and isobutyrate tended to increase from 0 to 3 ng/mL, but were not different among 3, 6, and 9 ng/mL (quadratic, $P \geq 0.12$), butyrate tended to decrease from 0 to 3 ng/mL cortisol, and was not different among 3, 6, and 9 ng/mL (quadratic, $P = 0.07$), and isovalerate was not different among 0, 3, and 6 ng/mL, but decreased from 6 to 9 ng/mL of cortisol (quadratic, $P = 0.06$). Digestibility of OM (g/d and % of intake) tended to be lower (quadratic, $P = 0.12$), and NDF digestion (g/d and % of intake) was lower (quadratic, $P = 0.09$) for 9 ng/mL cortisol compared to 0, 3, or 6 ng/mL. Digestibility of CP (g/d and % of intake) was not different ($P \geq 0.23$) among treatments. In the period after cortisol treatment, a cortisol × h ($P = 0.03$) was observed for isobutyrate, NH_3 decreased linearly ($P = 0.04$) with increasing cortisol, valerate tended to increase linearly ($P = 0.14$) with increasing concentrations of cortisol, and isovalerate was lower for 9 ng/mL than 0, 3, and 6 ng/mL cortisol (quadratic, $P = 0.10$). Digestibility (g/d and % of intake) of OM, NDF, and CP were not different ($P \geq 0.51$) among treatments. Results indicate that cortisol may influence rumen microbial fermentation and digestion when

present in saliva at 9 ng/mL.

Key Words: cortisol, fermentation, rumen

1671 WS Shifting the paradigm of liver abscess dogma in USA feedlots. Z. Bester*[1], M. Hubbert[2], R. E. Carey[1], K. L. Samuelson[1], and C. A. Loest[1], *[1]New Mexico State University, Las Cruces, [2]Clayton Livestock Research Center, NMSU, Clayton, NM.*

Liver abscesses in feedlot cattle are a major economic, welfare, and production concern to the cattle feeding industry. Severe liver abscesses (LA) reduce ADG by as much as 0.20 kg, DMI by 5%, trimming loss by 0.43%, carcasses grading choice by 7%, and HCW by 36 kg. In processing facilities, LA introduce operational and food safety concerns. These include a reduction in processing efficiency, lost time as a result of line stoppages, and offal condemnation in addition to the consumer risk associated with LA contamination of edible meat. Tylosin phosphate, a macrolide antibiotic, has been shown to reduce LA by 75% and level of *Fusobacterium Necrophorum* in the rumen by 80 to 90%. During this initial observational study, a total of 83 feedlot pens (each individual feed yard exceeding 40,000 head capacity) within three geographical regions (Arizona, Colorado, and the Texas Panhandle) were sampled. Feedlot pen data were collected within 1 wk before harvest and cattle were traced to the packing plant. Every third rumen and its matching liver were tagged (if condemned only). Rumens were scored for consolidation, scars, moderate and acute lesions, and a sample was taken. Livers were scored based on an adaptation of the Elanco Liver Check scoring system. Holstein cattle had a greater ($P < 0.05$) percentage of LA than beef breeds (30.3 vs. 20.0%). Additionally, Holstein cattle had 11% severe LA (A+) compared with 4% for beef breeds ($P < 0.05$). No geographical difference ($P \geq 0.10$) were detected for liver abscess prevalence and averaged 23, 25, and 26% for the Texas Panhandle, Arizona, and Colorado regions, respectively. Liver abscess rate and severe LA (A^+) incidence differed between feedlots ($P < 0.05$) with within feedlot variation. A correlation was observed for LA% and days on feed ($R^2 = 0.22$; $P = 0.04$) and for LA % and breed ($R^2 = 0.29$; $P = 0.01$). No correlation was observed between LA percentage and tylosin phosphate, and between LA percentage and rumen lesions ($P \geq 0.10$). These data indicated no association between LA and rumen damage as a result of acidosis. Rumen lesions averaged 12.2%, of which 9.3% were consolidated, 2.4% scar tissue, and the remainder moderate and acute lesions. This study justifies further investigation of feedlot soil and manure as the source of LA causing pathogens to evaluate the within feedlot variation observed for in LA percentage in cattle.

Key Words: cattle, feedlot, liver abscess

SMALL RUMINANT

1672 Protein supplementation and herbage allowance for pregnant ewes grazing low-quality pasture. C. H. E. C. Poli*[1,2], B. M. Paulino[1], A. B. Moraes[1], Z. M. S. Castilhos[3], F. C. A. Silva[3], N. M. Fajardo[1], C. M. Pimentel[4], D. B. David[5], E. B. Azevedo[6], and J. J. Villalba[2], *[1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [2]Utah State University, Logan, [3]Fundação Estadual de Pesquisa Agropecuária, Porto Alegre, Brazil, [4]Universidade de Brasília, Brasília, Brazil, [5]Fundação Estadual de Pesquisa Agropecuária, São Gabriel, Brazil, [6]Universidade Federal do Pampa, Itaqui, Brazil.*

Protein supplements mixed with mineral salt have been widely used in beef production in tropical countries, but few studies have been performed to test their use with sheep or pregnant animals. This study assessed the effect of protein supplementation under two herbage allowances aiming at overcoming ewe undernutrition during gestation and lactation in low-quality pastures during winter. At approximately fifty days of gestation, 36 ewes carrying singletons and of similar stage of pregnancy were chosen from a group of 50 using an ultrasound technique. Ewes were allocated into four treatments in a randomized block design with three replications, where each paddock with 3 ewes was considered the experimental unit. The treatments were arranged in 2 x 2 factorial design of two herbage allowances: 1) low (LH) 10 kg^{-1} dry matter (DM) per 100 kg liveweight (LW) and 2) high (HH) 20 d^{-1} DM per 100 LW; and two supplements: 1) protein plus a mineral salt mix (PS) and 2) mineral salt alone (S). Both supplements were offered in ad libitum amounts. Due to differences in daily nutrients requirements and pasture quality, the trial was divided into two periods: pregnancy and lactation. Animals grazed a low-quality *Brachiaria arrecta* cv. Napier (crude protein: 67 g kg^{-1}, neutral detergent fiber: 710 g kg^{-1}) pasture. Animal performance was assessed every 21 d. Other variables such as herbage structure and composition, lamb birth weight, daily supplement intake, and placenta weight were also measured. There was no effect ($P \geq 0.05$) of PS on ewe average daily gain (ADG), placenta weight, lamb birth weight or lamb ADG. Protein supplement intake was greater ($P \leq 0.05$) than mineral salt intake in both reproductive stages, being greater during lactation, but it was not enough to increase the productive performance of ewes during the last third of pregnancy or during lactation. In conclusion, regardless of herbage allowance, the use of protein supplements on low-quality pastures does not improve the nutritional status of ewes or lambs before weaning. **Key Words:** fetal development, maternal nutrition, sheep

Fig 1673.

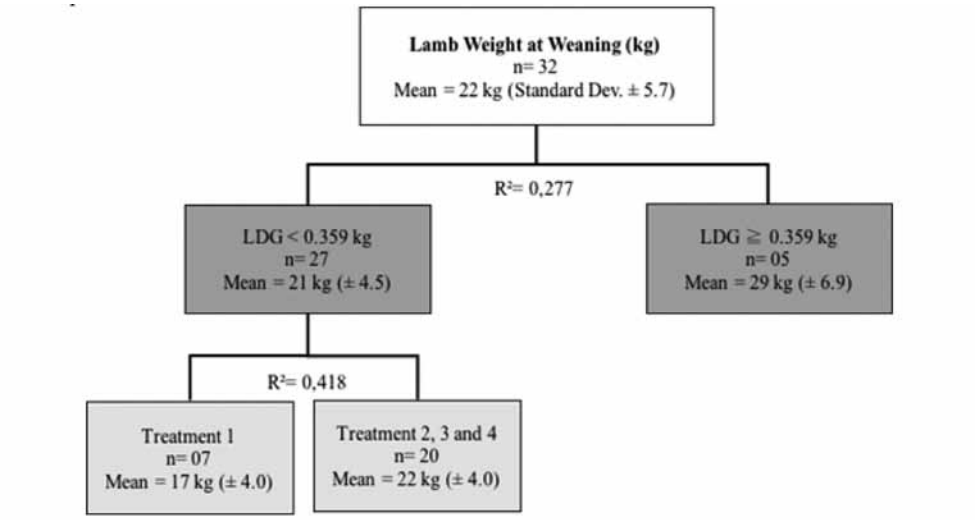

Figure 1 Decision Tree Test showing the lamb weight at weaning partitioned through R^2-values, explained by lamb daily gain (LDG) and treatments (food restriction during different ewe pregnancy periods).

1673 Food restriction in ewes during different pregnancy periods affects milk production and lamb growth. C. H. E. C. Poli[*1,2], L. A. Sphor[2], A. L. G. Monteiro[3], J. F. Tontini[2], C. Bremm[2], P. C. F. Carvalho[2], and J. J. Villalba[1]. *[1]Utah State University, Logan, [2]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [3]Universidade Federal do Paraná, Curitiba, Brazil.*

This study assessed the effect of food restriction during different periods of ewe pregnancy on milk production and lamb growth. Thirty-five adult pregnant ewes were assigned to four treatments (7–10 animals/treatment), which varied in the period when food restriction (removal of a supplement fed at 150 g/Kg BW/day) was applied: first third period of pregnancy (T1); second third period of pregnancy (T2); third third period of pregnancy (T3), or no supplement restriction (Control; T4). All ewes grazed together in a Bermuda grass cv. Tifton-85 pasture of low biomass (below 1000 kg DM/ha), and once a day they received the supplement [14% CP; 3.5% EE; 16% ADF], or not, according to treatment. Ewes were weighed every 14 d during pregnancy. Lamb birth weight (LBW) and placenta weight (PW) were assessed at lambing. Daily milk production (MP) and lamb daily gain (LDG) were recorded until weaning. The experiment was performed in a completely randomized design, and the data were analyzed by a Decision Tree multivariate analysis. Treatments explained 23% of MP, with greater milk production per day for T2 and T4 (3423 g ± 1047.7 g SD) than for T1 and T3 (2294 g ± 1091.1 g SD). LBW was best explained by the number of lambs per ewe (R^2 = 0.52), and PW had a positive correlation (R^2 = 0.72) with LBW, independent of the number of lambs per ewe. When the LDG was lower than 359 g, the lowest LDG and the lamb weight at weaning were observed in T1 (Fig. 1). Despite the relatively low nutrient requirements from ewes during early pregnancy, these results point to the importance of avoiding dietary restriction during this period to enhance MP and LDG. On the other hand, nutrient restriction during mid-pregnancy had no consequences on milk production or lamb growth.

Key Words: sheep nutrition, sustainability, fetal development

1674 Relationship between infrared thermography measures and feed efficiency in New Zealand sheep. S. P. Miller[*1], S. Dowling[2], J. C. Munro[3], Y. R. Montanholi[3], J. R. Webster[2], and P. L. Johnson[1], *[1]AgResearch, Mosgiel, New Zealand, [2]AgResearch, Hamilton, New Zealand, [3]Department of Plant and Animal Sciences, Faculty of Agriculture, Dalhousie University, Truro, Canada.*

A data set to investigate genetic parameters for feed efficiency in New Zealand maternal sheep is being collected. As measurement of this trait is expensive, route to market for breeders will be through genomic selection. Another potential way to enable breeders to select for this difficult to measure trait, combined with genomics will be through predictor traits. Using custom built electronic feeding stations, individual feed intake was collected on 197 ewe lambs born in September 2014 with the 6-wk feed intake trial taking place June-August 2015. Residual feed intake (RFI; MJ/day) was determined using a prediction model that included mid-point body weight ($kg^{0.75}$) and average daily gain. Infrared thermography measures were investigated as a potential indicator trait with images collected at two time points. A thermal video captured the left side of the head, and back of the ear (approximate distance of 0.5 m), using an infrared camera (ThermaCamS60, FLIR, Systems AB, Dandoryd, Sweden). Four head sub-regions were identified

and maximal and average temperature calculated for the eye, bridge of the nose, muzzle, and middle of the back of the ear. To identify potential regions of influence a sub-set of images from 30 individuals were interpreted representing the six most extreme RFI animals (three high RFI; three low RFI), and also individuals with extreme RFI values from four sires identified as the producers of the most extreme RFI progeny (two high RFI sires; two low RFI sires). The difference in RFI was significant ($P < 0.001$) between the extreme groups (-1.5 ± 0.28 MJ/day vs. $+1.6 \pm 0.29$ MJ/day). Within a time point, the average temperature measurements for the four different positions were significantly correlated (all $P < 0.01$). Between time points, back of the ear measurements showed the highest correlation ($r = 0.7$; $P < 0.001$) and the greatest mean temperature difference between groups at each measurement point. At the first time point, the estimated average ear temperature of the lowest RFI animals was 26.7 ± 0.67°C vs. 29.2 ± 0.69°C for the highest RFI animals ($P = 0.015$), with corresponding values at the second time point of 27.2 ± 0.55°C vs. 29.5 ± 0.59°C ($P = 0.011$). These results provide evidence of a relationship between thermal images and feed efficiency in maternal growing sheep that will be investigated further as a potential indicator trait for selection in industry.

Key Words: indirect, phenotyping, selection

1675 Ground redberry juniper and urea in supplements fed to Rambouillet ewe lambs on growth, blood serum, and fecal N. T. R. Whitney[*1] and J. P. Muir[2], *[1]Texas A&M AgriLife Research, San Angelo, [2]Texas A&M AgriLife Research, Stephenville.*

Effects of using ground redberry juniper and urea in dried distillers grains with solubles (DDGS)-based supplements fed to Rambouillet ewe lambs ($n = 48$; 42 kg ± 3.8) on growth, blood serum, and feces were evaluated. In a randomized design study (40 d), individually-penned lambs were fed a basal diet of ground sorghum-sudangrass hay (ad libitum) and of 1 of 8 supplements (fed separately from the hay; 6 lambs/treatment; 496 g/d; DM basis) in a 4 × 2 factorial arrangement with 4 concentrations of ground juniper (15, 30, 45, or 60% of DM) and 2 levels of urea (1 or 3% of DM); dried distillers grains with solubles was replaced as percentage of juniper increased. Lamb growth was evaluated on d 0, 5, 12, 19, 26, 33, and 40. Blood serum was evaluated on d 6 to 8, 20 to 22, and 34; feces were collected on d 34. A repeated measures analysis showed factorial by day interactions ($P < 0.001$) for hay DMI, total daily DMI, BW, ADG, and G:F, with only a few differences within day. Overall, hay and total DMI were similar among lambs ($P > 0.44$), but lambs fed 60% juniper-based supplements had the least amount of supplement intake ($P < 0.01$). Overall, lambs fed 15% juniper-based supplements had the greatest ($P < 0.04$) ADG and G:F vs. the other lambs. Percentage of urea in the supplement did not affect ($P > 0.23$) overall intake of hay or supplement, ADG, or G:F. However, lambs fed 15% juniper-based supplement tended to have greater ($P = 0.07$) final BW than lambs fed 60%, and urea used at 1% of supplement vs. 3% resulted in reduced final BW ($P = 0.03$). Fecal DM was similar ($P > 0.15$) among lambs, but fecal N was greater ($P < 0.02$) for lambs fed the 15% and 45% juniper-based supplements vs. 60% juniper-based supplement. In conclusion, when ewe lambs were fed a low-quality basal hay diet, growth performance declined when 60% juniper or 3% urea was used in supplements. This decline can be attributed to differences in supplement concentrate:forage ratio, fiber, degradable N, and plant secondary compounds, all of which can affect intake and growth. However, an economic analysis is needed to determine maximum inclusion rate of juniper and urea in rangeland supplements, especially when trying to only meet the maintenance requirement of the animal.

Key Words: juniper, lambs, supplement

1676 The relationship between body condition score and body weight, body linear measurements and real-time ultrasound body composition measurements in Alpine does before breeding and kidding. F. R. B. Ribeiro[*1], B. Barcelos[2], L. C. Nuti[1], W. B. Foxworth[1], S. K. Lewis[1], Y. Jung[1], S. Horner[1], B. L. Jackson[1], and G. R. Newton[1], *[1]Prairie View A&M University, Prairie View, TX, [2]School of Animal Science and Food Engineering, University of Sao Paulo, Pirassununga, Brazil.*

The objective of this study was to determine the relationships between body condition score (BCS) and body weight (BW), hip height (HH), wither height (WH), girth circumference (GC), and real-time ultrasound (RTU) measurements of body composition in Alpine does before breeding ($n = 66$) and before kidding ($n = 34$). Thirty-two animals were not included in the before kidding measurements due to culling or failure to give birth. The body composition traits measured by RTU were 12th–13th rib fat thickness (uBF) and rump fat thickness (uRUMP). Ultrasound measurements were taken using an Aloka 500 with a 12 cm 3.5 MHz transducer. Hair was clipped and vegetable oil was used as a coupling agent to enhance image quality. Data were analyzed using the Proc CORR and Proc REG procedures of SAS. Body condition score was highly correlated ($P < 0.01$) with uBF and uRUMP before breeding ($r = 0.45$ and 0.39, respectively) and before kidding ($r = 0.84$ and 0.74, respectively). Body weight and HH were highly correlated before breeding ($r = 0.63$; $P < 0.0001$), but not before kidding ($r = 0.27$; $P = 0.12$). Girth circumference was highly correlated to BW ($r = 0.78$; $P < 0.0001$) and correlated to HH ($R = 0.38$; $P = 0.037$) before kidding. Wither height and HH were highly correlated only when measured before kidding time ($r = 0.63$; $P < 0.001$). Prediction equations were developed to predict BCS using a stepwise procedure. Body condition score before breeding can be predicted from uBF with an R^2 of 0.21. Prediction of

BCS before kidding using uBF had an R^2 of 0.63, which was the first variable included in the model. Inclusion of three additional variables (uRUMP, HH, and WH) in the full model improved the R^2 to 0.76. Results indicate that RTU body composition traits are highly correlated with BCS in Alpine goats and that the accuracy of prediction was improved when does were close to parturition. More research is needed to refine the models and improve accuracy of prediction.

Key Words: body composition, goat, ultrasound

1677 Effects of selection for high and low juniper-consuming goats on rumen fermentation characteristics. W. C. Stewart*[1], T. R. Whitney[2], E. J. Scolljegerdes[3], D. F. Waldron[4], J. W. Walker[4], and J. M. B. Musser[5], *[1]Montana State University, Bozeman, [2]Texas A&M AgriLife Research, San Angelo, [3]New Mexico State University, Las Cruces, [4]TX A&M AgriLife, San Angelo, [5]Texas A&M, College Station.*

The objective of this study was to determine if ruminal fermentation characteristics differed in goat lines selected for high (HIGH) or low (LOW) juniper-consumption. Five Boer × Spanish-composite bucks (age = 2 yr; initial BW = 67.2 ± 4.3 kg) selected from each line were subjected to three different 25-d periods: 1) native range infested with juniper (Period 1); 2) group fed ad libitum sorghum × sudangrass hay (Period 2); 3) individually fed 3% BW of sorghum × sudangrass hay and ad libitum redberry juniper foliage offered fresh daily (Period 3). During each period, rumen fluid was evaluated for pH, VFA, ammonia N (NH_3–N), and IVDMD of juniper foliage. There was a period effect ($P < 0.02$) for all response variables. A selection line × Period interaction was observed for total VFA ($P < 0.01$) because HIGH, which exceeded LOW during Periods 1 and 3 was lower in Period 2. However, total VFA did not differ within period between HIGH and LOW. During Period 1, when goats grazed juniper infested native rangelands, rumen fluid from HIGH contained greater ($P < 0.05$) ruminal isovalerate, and tended to have greater ruminal isobutyrate ($P = 0.09$) and NH_3–N ($P = 0.07$) than LOW. When transitioned to a sorghum × sudangrass hay diet (Period 2), total ruminal VFA concentrations declined 26 and 4% for HIGH and LOW, respectively, and total VFA ($P = 0.08$) and valerate ($P = 0.09$) tended to be greater for LOW compared to HIGH. In vitro digestibility of juniper did not differ ($P = 0.48$), but declined 13 and 12% for HIGH and LOW, respectively, from Period 1 to 2. During Period 3, when transitioned to individual pens with ad libitum access to sorghum × sudan hay and juniper foliage, juniper intake did not differ ($P = 0.16$) with HIGH consuming 1.2 g/kg BW of juniper compared to 0.62 g/kg BW for LOW. Although no differences were detected ($P > 0.05$) for VFA, NH_3–N, pH, and IVDMD between HIGH and LOW goats during Period 3, total VFA from HIGH increased 48% vs. 7% in LOW from period 2 to 3. Propionate increased 16% in HIGH compared to a 5% decrease in LOW from Period 2 to Period 3. Overall, results indicate that ruminal fermentation characteristics differ between divergent goat lines selected for high and low juniper consumption when consuming diets with and without juniper.

Key Words: genetic selection, goats, juniper

1678 Ground redberry juniper and urea in DDGS-based supplements do not adversely affect ewe lamb rumen microbial communities. S. L. Ishaq*[1], C. J. Yeoman[1], and T. R. Whitney[2], *[1]Montana State University, Bozeman, [2]Texas A&M AgriLife Research, San Angelo.*

Effects of using ground redberry juniper and urea in dried distillers grains with solubles (DDGS)-based supplements fed to Rambouillet ewe lambs ($n = 48$; 42 kg ± 3.8) on ruminal parameters and microbial communities were evaluated. In a randomized design study (40 d), individually-penned lambs were fed ad libitum, a basal diet of ground sorghum-sudangrass hay and of 1 of 8 supplements (6 lambs/treatment; 496 g/d; DM basis) in a 4 × 2 factorial arrangement with 4 concentrations of ground juniper (15, 30, 45, or 60% of DM) and 2 levels of urea (1 or 3% of DM). Growth performance, serum, and fecal characteristics were reported. Ruminal fluid was collected via oral lavage at the end of the trial (d 34). Total VFA was unchanged ($P > 0.51$) with supplements. As a percentage of total VFA, propionic was similar ($P = 0.34$), acetic acid increased ($P = 0.004$) and butyric acid decreased ($P = 0.03$) as concentration of juniper increased in the supplement; urea did not have an effect ($P > 0.10$). Ammonia N was not affected ($P > 0.12$), but ruminal pH increased ($P < 0.001$) with juniper concentration; not with urea ($P > 0.89$). Treatment (individual juniper or urea concentrations, or juniper × urea) effects on operational taxonomic unit (OTU) abundance were not significant using ANOSIM ($P > 0.05$), AMOVA ($P > 0.01$), or PERMANOVA ($P > 0.05$). Treatments did not produce significantly different phylogenetic trees by structure ($P > 0.05$, unweighted UniFrac), but did produce some small, yet significant pairwise comparisons by abundance (weighted UniFrac). Samples did not significantly cluster by diet or supplements using metric multi-dimensional scaling plots. Families Prevotellaceae and BS11 gut group (Bacteroidetes) decreased with increasing concentrations of both juniper and urea, while families Acidaminococcaceae and S24–7 increased. Christensenellaceae and Lachnospiraceae increased with juniper concentration at a 1% urea. High concentrations of juniper were associated with Moraxella and Streptococcus, low concentrations of urea were associated with Fretibacterium, and high concentrations of urea were associated with Oribacterium and Pyramidobacter. In conclusion, on a low-quality basal hay diet, ewe lamb ruminal parameters can be attributed to differences in the concentrate:forage ratio, fiber, degradable N, and secondary compounds. Despite some differences in bacterial

diversity between treatments, due to changes in volatile fatty acid profile, ammonium, and pH, there was not a significant difference in OTU presence or abundance.

Key Words: bacterial diversity, lambs, supplement

1679 Fatty acid profile, sensory traits, and aromatic compounds of chops from lambs fed ground woody plants as roughage in feedlot finishing diets. K. R. Wall[*1], C. R. Kerth[1], T. R. Whitney[2], S. B. Smith[1], J. L. Glasscock[2], and J. T. Sawyer[3], [1]TX A&M University, *College Station, [2]Texas A&M AgriLife Research, San Angelo, [3]Tarleton State University, Department of Animal Science and Veterinary Technology, Stephenville, TX.*

We hypothesized that ground woody plants in feedlot diets would increase saturated fatty acids and modify sensory characteristics and volatile aroma compounds of loin chops. A completely randomized design study using Rambouillet wether lambs (n = 48) consisted of 2 feeding periods: Period 1 = fed a 70% concentrate (consisting mainly of 40% dried distillers grains with solubles, DDGS; 21.7% sorghum grain) diet from d 0 to 27 d and Period 2 = fed an 86% concentrate (consisting mainly of 40% DDGS and 37.5% sorghum grain) diet from d 28 to 57. In each feeding period, lambs were individually fed 6 diets that differed only by roughage source: cottonseed hulls (CSH; control) or ground wood consisting of either redberry (RED), blueberry (BLUE), or one-seed juniper (ONE), eastern red cedar (ERC), or mesquite (MESQ). After humanely harvesting the lambs and chilling the carcasses for at 48°C for 48 h, five chops, 2.54-cm thick, were cut starting from the posterior end of the LM; the first chop was designated the analysis of fatty acid composition, cut to straighten the LM face, vacuum-packaged separately, and stored at −80°C until analyzed. Subsequently, four, 2.54-cm-thick chops were serially cut for sensory and GC/MS/Olfactory analysis, labeled, vacuum packaged separately, and stored at −10°C until analyzed. Chops from lambs fed MESQ tended (P = 0.07) to have less total saturated fatty acids compared to chops from lambs fed either RED or ONE. No other fatty acids were affected (P > 0.10) by roughage source. Neither sensory traits nor cook loss percentage were affected (P > 0.17) by roughage source. A total of 95 aroma chemical compounds were detected by GC/MS/Olfactory methods and included alkanes, alcohols, aldehydes, acids, ketones, sulfur-compounds, and pyrazines. The CSH had greater (P < 0.05) amounts of 1-pentanol (bread or cereal aroma) compared to BLUE, ERC, or MESQ. Heptanal (medicinal aroma), pentanal (bread aroma), 1-(1H-pyrol-2yl)-ethanone, 2-heptanone (fruity aroma), and 2-pentyl furan (caramel aroma) amounts were greater (P < 0.05) in CSH than all other roughages. We conclude that woody plants can be included in feedlot rations of lambs with no adverse affects on fatty acid profile, sensory traits, or aromatic compounds.

Key Words: carcass, lamb, sensory

1680 Feeding behavior of grazing lambs in a silvopastoral system. F. de Oliveira Scarpino van Cleef[*1,2], T. Silva do Nascimento[1], L. Ariel Tosi[1], D. J. A. Santos[1], and A. C. Ruggieri[1,2], *[1]Sao Paulo State University, Jaboticabal, Brazil, [2]CNPq, Brasilia, Brazil.*

Silvopastoral systems may contribute to the reduction of the effects caused by climate change in grazing animals. The aim of this study was to evaluate the presence of trees (*Eucalyptus urophylla* × *Eucalyptus grandis*) on the behavior of grazing finishing lambs in Massai grass (*Panicum maximum* × *Panicum infestum*). Twenty-four crossbred lambs (27 ± 3.3 kg BW and approximately 90 d old) were blocked by initial BW and assigned into three experimental treatments: TA = unshaded Massai grass pasture; TB = Massai grass pasture with eucalyptus trees spaced 12 × 2m; TC = Massai grass pasture with eucalyptus trees spaced 6 × 2m. Light interception was the criteria for starting grazing period and the residual pasture height was fixed in 20 cm. Animals were observed over 9 consecutive days (3 d of occupation in each of 3 paddocks) to assess the grazing activities: feeding (FE), lying ruminating (LR), standing ruminating (SR), lying (LY), standing still (SS), searching for food (SF), and other activities (OT). Three trained observers recorded the behavioral activities, every 10 min, for 12 h (from 0700 to 1900 h). Data were submitted to analysis of variance and F test at 5% significance, using the GLM procedure of the statistical package SAS, and the treatments' means were compared using Tukey test at 5% significance. They were included in the model the treatment, block, day of occupation, day of occupation nested within the treatment, and interactions of treatment × block, and treatment × day of occupation. Animals in TA spent more time on FE (TA = 59%, TB = 53%, TC = 50%, P < 0.0001), with no differences observed between treatments with trees. Time of LR was greater for TB (TA = 25.7%, TB = 30%, and TC = 23%, P < 0.0001), and the interaction was observed between TB and day of occupation (P = 0.02), with animals spending more time on this activity at second and third occupational d. On the other hand, animals in TC stayed more time on LY (TA = 5.7%, TB = 7.7%, and TC = 11.8%,P < 0.0001), SS (TA = 2.5%, TB = 3,01%, and TC = 4,2%, P = 0.0001), and having other activities (TA = 0.7%, TB = 0.6%, and TC = 2.9%, P < 0.0001) than animals in TA and TB. The activities SR and SF did not differ among treatments (P = 0.08 and P = 0.14, respectively). Because of the greater availability of shade, the silvopastoral system improved the state of welfare of the lambs, shown by the greatest time spent on ruminating.

Key Words: eucalyptus, silvopastoral, sheep

Table 1681.

Table 1. Digestibility and performance of hair sheep lambs fed with ammoniated cotton gin trash treated with exogenous fibrolytic enzymes (EFE).

Variables	EFE					CV (%)	Regression		R^2
	Control	0%	2%	4%	6%				
DM	39.1	40.2	45.3*	48.2*	50.7*	8.2	$\hat{Y}$= 40.948 + 1.718x		0.97
OM	40.7	42.3	45.7	48.3	50.1	9.2	$\hat{Y}$= 42.708 + 1.299x		0.98
CP	45.5	40.8	48.3	46.1	48.8	16.7	$\hat{Y}$= 46.0		-
EE	44.4	44.5	44.7	45.1	45.3	18.0	$\hat{Y}$= 44.9		-
NDF	45.3	40.1	39.9	39.1*	38.4*	9.3	$\hat{Y}$= 40.262 - 0.295x		0.95
ADF	44.4	39.6	38.0	37.3*	36.5*	10.6	$\hat{Y}$= 39.354 - 0.505x		0.96
FC	42.0	37.1	36.8	35.6*	35.0*	8.1	$\hat{Y}$= 37.252 - 0.375x		0.95
NCF	26.2	51.5*	54.4*	56.3*	59.0*	23.6	$\hat{Y}$= 51.642 + 1.223x		0.99
TDN	41.1	45.6	48.7*	50.6*	53.2*	11.5	$\hat{Y}$= 45.814 + 1.240x		0.99
								Males	Female
IW (kg)	20.0	20.7	20.6	21.2	21.2	8.7	$\hat{Y}$= 20.9	20.3 a	21.2 a
FW (kg)	30.7	33.1	33.6	34.5	34.8	7.2	$\hat{Y}$= 34.0	35.5 a	31.2 b
TG (kg)	10.7	12.4	13.0	13.3	13.6	15.8	$\hat{Y}$= 13.1	15.2 a	10.0 b
DLG (g d^{-1})	170.1	196.2	206.0	210.9	215.1	15.8	$\hat{Y}$= 207.0	240.9 a	158.4 b
FCR (kg/kg)	15.3	15.9	14.8	15.0	15.1	18.5	$\hat{Y}$= 15.2	16.2 a	14.2 a

R^2 = coefficient of determination. C.V. (%) = coefficient of variation. IW = initial weight. FW = final weight. TG = total gain. DLG = daily liveweight gain. FCR = feed conversion ratio. Mean followed by same letters are not significantly different by F test (5%). * P< .05

1681 Intake, digestibility, and performance of hair sheep lambs fed with ammoniated cotton gin trash treated with exogenous fibrolytic enzymes. D. G. Quadros*, *Bahia State University, Barreiras, Brazil.*

This study was performed to evaluate intake, digestibility, and performance of Santa Ines lambs fed with diets containing ammoniated cotton gin trash (CGT) treated with exogenous fibrolytic enzymes (EFE). CGT was pre-treated with 6% urea (25% of moisture for 80 d) according previous studies. Treatments were 0, 2, 4, and 6% of EFE (75% cellulase and 25% hemicellulase), applied 24h before feeding. In addition, there was a control group fed with non-ammoniated and untreated CGT. The experiment was a completely randomized block design with five treatments and six replications (animals), with three males and three females per treatment, from February to May 2014 in Animal Science Center at UESB, in Vitoria da Conquista, Bahia, Brazil. Isonitrogenous and isocaloric diets were balanced according to NRC for 20 kg animals, liveweight gain of 200 g with estimated intake of 4.5% of bodyweight (61% TDN and 15% CP). Concentrate contained corn, soybean meal, and minerals, fed in a concentrate:roughage ratio of 50:50. The lambs were feedlotted for 84 d, being the first 21 d of adaptation and three periods of data collection of five consecutive days in each 16 d. For evaluating intake and digestibility, feed, orts, and feces were collected, using NDFi as an internal marker. There was no effect of EFE on intake, with the average values of 1311.4, 1189.9, 254.1, 748.9, and 810.0 g per day for DM, OM, CP, NDF, and TDN, respectively. EFE increased NFC intake ($P < 0.05$), by 17.0% units for each 1% of EFE. There were no differences on apparent digestibility of CP and EE ($P > 0.05$) with EFE application; however, digestibility of DM, OM, NDF, ADF, FC, NFC, and TDN were increased linearly ($P < 0.05$). Males (240 g) gained daily more weight than females (158.4 g) ($P < 0.05$), although there was no effect of EFE ($P > 0.05$). Despite the benefits of ammonization and EFE on digestibility and intake of CGT, there was no significant effect on performance.

Key Words: cellulase, feedlot, hemicellulase, ruminants.

1682 Effects of forage quality and breed on rumination time in goats. S. N. LeShure*, T. A. Gipson, A. L. Goetsch, R. Puchala, and T. Sahlu, *American Institute for Goat Research, Langston University, Langston, OK.*

Rumination time is one of the many key factors in determining animal wellbeing. The objective was to investigate effects of forage quality and breed on rumination time in goats. The experiment was 2 simultaneous 4 × 4 Latin squares having a 2 × 4 factorial treatment arrangement with 2 breeds (Alpine and Spanish) and 4 treatments [24 h fasting (FAST), low-quality hay (LOW; mixed grass), LOW plus concentrate (CONC; 80% corn and 20% soybean meal at 1% BW(DM)), and high-quality hay (HIGH; alfalfa)]. Twelve mature does of each breed were placed in individual metabolic crates and given free access to hay unless fasting. There were 4 periods of 72 h with 3 rotations of 8 does/day (24 h × 3 d). Does were digitally recorded for 24 h, then observations were encoded for ruminating bouts and bout duration. Data were analyzed using a mixed model consisting of DMI as a covariate, treatment, breed, and treatment x breed as fixed effects and animal within square as a random effect. Feed intake relative to $BW^{0.75}$ was 0, 17, 28, and 21 g/kg $BW^{0.75}$ for FAST, LOW, CONC, and HIGH, respectively (SEM = 1.6) and 17 and 16 g/kg $BW^{0.75}$for Alpine and Spanish, respectively (SEM = 1.4).

Total rumination duration was affected by breed ($P < 0.01$) and treatment ($P < 0.01$). Alpine goats ruminated longer ($P < 0.01$) than Spanish (310 vs. 249 min, respectively; SEM = 12.8) and rumination duration while fasting was lower ($P < 0.01$) than for other treatments (229, 313, 282, and 295 min for FAST, LOW, CONC, and HIGH, respectively; SEM = 17.6). Treatment did not affect ($P > 0.10$) the number of rumination bouts; however, Alpines had a greater ($P < 0.01$) number of bouts than Spanish (29 vs. 20 bouts, respectively; SEM = 1.9). Average bout duration was affected by both treatment ($P < 0.01$) and breed ($P < 0.01$). Average bout while fasting was shorter ($P < 0.01$) than for other treatments (10, 13, 13, and 15 min for FAST, LOW, CONC, and HIGH, respectively; SEM = 0.9). Spanish had longer ($P = 0.03$) rumination bouts than Alpine (14 vs. 11 min, respectively; SEM = 0.8). In conclusion, similar dry matter intake among non-fasting treatments may have prevented effects on rumination, although greater differences between breeds and fasting state had marked influences.

Key Words: forage quality, goats, rumination

1683 Genome-wide association analysis of residual feed intake and milk yield in dairy goats.

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Interest in both dairy and meat goat production in the US has been increasing, and there is tremendous opportunity for genetic progress in traits that are easy to measure (e.g., milk yield) and those that are more difficult (e.g., residual feed intake, RFI). However, there is little research or infrastructure within the goat industry for implementation of large-scale genetic evaluation. The objective of this study was to conduct a genome-wide association study (GWAS) for RFI and total milk yield in dairy goats. Forty-eight Alpine females (56.4 ± 7.15 kg BW; 423 ± 146.1 kg milk; 225 ± 20.9 d in milk; 16 primiparous) were used. Data in mid- to late lactation were used to calculate RFI. Milk yield and components were collected over a 12-wk period in mid- to late lactation and were used to calculate energy-corrected milk yield (ECMY). ECMY DMI, and BW from the same period were used to calculate RFI, which ranged from −794 to 594 g. DNA was collected via venipuncture and stored on Whatman FTA cards. Genotypes were assayed using the Illumina 52K goat SNP chip. SNPs with a minor allelic frequency < .01 were removed, resulting in 48,632 SNPs available for analysis. Missing genotypes were imputed using BEAGLE and SNP effects were estimated using GenSel on the iPlant platform. For RFI, the posterior mean of the residual variance was 47,934 and the posterior mean of genetic variance was 14,428, giving an estimated heritability of 0.23. For total milk yield, the posterior mean of the residual variance was 10,141 and the posterior mean of genetic variance was 9826, giving an estimated heritability of 0.49. The 100 SNP with the greatest effects contributed 3.1% and 3.3% of the total genetic variance for RFI and total milk yield, respectively. Although the sample size in this study is very small and the ideal usage of genomic information would be to supplement large-scale genetic evaluation programs, it illustrates the potential of utilizing genomic selection with phenotypes on large populations of dairy goats to make genetic improvement. Genetic selection for RFI and milk yield in dairy goats may be expedited by selection programs that incorporate genomic information, particularly in the absence of large, nationwide breeding value prediction programs.

Key Words: dairy goats, residual feed intake, SNP

1684 Effect of Narasin on nutrient intake and digestibility in wethers fed high-forage diets.

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The objectives in this trial were to determine the effects of adding increased levels of narasin on nutrient intake and digestibility in wethers fed low quality forage. Five White Dorper x Santa Inês wethers (BW 68.7 ± 2.1 kg), cannulated in the rumen, were used in a 5 × 5 Latin square design. Animal were fed daily and diet was composed of coastcross bermudagrass hay (91.0% DM; 67.2% NDF; 32.1% ADF; 6.8% CP; 3.2% EE; 17.3% NFC; 5.5% ash). Narasin was offered twice a day and levels were 0 (control, N0), 8 (N8), 16 (N16), 24 (N24), or 32 (N32) mg/kg DM, corresponding to 0, 80, 160, 240, and 320 mg of Zimprova 100®. The delivery vehicle of narasin was 20 g of ground corn containing the set dosage of narasin in 1 kg of DM. Every experimental period lasted 20 d. The first 15 d were used to adapt the wethers with the experimental diets. Daily feed intake and fecal output were determined on Days 16, 17, 18, and 19 of each period. For total collection of feces, harnesses with collection bags were used to avoid contamination of feces by urine. Data were analyzed using the MIXED procedure (SAS Inst. Inc.) and the LSMEANS option was used to generate individual means. The effect of narasin levels were evaluated using linear and quadratic orthogonal contrasts. The effects were considered significant when $P < 0.10$. Increasing levels of narasin did not affect dry matter (1.1 ± 0.2 kg; $P = 0.70$), organic matter (1.0 ± 0.2 kg; $P = 0.69$), NDF (0.7 ± 0.1 kg; $P = 0.69$), and ADF (0.3 ± 0.01 kg; $P = 0.68$) intakes. Experimental diets did not affect DM (50.5 ± 2.6%; $P = 0.57$) and OM (50.9 ± 2.6%; $P = 0.63$) digestibilities. However, narasin increased linearly NDF digestibility (N0: 50.4%; N8: 53.7%; N16: 51.8%; N24: 55.0%; N32: 55.2%; $P = 0.06$). ADF digestibility tended to differ with increased levels of narasin (N0: 49.1; N8: 51.1; N16: 49.2; N24:

53.4; N32: 53.0%; $P = 0.15$). Levels of narasin improve NDF digestibility in wethers fed a low quality forage diet without affecting nutrient intake.

Key Words: intake, ionophore, narasin.

1685 Effects of different levels of zilpaterol hydrochloride on feedlot performance and carcass characteristics of hair-breed ram lambs.

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Twenty-four Dorper × Pelibuey ram lambs initially weighing 30.73 ± 1.04 kg were used in a randomized complete block experimental design to evaluate effects of different levels of zilpaterol hydrochloride (ZH; 0, 0.1, 0.2, and 0.3 mg/kg BW) on feedlot performance and carcass characteristics of ram lambs. After a 30-d feeding period, all lambs were harvested. All data collected were analyzed with analysis of variance using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Means were separated with a PDIFF STDERR statement. Significance was declared at $P \leq 0.05$ and tendency when $0.05 < P \leq 0.10$. The doses of ZH improved ($P < 0.05$) feed intake, water consumption, ADG, and G:F. Carcass characteristics as HCW, CCW, KPH, dressing %, LM area, LM pH at 24 h, leg perimeter were not affected ($P > 0.05$) by ZH level supplementation. Inclusion of different levels of ZH in feedlot finishing diets improve feedlot performance; without affecting carcass characteristics.

Key Words: β-adrenergic agonist, carcass characteristics, feedlot sheep, growth rate

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1686 Performance of lambs fed high concentrate-diets containing monensin or narasin.

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The objective in this trial was to determine the effect of ionophore inclusion (monensin or doses of narasin) on performance of lambs fed high-concentrate diet. Forty-five (30 males and 15 females) Dorper x Santa Inês lambs were assigned to a randomized complete block design, defined by age (90.5 ± 0.8 d old), sex, and initial BW (25.3 ± 0.5 kg). Lambs were housed in "tie stalls" and fed a TMR composed of 90% concentrate. Diets were isonitrogenous (15.5% CP, DM basis) and treatments were Control (without ionophore), monensin (25 mg/kg DM), and three doses of narasin (5, 10 or 15 mg/kg DM), corresponding to the experimental diets C, M, N5, N10, and N15, respectively. Feed ingredients (ground corn, ground hay, soybean meal, limestone, mineral salt, urea, and ammonium chloride) and ionophores were mixed using a horizontal mixer. The experiment lasted 56 d and lambs were weighted after a fasting period of 14 h on Days 0, 14, 28, 42, and 56. Average daily gain (ADG), dry matter intake (DMI), and feed efficiency (FE) were determined in each period. Data were analyzed using the MIXED procedure (SAS Inst. Inc.). There were two contrasts previously defined (I: control vs. ionophores; II: monensin vs. narasin). The effects of levels of narasin (control, N5, N10, and N15) were evaluated using linear and quadratic orthogonal contrasts. The effects were considered significant when $P < 0.10$. Inclusion of ionophores did not affect BW 14d after start receiving the experimental diets. However, on d 28 animals fed the diets containing narasin (5, 10, or 15 mg/kg) were heavier ($P = 0.01$) than those fed monensin (C: 32.7; M: 31.3; N5: 32.2; N10: 33.2; N15: 33.2 kg). On d 42 there was an increased linear effect ($P = 0.04$) for levels of narasin and animals fed monensin were lighter than animals fed narasin (C: 36.8; M: 36.1; N5: 36.1; N10: 38.0; N15: 37.8 kg; $P = 0.07$). There was an increased linear effect ($P = 0.02$) on final BW (d56) and animals fed narasin were heavier than those fed monensin (C: 40.9; M: 40.2; N5: 40.5; N10: 42.4; N15: 42.5 kg; $P = 0.02$). There was no effect ($P = 0.40$) on DMI (1.09 ± 0.04 kg/d). Narasin increased ($P = 0.04$) feed efficiency (C: 0.25; M: 0.25; N5: 0.25 N10: 0.26; N15: 0.27). Narasin improved lamb performance compared to a monensin dosage of 25 mg/kg.

Key Words: feed efficiency, ionophore, narasin.

1687 Effects of high concentrations of crude glycerin on blood parameters of energy metabolism in finishing lambs.

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Forty crossbred (Santa Ines × Dorper) ram lambs (21.7 ± 2.7 kg BW, 90 d old) were used to evaluate the effects of high concentrations of crude glycerin on some blood parameters of energy metabolism. Lambs were assigned to a complete randomized block design (initial BW) and fed four isonitrogenous (18.4% CP) and isocaloric (2.7 Kcal ME/kg) experimental diets containing corn silage (40%), and concentrate (60%) composed of soybean hulls, soybean meal, mineral premix, and crude glycerin replacing 0 (G0), 10 (G10), 20 (G20), or 30% (G30) corn cracked grain, on a DM basis. Crude glycerin totally replaced corn grain in G30 and it was composed of 83% glycerol, 95% DM, 6% salt, and less than

0.01% methanol. The feedlot period lasted 66 d (21 d adaptation [three step-up diets] and 45 d finishing period). Animals were fed twice daily (0700 and 1900 h). Blood samples were collected from the jugular by venipuncture on the d 0 and d 45 of finishing period (day effect), before morning feeding and 4 h after feeding (prandial effect). Serum total cholesterol (TC), serum triglycerides (TG), blood glucose (BG), serum HDL-cholesterol (HDL), serum LDL-cholesterol (LDL), and serum VLDL-cholesterol (VLDL) were evaluated. Data were analyzed using a linear mixed model with Kenward-Rogers adjustment for calculation of degrees of freedom. Whenever the F-test was significant, contrast analyses were performed and differences of least squares means were determined using the pairwise Tukey–Kramer multiple test. Crude glycerin did not change BG concentrations, but a day effect was observed ($P < 0.001$) for this variable. A linear decrease in TC was observed with increasing concentrations of crude glycerin in the diets ($P = 0.02$). A prandial effect was observed for TG ($P = 0.001$) and for VLDL ($P < 0.0001$), while HDL concentrations linearly decreased ($P < 0.001$), and showed a day effect ($P < 0.001$) and a prandial effect ($P = 0.02$). The concentration of LDL linearly decreased with crude glycerin inclusion, and showed a significant day effect ($P < 0.001$). The average values (mg/dL) observed for treatments G0, G10, G20, and G30 were, respectively: TC = 41.0, 41.2, 36.4, 36.1; TG = 12.5, 13.2, 12.1, 15.3; BG = 83.6, 85.7, 82.1, 87.2; HDL = 13.3, 12.7, 11.4, 10.7; LDL = 25.2, 22.9, 23.8, 22.3; VLDL = 2.5, 2.6, 2.4, 3.1. Feeding crossbred finishing lambs up to 30% crude glycerin can decrease the concentration of some blood parameters of energy metabolism, such as total cholesterol, HDL and LDL.

Key Words: blood, glycerol, sheep

1688 Effect of diets rich in starch or digestible fiber on glucose metabolism of ewes and goats in mid-lactation. M. F. Lunesu*[1], G. C. Bomboi[2], M. Decandia[3], G. Molle[3], G. Gaspa[1], A. S. Atzori[1], L. S. Knupp[4], and A. Cannas[1], *[1]Dipartimento di Agraria, University of Sassari, Sassari, Italy, [2]Dipartimento di Medicina Veterinaria, University of Sassari, Sassari, Italy, [3]Dipartimento per la Ricerca nelle Produzioni Animali, Agris Sardegna, Sassari, Italy, [4]Departamento de Zootecnia, Universidade Federal de Vicosa, Vicosa, Brazil.*

This study evaluated if dietary carbohydrate type (starch vs. fiber) can modulate glucose metabolism in ewes and goats in mid-lactation. At c.a. 95 d in milk (DIM), 20 ewes and 20 goats were subdivided into two groups. The first one (10 sheep and 10 goats) received a high-starch diet (HS; 24.1% starch, 36.4% NDF, 15.4% CP, DM basis) and the other (10 sheep and 10 goats) a highly-digestible fiber diet (HF; 10.5% starch, 46.8% NDF, 15.4% CP, DM basis), obtained by replacing corn and barley meal with soybean hulls. At 153 DIM, glucose tolerance tests (GTT) were performed on 10 sheep and 10 goats selected from each group. Diet was withdrawn in the afternoon of the day before the test. One mL of a 50% glucose solution per kg of BW was injected into the jugular vein of each animal. Blood samples were collected 15 min before and at 5, 10, 15, 30, 45, and 90 min after glucose injection. At 165 DIM, all the animals were subjected to blood postprandial sampling at 30, 60, 120, 180, and 240 min post feeding. Blood glucose was assayed by an enzymatic-colorimetric method. Blood glucose concentration data were analyzed by the PROC MIXED of SAS with repeated measurements. For GTT the incremental area under the curve (AUC), the fractional turnover rate (k), and the half-life were calculated and data were analyzed with a two-factor (diet within species and species) ANOVA. The −15-min glucose concentration was higher in sheep than goats (73.5 vs. 53.6 mg/dl; $P < 0.005$) but was not affected by diet. During the GTT, the mean blood glucose concentration was greater in sheep than goats (228.1 vs. 209.2 mg/dl; $P < 0.05$) and in HS goats than HF goats (217.9 vs. 198.6 mg/dl $P < 0.01$), whereas it did not differ between HS sheep and HF sheep. The values of AUC, k and half-life were not affected by species or diet. Regarding the postprandial sampling, mean blood glucose concentration was higher in sheep than goats (60.3 vs. 50.3 mg/dl; $P < 0.001$) and in HS goats than HF goats (52.2 vs. 48.1 mg/dl; $P < 0.001$), whereas it did not differ between HS sheep and HF sheep. In conclusion, it seems that the source of carbohydrates modulated blood glucose metabolism in goats but not in sheep.

Key Words: fiber, glycemia, goats, sheep, starch

1689 Reproductive parameters of Dorper ewes in south Texas. E. C. Taylor*[1], J. A. Reyes[1], M. R. Garcia[1], and R. Stanko[2], *[1]Texas A&M University-Kingsville, Kingsville, [2]Texas A&M University-Kingsville, Texas A&M AgriLife Research, Kingsville.*

The overall objectives of two studies were to determine reproductive characteristics of Dorper ewes in south Texas and their potential use in accelerated mating. The initial study characterized month of puberty and subsequent anestrus in 16 spring-born, pre-pubertal ewe lambs (34.9 ± 0.43 kg). Lambs were monitored over a 13-mo period (September to October). Lambs were housed together and fed commercial pellets (2% BW, DM basis) and ad libitum hay. The second study determined the effect of a 9-d controlled vaginal insert (CIDR; 0.3 g progesterone) administered on d 0 of a 30-d anestrus breeding season (June). Thirteen non-lactating, postpartum (90 ± 4.5 d) ewes of second parity were randomly allocated into one of two treatment groups. All ewes were bled weekly for serum progesterone analysis to confirm anestrous, ovulation, and pregnancy. Ewes were continuously exposed to a fertile ram during the 30-d anestrous breeding season. Six ewes received a CIDR on d 0 to 9 (CT) and were housed separately and away from seven control ewes (CON). Two additional ewes were

housed in isolation and served as anestrous sentinels. Rams were alternated between CT and CON on d 16. Cumulative percentage of spring-born ewe lambs attaining puberty by September and December was 25% and 100%, respectively. Lambs had a mean BW of 39.1 ± 0.72 kg at 100% pubertal. During January, 62.5% of ewe lambs became anestrous and all were in anestrous by the seventh day of March. Resumption of estrous cycles began in May (6.25%) and continued through September (100%). Postpartum, CT ewes had a reduced ($P <$ 0.02) ram introduction to lambing interval (152.8 ± 3.2 d) as compared to CON ewes (165.7 ± 3.0 d). Ram introduction to lambing interval for CT ewes which conceived first service was further reduced as compared to CON ewes conceiving at first service (149.3 ± 1.3 d vs. 160.7 ± 1.5 d; $P < 0.01$). However, CT and CON ewes had similar conception rate (83.3% vs. 87.7%), days to conception (5.0 ± 4.5 vs. 14.7 ± 4.1), and lambs per ewe (1.4 ± 0.3 vs. 2.0 ± 0.3). We conclude that Dorper ewe lambs are sexually mature during the first fall-breeding season and enter anestrus as yearlings (March to May). Ram exposure alone is as effective as progesterone co-treatment to induce breeding of 90-d, postpartum Dorper ewes during the late anestrus season.

Key Words: anestrus, CIDR, Dorper

1690 Comparison of linear model and artificial neural network using antler beam diameter and beam length of white-tailed deer (*Odocoileus virginianus*).

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A thirty-one-year (1977–2008) record of field-dressed weight (FDW), antler diameter (AD), and beam length (BL) of male white-tailed deer (WTD) harvested at Berry College Wildlife Management Area (WMA), Mount Berry, Georgia, was analyzed using linear model and Artificial Neural Network (ANN). A total of 3564 male WTD were harvested at the WMA during the period under study. Of the total deer harvested, 63.95% were 1.5 yr old and 22.42%, 8.64%, 3.87%, and 0.67% for 2.5, 3.5, 4.5, and 5.5 yr old, respectively. The mean FDW of deer was 32.33 kg. Linear model and ANN were used to predict antler diameter and beam length of WTD. Linear model used to analyze AD and BL of deer includes the factors of year and month of harvest, and the covariates of age and FDW. For ANN, the two-layer feed-forward perceptron, also called single hidden layer feed-forward neural network was used to estimate AD and BL of deer. In the training phase of ANN, year, month of harvest, age, and FDW were linearly combined with a vector of weights. The resulting linear score was then transformed using an activation function to produce the output of the single hidden neuron. The estimates of correlation coefficients between FDW and AD, FDW and BL, and AD and BL were 0.75, 0.77, and 0.85 ($P < 0.01$), respectively. The estimates of regression coefficients indicated that FDW of the deer affected ($P < 0.05$) AD (0.92 ± .03) and BL (0.74 ± .02). Correlation coefficients between observed and predicted values of AD and BL from linear model are 0.81 and 0.83. However, ANN results in higher correlation coefficients (0.94 and 0.86) between observed and predicted values of AD and BL than linear model. This result demonstrates the utility of ANN in multidimensional data analysis.

Key Words: linear model, neural network, white-tailed deer

1691 Induction of sexual activity in Dorper ewes: Effect of two intramuscular doses of progesterone vs. progesterone vaginal sponges + eCG.

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The use of intravaginal sponges is a high-cost treatment which requires trained personnel while can generate reproductive problems in the animals. Therefore, the use of intramuscular (im) progesterone (P4) could be an alternative to avoid such a scenario. The reproductive outcomes of Dorper anestrus ewes using different im doses of P4 regarding the use of P4-intravaginal sponges + eCG, was evaluated. The study was carried-out in northern Mexico during the anestrus season (26°N, February). Anestrus ewes (n = 52, 3–5 yr old) similar body weight (BW) and body condition score (BCS) were subjected to two transrectal ultrasound screenings on Days 14 and 7 prior to the onset of the experimental treatments to confirm the absence of functional corpora lutea. Thereafter, ewes were randomly distributed to three experimental groups: 1) IMG1 (n = 21; 41.7 ± 4.0 kg BW, 2.1 ± 0.2 BCS) receiving 30 mg-im of P4 on Days 5 and 2 prior to eCG administration, 2) IMG2 (n = 17; 41 ± 7 kg BW, 2.0 ± 0.6 BCS) receiving 20 mg-im of P4 on Days 5 and 2 prior to eCG application, and 3) IVS (n = 14; 41.5 ± 3.0 kg BW, 2.0 ± 0.2 BCS), receiving an intravaginal sponge Chronogest® during 6 d and removed 24 h prior to eCG application (d 0). The three groups received a single dose of 300 IU eCG im on d 0. Estrus activity was recorded after exposure to one sexually active male during 15 min twice per day (0800 and 1800 h) × 5 d. On Day 10, the percentage of ovulations across treatments was determined by detecting the presence of corpora lutea throughout ultrasonographic scanning (USS). Then, on Day 45, another transrectal-USS was performed to determine pregnancy rate. Estrus activity,

ovarian activity and pregnancy were evaluated among treatments thru X^2considering the daily and cumulative proportions of these variables (MYSTAT 12 X2 program). The percentage of estrus were different ($P < 0.05$) between all the groups (43% IMG1, 35% IMG2, and 100% IVS). The largest ovulation percentage and gestation rate ($P < 0.05$) were observed in IVS group (93% and 79%, respectively), and similar ($P > 0.05$) for both IMG groups (62% IMG1 and 59% IMG2 for ovulation percentage, and 24% for gestation rate in both groups). Results demonstrated a better reproductive performance of previously anestrus Dorper ewes treated with intravaginal P4-sponges + eCG with respect to those receiving the im administration of P4. In conclusion, the synchronization protocol using two injections of progesterone had less sexual response compared to the use of vaginal sponges.

Key Words: anestrus, ewes, progesterone

1692 Effect of supplementation with antioxidants in goats and their newborns evaluated during the transition period.

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The objective of this study was to evaluate hematological parameters of dam and newborn goats of the does that were supplemented with Selenium and Vitamin E. Also, the amount of Selenium and Vitamin E of the serum and milk was measured for evaluation of amount that was transferred from dam to newborns. Fifteen Saanen does that were supplemented starting on the fourth month of pregnancy until the end of the experiment and twenty-one kids from these does were used. The does and the newborns were divided into three groups based on the dam treatments: Control and Control milk (base diet with 50% forage and 50% concentrate); Se and Se milk (2.5 mg of Se/Kg Dm added to the diet) and Sev and Sev milk (2.5 mg of Se/Kg DM and 1000 IU/day of Vitamin E/kg DM), for does and kids, respectively. The kids started receiving ad libitum access to feed from 7 d postpartum. The experiment continued for 56 d. Blood samples were collected from dam before the supplementation, during the partum and 2, 7, 14, and 28 d postpartum. Milk was collected during partum and 28 d postpartum. Blood samples were collected from newborns before ingesting of colostrum and 2, 7, 14, and 28 d postpartum. Blood samples were analyzed for Selenium, Vitamim E, Erythrocyte (red blood cell- RBC- 10^6/mm^3), Hemoglobin (Hb-g/dL), Hematocrit (Hct-%), Mean Corpuscular Volume (MCV-μ^3), Mean Corpuscular Hemoglobin (MCH-pg), Mean Corpuscular Hemoglobin Concentration (MCHC-%), Red Cell Distribution Width (RDW-%). Milk samples were analyzed for Selenium and Vitamin E. Kids were weighed at birth and 7, 14, 21, and 28 after birth. The experimental design was a complete randomized design with repeated measures, with replications. Data were analyzed by analysis of variance and the means were compared by Tukey test ($P \leq 0.05$). There was no significant effect of treatment ($P > 0.05$) for all hematological parameters, Vitamin E for dam and newborns nor for weight of the kids. For Se the results showed significant increase ($P < 0.05$) of the transfer from dam to the kids with values of 0.20, 0.17, and 0.08 mg/kg of dam serum; 0.49, 0.25, and 0.062 mg/kg of dam milk and 0.15, 0.18, and 0.057 mg/kg of kids serum of treatments Sev, Se, and control, respectively

Key Words: birth, nutrition, selenium, vitamin E

1693 Effects of feeding varying levels of deoiled distillers dried grains with solubles on fatty acid composition of subcutaneous adipose tissue in meat goats.

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Deoiled distillers dried grains with solubles (D-DDGS), a by-product of the fuel ethanol industry, have increasingly been used as ingredients in livestock feed. These D-DDGSs have a reduced fat content and increased protein content making them attractive ingredients, however, feeding D-DDGS can affect carcass composition. The objective of this study was to investigate the effect of D-DDGS on fatty acid (FA) composition of subcutaneous (s.c.) adipose tissues in goats. Four experimental diets containing 50% Bermuda grass hay plus 50% concentrate mix containing 0 (CON), 10, 20, or 30% D-DDGS (D-DDGS10, D-DDGS20, or D-DDGS30, respectively) in the diet were randomly assigned to twenty-four castrated male Kiko goats ($n = 6$ per treatment). The goats were slaughtered at 84 d and s.c. fat was collected from directly over the sternum of the carcass, and were then pulverized, and stored at −80°C. The fat samples were directly derivatized for fatty acid identification and quantification on a gas chromatography system (Agilent Technologies, Santa Clara, CA) using internal standard calibration. Fatty acid methyl ester concentrations were used to calculate fatty acid concentrations and percentages. Statistical analysis was performed using the GLIMMIX procedure of SAS 9.4 (SAS Institute Inc., Cary, NC.) and statistical significance was determined at $P \leq 0.05$. D-DDGS did not affect total FA content ($P \leq 0.395$) of adipose tissues, however, their inclusion changed concentrations and percentages of important FA ($P < 0.038$). Concentrations of 18:1 t, 18:2 n6c, 20:1 n9c, and polyunsaturated (PUFA) of s.c. fat from D-DDGS30 goat were 16.26, 16.29, 9.35, and 19.74 mg/g, respectively, which were greater than those from D-DDGS10 and CON

goats ($P < 0.026$). Because of the similar total FA content, the percentages of 18:1 t, 18:2 n6c, 20:1 n9c, and PUFA (2.12, 2.11, 1.25, and 2.56%, respectively) were also greater in s.c. fat of D-DDGS30 goats than those of D-DDGS10 and CON goats. Although concentration of 20:4 n6c was similar among CON and D-DDGS treatments ($P = 0.408$), its percentage was greater in s.c. fat of D-DDGS30 goats than that of CON goats ($P = 0.018$). These data indicate that feeding D-DDGS30 increased the percentages of unsaturated fatty acids in the s.c. depot of the meat goats in the current study and may be used to alter carcass fat composition.

Key Words: adipose tissue, distillers, goat

1694 Dietary effects of grass hay and alfalfa hay on the digestive microbiome of the alpaca. C. Carroll*, K. D. Olsen, J. M. Chaston, and T. F. Robinson, *Brigham Young University, Provo, UT.*

The purpose of this study is to identify the effects of a grass hay diet (GH) and an alfalfa hay diet (AH) on the digestive microbiome of the alpaca. Ten adult male alpacas were randomly selected for the study and divided into two groups; each group was fed a different diet (GH or AH) for thirty days. Both groups were fed once daily ad libitum. At the end of the feeding period, digesta samples were taken from the first stomach compartment (C1), duodenum, jejunum, ileum, cecum, and large intestine of each alpaca. Bacterial DNA was isolated from each sample and sequenced to identify operational taxonomic units, or bacterial taxa. All data were analyzed using QIIME software. Comparisons of the microbial composition of samples from grass-fed and alfalfa-fed alpacas at each digestive tract sample site showed that the microbiome at any single body site differed with diet ($P < 0.05$). Among the differences noted in the microbiomes of alpacas fed AH include a shift toward a higher proportion of phylum *Euryarchaeota* and a lower proportion of phylum *Actinobacteria* in the duodenum, ileum, and jejunum; and a higher proportion of phylum *Euryarchaeota* with a lower proportion of phylum *Bacteroidetes* in the cecum and large intestine. Analyses of the microbial composition of each body site revealed the presence of three different microbiomes per diet treatment group ($P < 0.05$); that of C1, the small intestine (duodenum, jejunum, and ileum), and the distal intestine (cecum and large intestine). The predominant phyla were *Firmicutes* (all sites), *Bacteroidetes* (C1, cecum, and large intestine), *Actinobacteria* (duodenum, jejunum, and ileum), and *Euryarchaeota* (duodenum, jejunum, and ileum). These data demonstrate that, in alpacas, forage type does affect the predominant microbes and though taxa are similar between tract sites, there are shifts in the populations.

Key Words: alpaca, forage, microbiome

1695 Sunflower and palm cake as supplemental fatty acid sources to feedlot lambs. J. G. de Souza[*1,2], P. G. Cirqueira[2], J. P. I. S. Monnerat[3], and C. V. D. M. Ribeiro[2], *[1]Penn State University, University Park, [2]Federal University of Bahia, Salvador, Brazil, [3]Federal University of Pernambuco Rural, Recife, Brazil.*

The sunflower cake and palm cake are two by-products of the biodiesel industry with different profiles of fatty acids (FA). The sunflower cake has 60% of unsaturated FA and the palm cake is rich in medium-chain fatty acids (MCFA). Feeding both sources to ruminants may increase FA digestibility and improve energy intake. Therefore, the objective of this study was to evaluate the interaction of the dietary supplementation of sunflower cake and palm cake on DMI and blood parameters of feedlot lambs. Twenty non-castrated lambs [23.81 ± 4.3 kg] were individually penned and used in a completely randomized design. The animals were fed 40% Tifton hay plus 60% concentrate, with 5% of supplemental FA (% DM). The treatment diets consisted of the contribution of each fat source to the total FA supplementation, as follows: 1) 100% of supplemental FA from sunflower cake; 2) 66% from sunflower cake and 33% from palm cake; 3) 33% from sunflower cake and 66% from palm cake; and 4) 100% of supplemental FA from palm cake. The collection period started on the 35th d of the feedlot period and lasted for 5 d, when the DMI was determined. Blood parameters were taken on the 36th d at 0, 3, 6, and 9 h after the morning feeding. Data were compared by orthogonal polynomial contrasts to determine linear and quadratic effects of the substitution of sunflower cake by palm cake, and significance was declared at 5%. No effect was observed for the daily average serum concentrations of AST (199.80, 197.51, 196.78, 185.56 UI/L), ALT (36.07, 45.21, 41.96, 38.09 UI/L), urea (39.31, 43.55, 48.96, 47.11 mg/dL), triglycerides (18.35, 18.53, 16.16, 17.05 mg/L), and NEFA (1.01, 1.15, 1.17, 1.31 mmol/L) as sunflower cake was substituted by palm cake. A treatment by time interaction ($P < 0.05$) was observed only for triglycerides and NEFA. There was a linear effect ($P < 0.05$) for DMI (1.266, 1.017, 1.177, 0.902 kg/d) and ether extract intake (0.09, 0.05, 0.05, 0.03 kg/d) as sunflower cake was substituted by palm cake. In conclusion, replacement of sunflower cake by palm cake decrease DMI without affecting blood metabolites.

Key Words: blood parameters, sheep, supplemental fatty acids

Table 1697.

Table 1. Reproductive response of Alpine goats receiving 20 mg of progesterone and 100 IU eCG, treated with 4 mg GnRH i.m. or non-GnRH treated in Northern Mexico[1]

	GnRH Group	Control Group
Estrus latency (h)	**44.6±3.7ª**	**52.0±3.7ª**
Estrus response (%)	14/14, 100%	12/12, 100%
Ovulation rate (%)	**12/14, 85.7%**	**10/12, 83.3%**
Pregnancy rate (%)	7/14, 50%	8/12, 67%

[1] No differences occurred for any variable between treatments

1696 Ground chevon as influenced by different concentrations of rosemary extracts. M. Y. Muñoz[1], J. H. Lee[2], C. D. Santos[1], X. Ma[2], A. Discua[*2], and B. Kouakou[2], *[1]Universidad Nacional de Agricultura, Catacamas, Honduras, [2]Fort Valley State University, Fort Valley, GA.*

Rosemary extracts (RE), containing high concentrations of polyphenol compounds that have antioxidant and antimicrobial properties, which could increase the shelf-life of fresh meat. Numerous studies have been conducted to enhance the quality of fresh meat from ruminants by feeding dietary supplements containing high amounts of polyphenol compounds. However, limited information is available on the effectiveness of RE on shelf-life of ground chevon (goat meat). The aim of this study was to determine the effect of different concentrations of RE on the physicochemical and microbial properties of ground chevon stored under retail display conditions. Ground chevon was prepared with shoulder and leg cuts from Kiko crossbred (8 mo old, BW = 39.7 ± 2.55 kg) male goats, treated with four different concentrations of RE (0, 0.02, 0.1, or 0.25%). Each batch of RE treated ground chevon (3/RE; 8.0 kg/batch) was placed on high barrier polypropylene trays and sealed with lidding films (30 trays/batch), and stored in a display case at 4°C over a 15-d period. Six packages (250 g/package) from each RE treatment (30 packages/RE) were analyzed for color properties (CIE L*a*b* values), lipid stabilities (thiobarbituric acid-reactive substances, TBARS), and bacterial counts (total aerobic bacteria, coliforms, *Escherichia coli*, yeasts, and molds) after 1, 4, 8, 12, 15 d of storage. All data were analyzed as a randomized block design, blocked by batch, with a 4 × 5 factorial treatment arrangement using the MIXED procedure of SAS. Ground chevon that contained 0.1 or 0.25% RE had higher ($P < 0.01$) CIE L*(lightness) values than that contained 0% RE. The CIE a* (redness) and b* (yellowness) values of ground chevon significantly decreased after 12-d of storage. Ground chevon containing 0.1 or 0.25% RE had lower ($P < 0.01$) total aerobic bacteria than that containing 0.02 or 0% RE. Furthermore, total aerobic bacteria counts increased ($P < 0.01$; 2.32 to 4.39 ± 0.073 log CFU/g) with storage time in ground chevon containing all different concentrations of RE. This trend was also found in the yeast and mold counts in the ground chevon. The TBARS values varied for all RE treated groups and remained lower than 1.0 mg MAD/kg over the storage period. The results indicated that higher concentrations of rosemary extracts in ground chevon might inhibit the growth of aerobic bacteria. However, the lipid stability of ground chevon was not enhanced by the inclusion of rosemary extracts.

Key Words: ground chevon, rosemary extracts, shelf-life

1697 Post-estrus GnRH administration does not improve fertility in Alpine goats in northern Mexico. Z. Santos[*1], C. A. Meza-Herrera[2], J. M. Guillen[1], F. Arellano[1], R. Rodriguez[1], and F. G. Véliz-Deras[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Mexico, [2]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Mexico.*

The aim of this study was to evaluate the possible effect of GnRH administration during the implantation process in Alpine goats in northern Mexico (26° 23 'N). The study included sexually active bucks ($n = 4$) and multiparous anestrus Alpine goats ($n = 26$). Early in May, goats with homogeneous body condition score (3.0 ± 0.11) were treated with 20 mg of progesterone i.m (d0) and 24 h later (d1) received 100 IU of eCG. Thereafter, on d-13 post-estrus, goats were randomly distributed into the following experimental groups: 1) the GG group ($n = 14$) received 4 mg of GnRH i.m. (synthetic analog) and 2) the GC ($n = 12$) served as a control, receiving saline. Estrus activity was confirmed every 12 h for 5 min using an aproned male from d 0 to d 15. Once in standing estrus, goats were bred by a sexually active male. Then, on d45, a transrectal ultrasonographic scanning (USS; HS-2000, Honda Electronics Co, LTD) was performed to determine pregnancy rate. The response variables estrus response (ER), ovulation (OR) and pregnancy (PR) rates were analyzed by X^2 and estrus latency (EL) with a t-student test (SYSTAT 12, Evanston, IL, USA). None of the response variables EL, ER, OR, and PR differed ($P > 0.05$) between experimental groups. Administration of GnRH on d-13 post-estrus did not improved fertility in Alpine goats from northern Mexico.

Key Words: GnRH, progesterone, synchronization

Table 1699.

Table 1. Reproductive performance of anovulatory goats exposed to males previously treated with estrogenized females either changed every 12 h (GR) or not-changed (GN) and males with control saline-treated females (GC) under the anestrus season (Feb-Mar) and natural photoperiod at 26°N

	GR	GN	GC
Goats (n)	(24)	(24)	(24)
Estrus response (n)	19/24[a]	19/24[a]	0/24[b]
	80%	80%	0%
Estrus latency (h)	89.68±5.8[a]	106.74±5.4[a]	0[b]
Pregnancy rates (n)	14/24[a]	14/24[a]	0/24[b]
	58%	58%	0%

[ab] Means with different superscripts differ (p=0.05)

1698 Quality of chevon chops as influenced by different packaging atmospheres. C. D. Santos[1], J. H. Lee[2], M. Y. Muñoz[1], A. Discua[2], X. Ma[2], D. Kafle[*2], and B. Kouakou[2], *[1]Universidad Nacional de Agricultura, Catacamas, Honduras, [2]Fort Valley State University, Fort Valley, GA.*

Vacuum and modified atmosphere packaging (MAP) techniques are used to extend the display life of fresh meat. The aim of this work was to evaluate the microbial and physicochemical properties of goat meat (chevon) cuts packaged under different atmospheres. Chevon chops from Kiko crossbred (8 mo. old, BW = 39.7 ± 2.55 kg) male goats were packaged under high carbon dioxide (CO_2; 80%), nitrogen (N_2; 80%), vacuum (VAC), or ambient air (AIR) atmospheres (30 packages/atmosphere) using an MAP tray sealer. All treated packages were stored at 4°C under 1700 lux of fluorescent lighting for 15 d. Six packages (4 chops/package) from each packaging treatment (6 packages/d) were analyzed for color properties (CIE L*a*b* values), lipid stabilities (thiobarbituric acid-reactive substances, TBARS), and bacterial counts (total aerobic bacteria, coliforms, *Escherichia coli*, yeasts, and molds) after 1, 4, 8, 12, 15-d of storage. All data were analyzed as a completely randomized design with a 4 × 5 factorial treatment arrangement using MIXED procedure of SAS. Chevon chops from high N_2 packages had higher ($P < 0.01$) CIE a*(redness) and lower b* (yellowness) values than those from VAC packages. The CIE a* and b* values of chevon chops significantly decreased with storage time; however, the CIE L* (lightness) values increased ($P < 0.01$) with storage time with some variations. No significant differences were found in the bacterial counts in chevon cuts from vacuum and high-CO_2 and-N_2 packages. Coliforms (1.26 to 5.11 ± 0.158 log CFU/g), *E. coli* (1.26 to 5.11 ± 0.073 log CFU/g) yeasts (1.02 to 3.06 ± 0.085 log CFU/g) and molds (1.72 to 5.55 ± 0.135 log CFU/g), and total aerobic bacterial (2.08 to 5.42 ± 0.243 log CFU/g) counts increased ($P < 0.01$) with storage time in chevon chops from all packaging treatments. The TBARS values of chevon chops varied for all packaging treatments and increased ($P < 0.01$) as the storage time progressed (0.13 to 0.31 ± 0.026 mg MAD/kg). The results indicated that high nitrogen atmosphere packaging might improve the color property of fresh chevon cuts. However, neither vacuum nor modified atmosphere packaging methods might significantly inhibit the lipid oxidation and microbial growth in fresh chevon cuts during 15 d storage.

Key Words: chevon chops, packaging atmospheres, shelf-life

1699 Reproductive performance of anovulatory goats stimulated by bucks previously exposed to estrogenized does. J. M. Guillen[*1], C. A. Meza-Herrera[2], Z. Santos[1], and F. G. Véliz-Deras[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, Mexico, [2]Universidad Autónoma Chapingo, Unidad Regional Universitaria de Zonas Áridas, Bermejillo, Mexico.*

The aim of this study was to evaluate the effectiveness to induce estrus response of cross-mix dairy anovulatory goats by the stimulus of either sexually active bucks or estrogenized does. Bucks (n = 12) were randomly allotted to three experimental groups (n = 4 per group): A) (GR) males in contact with 2 estrogenized females (EF) for 12 h, and then changed for 2 different EF for 12 h: B) (GN), males were exposed to 2 EF for 12 h, separated 1 h and returning the same goats for 12 h, C) (GC) males were exposed 12 h to 2 anestrous does treated with saline, separated 1 h and returning the same goats for 12 h. While the EF received 2 mg of estradiol cyprionate × 3 d, control females received 1 mL of saline × 3 d. On May 15, 72 cross-mix dairy multiparous females were distributed in 3 homogeneous groups (24 goats each) according to body condition (3.0 ± 0.11 units), and exposed to the previously treated males (GR, GN, GC). Females goats were checked every 12 h × 5 min with a male; on estrus manifestation, females were bred. On Day 45, a transrectal ultrasound scanning was performed to determine pregnancy rate. The estrus response, ovulation, and pregnancy rates were analyzed by X^2while estrus latency considered a t-student test (SYSTAT 12, Evanston, IL, USA). The reproductive response of treated goats is presented in Table 1. Results demonstrate that induction of males with estrogenized females is an effective method to induce out-of-season reproductive function in northern Mexico.

Key Words: buck effect, estrogenized goats, estrus induction

1700 Effect of dried distillers grains on diet digestibility, body weight gain, and carcass composition of lambs. J. R. Bárcena-Gama[*1], K. R. Curzaynz-Leyva[1], C. Sánchez del Real[2], J. C. Escobar-España[1], M. I. Rivas-Martínez[1], E. A. Santillán-Gómez[1], and S. S. Gonzalez-Muñoz[3], *[1]Colegio de Postgraduados, Montecillo Texcoco, Mexico, [2]Universidad Autónoma Chapingo, Chapingo Texcoco, Mexico, [3]Colegio de Postgraduados, Montecillo Estado de Mexico, Mexico.*

Dried corn distillers grains with solubles (DDGS) can partially replace grains and forages in diets for ruminants. Therefore, the objective of this study was to evaluate the effect of diets with or without DDGS on DM, NDF and ADF digestibility, DM intake, ADG, and carcass composition of lambs. The experimental design was completely randomized with four treatments: 1) control, 0.0% DDGS, 2) 15% DDGS, 3) 30% DDGS, and 4) 45% DDGS. Thirty-two Criollo lambs (28.56 ± 2.19 kg initial BW) housed in individual metabolic cages were used in this experiment during 60 d (n = 8). Data were analyzed with PROC MIXED of SAS and treatments means were compared using Tukey test ($P < 0.05$). As compared to control, DDGS increased DM intake (1.7 kg vs. 1.4 kg control), ADG only for lambs fed 15% DDGS (288 g d^{-1} vs. 238 g d^{-1}control), and decreased DM digestibility (7.0%) in lambs fed 45% DDGS ($P < 0.05$). Lambs fed diets with DDGS showed higher weight (8.0%) and yield (2.0%) of hot and cold carcass, but rib eye area was lower for lambs fed 15% DDGS ($P < 0.05$), and no differences were found for back fat ($P > 0.05$). Therefore, the inclusion of DDGS in diets for lambs increased DM intake and improved carcass weight and yield, without affecting back fat.

Key Words: DDGS, lambs, performance.

1701 Effect of high concentrations of crude glycerin on feed intake and growth of feedlot ram lambs. M. Almeida[*1,2], J. M. Bertocco Ezequiel[3], J. R. Paschoaloto[3], H. L. Perez[1,2], V. B. Carvalho[3], E. S. Castro Filho[3], and E. H. C. B. Van Cleef[2,3], *[1]São Paulo State University, Jaboticabal, Brazil, [2]FAPESP, São Paulo, Brazil, [3]Unesp, São Paulo State University, Department of Animal Science, Jaboticabal, Brazil.*

The objective of this study was to evaluate the effects of high concentrations of crude glycerin (CG) on feed intake and growth of finishing lambs. Forty crossbred (Santa Ines × Dorper) ram lambs (21.7 ± 2.7 kg BW and approximately 90 d old) were assigned to a complete randomized block design and fed four isonitrogenous (18.4% CP) and isocaloric (2.7 Kcal ME/kg) experimental diets containing 0, 10, 20, or 30% of CG (83% glycerol), on a dry matter basis. In the diet containing 30% CG, the by-product totally replaced corn grain. The experimental diets were formulated with 30% corn silage and 70% concentrate (corn grain [except the diet with 30% CG], soybean hulls, soybean meal, urea, minerals, and crude glycerin [except the control treatment]). Lambs were housed in a naturally ventilated barn with individual pens, and fed ad libitum twice daily. Animals were weighed at 14-d intervals and were harvested when they reached approximately 35 kg BW. Feed intake and growth were evaluated during the initial (d 0 to d 14), intermediate (d 14 to d 28), and cumulative feedlot period. Data were analyzed using a MIXED procedure, with treatment included as fixed effect and block as random effect. The increasing inclusion of CG in the diets linearly increased days on feed ($P = 0.02$). Dry matter intake (DMI) during the initial feedlot period was decreased with CG inclusion (Linear, $P = 0.03$), while during the intermediate feedlot period, a tendency was observed for DMI to reduce when animals were fed CG (Linear $P = 0.09$). Regarding the cumulative feedlot period, a quadratic effect was observed on DMI ($P = 0.04$), with greater intakes for animals fed treatment containing 10% CG. There was a tendency for reduced average daily gain (ADG) in animals fed CG during initial feedlot period (Linear, $P = 0.08$). The CG also decreased ADG during intermediate feedlot period ($P = 0.02$), and during the cumulative finishing period (Linear, $P = 0.003$). When all treatments with CG were compared with controls, there was a tendency for reduced ADG during intermediate and cumulative periods ($P = 0.07$, $P = 0.09$, respectively). There was also a tendency for reduced cumulative feed efficiency (Linear, $P = 0.07$), when CG was added to the diets. In conclusion, adding up to 10% of CG in diets for crossbred finishing lambs improves feed intake and animal growth.

Key Words: by-product, glycerol, sheep

1702 Conditions to evaluate differences among individual sheep and goats in resilience to restricted drinking water availability. U. L. Mengistu[1,2], R. Puchala[1], T. Sahlu[1], T. A. Gipson[1], L. J. Dawson[1,3], and A. L. Goetsch[*1], *[1]American Institute for Goat Research, Langston University, Langston, OK, [2]School of Animal and Range Sciences, Haramaya University, Dire Dawa, Ethiopia, [3]Center of Veterinary Health Sciences, Oklahoma State University, Stillwater.*

Thirty-six yearling Boer goat (BOE), Katahdin sheep (KAT), and Spanish goat wethers (SPA) were used to study appropriate conditions to evaluate resilience to restricted drinking water availability. Moderate quality grass hay was consumed ad libitum with concentrate (80% corn, 20% soybean meal) supplemented at 0.5% BW. Baseline conditions were determined in the last 2 wk of a 3-wk period (i.e., 100% level). Thereafter, water availability was decreased by 10% every 1 (1X) or 2 wk (2X) to 40% of baseline intake (i.e., 90, 80, 70, 60, 50, and 40% levels), but also with 2 wk at 40% for the 1X restriction

treatment. There was an interaction (P < 0.001) between animal type and restriction level in hay DMI, with values of 346, 360, 358, 276, 286, 235, and 176 g/d for BOE, 656, 592, 592, 469, 522, 407, and 307 g/d for KAT, and 392, 390, 368, 273, 298, 298, and 219 g/d for SPA at levels of 100, 90, 80, 70, 60, 50, and 40%, respectively (SE = 29.1). Moreover, hay DMI by 2X wethers was much lower in wk 2 vs. 1 at the 40% level (week × level interaction, P = 0.008; 409, 369, 345, 377, 336, and 276 g/d in wk 1 and 428, 398, 312, 352, 310, and 203 g/d in wk 2 at 90, 80, 70, 60, 50, and 40% levels, respectively; SE = 23.4). Restriction level affected (P < 0.001) plasma cortisol concentration in 2X wethers on the last day at each level (12.4, 14.0, 23.3, 26.4, and 32.6 nmol/l for 100, 70, 60, 50, and 40% levels, respectively; SE = 3.62). Plasma vasopressin concentration in 2X wethers at the end of each week at 60, 50, and 40% levels was affected by an interaction (P = 0.006) between week and restriction level (3.98, 5.61, and 7.84 in wk 1 and 6.40, 7.22, and 7.06 pmol/l in wk 2, respectively; SE = 0.564). In conclusion, there was some indication that DMI by KAT was more subject to adverse effects of very low water availability but not mild restriction compared with goats. Based on vasopressin concentration, a length of at least 2 wk rather than 1 with a set level(s) of restricted water availability seems desirable, which might also increase meaningfulness of measures such as BW. Results for DMI and cortisol concentration suggest appropriateness of a maximum restriction level of 50%.

Key Words: goats, sheep, water

1703 High concentrations of crude glycerin change ruminal in vitro greenhouse gas emissions in feedlot sheep.

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The objective of this study was to evaluate the effects of high concentrations of crude glycerin (CG) on in vitro greenhouse gas emissions in feedlot sheep. Eight crossbred (Santa Ines × Dorper) ruminally cannulated male sheep (64.5 ± 8.5 kg BW) were distributed in a replicated 4 × 4 Latin square design. Treatments consisted of isonitrogenous (18.4% CP) and isocaloric (2.7 Kcal ME/kg) diets containing 0, 10, 20, or 30% CG, on diets' dry matter basis. In the diet with 30% CG, corn grain was totally replaced. The experimental diets contained 30% corn silage and 70% concentrate (corn grain [except the diet with 30% CG], soybean hulls, soybean meal, urea, minerals, and crude glycerin [except the control treatment]). The animals were housed in semi-covered individual pens and fed ad libitum twice daily. After 21-d adaptation period, rumen content was sampled to serve as inoculum for in vitro incubations. Approximately 200 mg (DM basis) of each diet and buffered rumen fluid (20 mL McDougall's buffer and 10 mL rumen fluid) were placed into 60-mL penicillin glass bottles, purged with helium gas and sealed. The gas production (mL/g DM and mL/g DM disappeared), terminal pH, and DM disappearance were evaluated after 24-h incubation at 39°C. DM disappearance was obtained filtering and drying incubation residues. Gas production was estimated using a digital pressure meter and a transducer, while CH_4 and CO_2concentrations were obtained using gas chromatography. Data were analyzed using MIXED procedure, with fixed effects of diet and period, and random effects of sheep (diet). Orthogonal contrasts were used to determine the linear and quadratic effects of CG. Total gas production was linearly increased with inclusion of CG to the diets ($P = 0.04$), while CO_2 production tended to decrease ($P = 0.10$), decreasing proportion of CH_4 in total gas. DM disappearance was not affected by treatments (average = 46.7%), and when this parameter was taken into account in the gas production calculation, the same effect was observed for total gas production ($P = 0.04$), and CO_2 production linearly decreased ($P = 0.03$). The increasing inclusion of CG in the diets linearly increased terminal pH ($P = 0.02$). In conclusion, high concentrations of crude glycerin have no effect on diets' DM disappearance, but increase in vitro total gas production, decreasing proportion of CH_4 and increasing terminal pH.

Key Words: by-product, glycerol, methane

1704 Factors influencing estimates of energy used for activity by grazing meat goats.

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Ten yearling Boer goat wethers (45.4 ± 0.92 kg) consuming fresh Sudangrass ad libitum while grazing (GRA) a 0.8-ha pasture or individually confined (CON) were used in a crossover experiment with 3-wk periods to evaluate factors influencing estimates of energy used for activity (AEC) when grazing. Fresh forage offered to CON wethers was 15.9 and 13.4% CP and 65.0 and 67.4% NDF in periods 1 and 2, respectively. Based on forage and fecal AIA, forage DE concentration for CON averaged 67.9 and 56.5% in periods 1 and 2, respectively. From these values and fecal DM, least squares means of ME intake were 405 and 484 kJ/kg $BW^{0.75}$ for CON and GRA, respectively (SE = 15.4). Heat energy (HE) determined from heart rate (HR) measured over 1 d and the ratio of HE to HR estimated earlier was less (P < 0.001) for CON than for GRA (482 and 642 kJ/kg $BW^{0.75}$; SE = 17.2). To estimate the AEC from total HE and the partitioning of its sources, a ME requirement for maintenance of 427 kJ/kg $BW^{0.75}$) was assumed; HE expended for tissue energy gain was determined from recovered energy (RE) when greater than 0 and an efficiency of ME use for gain of 0.40 ± 0.009 ([0.0423 × forage ME in MJ/kg DM] + 0.006); and, when RE was less than 0,

the efficiency of use for maintenance of energy from forage and mobilized tissue was 0.68 ± 0.004 ([0.019 × forage ME in MJ/kg DM] + 0.503). The resultant AEC was 39 and 213 kJ/kg $BW^{0.75}$ for CON and GRA, respectively (SE = 21.9). Assuming that mobilized tissue energy was used for maintenance more efficiently (i.e., 0.80) than forage ME yielded slightly greater AEC of 57 and 241 kJ/kg $BW^{0.75}$ for CON and GRA, respectively (SE = 23.9). The former AEC value for GRA and that determined from the difference between GRA and CON HE were much greater than AEC based on time spent in different activities (i.e., lying, standing, grazing, and walking) multiplied by corresponding HE and assuming that AEC resulted from HE when standing, grazing, and walking (217 ± 19.7, 165 ± 19.3, and 46 ± 4.85 kJ/kg $BW^{0.75}$, respectively). In conclusion, determining the AEC of meat goats while grazing by subtraction of other sources of HE is influenced by specific assumptions of energy requirements and efficiencies of use for different physiological functions.

Key Words: activity, energy, goats, grazing

1705 The response to artificial infection with *Haemonchus contortus* and growth performance of sheep and goat progeny of selected parents in a central performance test.

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Fifteen Katahdin (KS-A; 4.0 mo old, 38 kg), 5 Katahdin (KS-B; 3.0 mo, 20 kg), 16 Dorper (DS; 3.4 mo, 25 kg), and 17 St. Croix sheep (CS; 4.2 mo, 18 kg) and 20 Kiko (KG; 3.9 mo, 19 kg), 16 Boer (BG; 4.4 mo, 16 kg), and 18 Spanish goat (SG; 4.3 mo, 18 kg) males from 5 commercial farms in KS, MO, and AR and Langston University (LU) were used to investigate growth performance and response to artificial infection with *Haemonchus contortus* in year 3 of a central test at LU. Animals tested were progeny of dams (based on on-farm data) and sires classified as Resistant and Moderate in year 2. The test entailed an adjustment period of 2 wk followed by 8 wk of data collection. Animal groups were housed separately in adjacent pens with automated feeders allowing free-choice access to a 15% CP diet. During adaptation, anthelmintic treatment resulted in low fecal egg count (FEC; < 600 eggs/g), after which 10,000 larvae were administered orally. Packed cell volume (PCV) was measured weekly and FEC was determined 5 times in wk 5-9. The cubic clustering criterion of SAS® categorized resistance classes. The GLM procedure included animal group and resistance classification, initial BW, PCV, and FEC were covariates, and the logarithmic transformation ln(x+100) was used for mean FEC. Animal group affected (P < 0.01) ADG (308, 264, 321, 254, 139, 243, and 147 g; SEM = 14.6), DMI (2.34, 1.65, 1.65, 1.32, 0.79, 1.28, and 0.94 kg/d; SEM = 0.069), and PCV (25.4, 24.3, 28.6, 29.3, 25.8, 22.9, and 25.7% for KS-A, KS-B, DS, CS, KG, BG, and SG, respectively; SEM = 0.65). The resistant males had highest (P = 0.04) ADG (256, 237, and 225 g for Resistant, Moderate, and Susceptible, respectively; SEM = 8.8). There was an animal group × resistance classification interaction (P = 0.04) on FEC (270, 2346, and 4633 with KS-A, 1088, 5272, and 8263 with KS-B, 442, 1140, and 2370 with DS, 209, 870, and 2368 with CS, 248, 994, and 2431 with KG, 1182, 2164, and 4523 with BG, and 215, 1203, and 3132 eggs/g (untransformed) with SG for Resistant, Moderate, and Susceptible classes, respectively; SEM = 295.0). The correlation coefficient between sire and progeny FEC was 0.27 (P = 0.004) and that of PCV was 0.44 (P < 0.001). In conclusion, selection for resistance did not adversely affect performance of males, and there were moderate relationships between indices of parasite infection of sires and progeny.

Key Words: goats, internal parasitism, sheep

1706 Species and breed differences of small ruminants in response to experimental infection with *Haemonchus contortus* and growth performance in a centralized performance test.

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The response to experimental infection with *Haemonchus contortus* and growth performance of small ruminant males were compared in a central performance test at Langston University (LU). Seventy-five Boer (3.8 mo of initial age, 19 kg), 51 Kiko (3.7 mo, 19 kg), and 50 Spanish goats (3.9 mo, 18 kg) and 43 Dorper (3.9 mo, 29 kg), 75 Katahdin (3.7 mo, 28 kg), and 42 St. Croix sheep (4.2 mo, 20 kg) from 8 commercial farms in AR, KS, MO, and OK and LU were housed separately in adjacent pens with automated feeders allowing free-choice access to a 15% CP (DM) and 50% concentrate pelletized diet. The test entailed an adjustment period of 2 wk followed by 8 wk of data collection. Body weight was determined weekly. During adaptation, anthelmintic treatment resulted in low fecal egg count (initial FEC = 64 eggs/g; SEM = 7.0), after which a dose of 10,000 larvae was administered orally. After the infection, packed cell volume (PCV) was measured weekly and FEC was determined 5 times in wk 5-9. Data were analyzed using the GLM procedure of SAS® with fixed effects of species and breed within species. Initial BW, PCV, and FEC were covariates and the logarithmic transformation was used for individual mean FEC. Species differed in ADG (P < 0.01; 176 and 305 g; SEM = 4.1), DMI (P < 0.01; 1.14 and 1.81 kg/d; SEM = 0.032), FEC (P = 0.02; 1897 and 1488 eggs/g in untransformed scale; SEM = 135.1), and PCV (P < 0.01; 26.7 and 29.1% for goat and sheep; SEM = 0.20). Dorper and Katahdin had greatest (P < 0.01) ADG (231, 154, 144, 329, 316, and 270 g; SEM = 6.8) and DMI (1.37, 0.94, 1.11, 1.98, 1.94, and 1.51 kg/d

for Boer, Kiko, Spanish, Dorper, Katahdin, and St. Croix, respectively; SEM = 0.054). St. Croix had the lowest ($P < 0.05$) FEC (1701, 2548, 1442, 1957, 1587, and 921 eggs/g; SEM = 233.9) and highest ($P < 0.01$) PCV (25.8, 27.8, 26.5, 29.0, 27.7, and 30.7% for Boer, Kiko, Spanish, Dorper, Katahdin, and St. Croix, respectively; SEM = 0.34). In conclusion, there was considerable variability between species, among breeds, and within breeds in resistance to internal parasite based on FEC and PCV after an artificial challenge with *H. contortus* larvae in a standardized environment.

Key Words: goat, internal parasite, sheep

1707 Effects of adding water to total mixed ration on water consumption, nutrient digestibility, wool cortisol, and blood indices in Corriedale ewes under hot and humid conditions.

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The objective of this study was to determine the effect of adding water to total mixed ration (TMR) on water consumption, nutrient digestibility, wool cortisol, and blood indices in Corriedale ewes under hot and humid conditions. Nine Corriedale ewes (ave. BW = 41 ± 3.5 kg) were individually fed diets based on maintenance requirements in metabolic crates. Sheep were assigned to three treatment groups according to a 3 × 3 Latin square design for 3 periods of 21 days duration each (9 sheep per treatment). Treatments were TMR moisture for 40%, 50%, and 60%. No differences were found in body weight gain among all treatment groups ($P > 0.05$). Nitrogen balance including digestible N, retained N, and urinary and fecal N showed no change among the treatment groups ($P > 0.05$). Water consumption was the lowest in 50% TMR moisture group than the other groups ($P < 0.05$). Other than ether extract which was higher in 60% TMR moisture group ($P < 0.05$) the differences among nutrient digestibilities including CP, crude fiber, OM, DM, NDF, ADF, and NFC were not significant ($P > 0.05$). No significant difference was observed for serum protein, BUN, glucose, and TG among the treatment groups ($P > 0.05$). Wool and blood cortisol were not different among the treatment groups ($P > 0.05$). Blood hematology including RBC, WBC, hemoglobin, hematocrit, basophils, and eosinophils were not different among the treatment groups ($P > 0.05$). It is concluded that the increase of TMR moisture at 40%, 50% and 60% had no effects on water consumption, N balance parameters, and nutrient digestibilities except for the ether extract under hot and humid environmental conditions. Additionally there were no effects on stress conditions (chronically known as wool cortisol levels), as well as blood cortisol levels, and immune functions of ewes.

Key Words: blood parameters, Corriedale ewes, digestibility, stress, TMR moisture, wool cortisol

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1708 Effects of pasture access regimen on grazing behavior and energy utilization by Alpine goats.

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Twenty-eight Alpine goats (initially 53.2 ± 1.80 kg BW and 26 ± 2.5 days in milk; 11 primiparous) were used to evaluate effects of different pasture access regimens on grazing behavior and energy utilization in a 16-wk experiment with 4-wk periods. Treatments were access to grass and(or) legume pasture from 0800 h, after the morning milking at 0700 h, to 1600 h (SET); continually other than during milking (CG); from the time of no moisture on leaf surfaces until milking at 1600 h (ND-M); and from the time of no leaf surface moisture until sunset (ND-D). The SET, CG, and ND-M goats were supplemented with 1.5% BW (DM) of concentrate immediately after the afternoon milking, whereas ND-D goats were supplemented at sunset. The ND-M and ND-D goats were fed alfalfa hay when length of pasture access was less than 6 h, with the level based on length of pasture access. Digestibility of OM determined each period from fecal DM and AIA in feedstuffs and feces was 77.0, 79.1, 81.3, and 77.8%, respectively (SE = 1.46), and ADG was similar among treatments (−12, −15, 2, and −6 g for CG, ND-D, ND-M, and SET, respectively; SE = 10.9). Neither fecal egg count nor FAMACHA score was affected by treatment ($P > 0.05$). Based on data from GPS collars and leg activity monitors, treatment affected ($P < 0.05$) time spent grazing (7.43, 6.93, 5.86, and 6.18 h, respectively; SE = 0.343), resting while lying (8.48, 8.82, 10.63, and 9.11 h, respectively; SE = 0.480) and standing (6.33, 7.29, 6.85, and 7.82 h, respectively; SE = 0.338), and walking (1.75, 0.95, 0.66, and 0.90 h for CG, ND-D, ND-M, and SET, respectively; SE = 0.093). Intake of ME was similar among regimens ($P > 0.05$; 26.73, 24.54, 26.25, and 22.37 MJ/d, respectively; SE = 1.522), although heat energy determined from heart rate and heat energy per heart beat was greatest for CG ($P < 0.05$; 14.41, 13.11, 12.90, and 13.03 MJ/d for CG, ND-D, ND-M, and SET, respectively; SE = 0.392). Milk energy yield was similar among treatments (5.41, 5.06, 5.34, and 5.55 MJ/d, respectively; SE = 0.35), but milk energy:ME intake was greatest ($P < 0.05$) for SET (0.228, 0.219, 0.220, and 0.275 for CG, ND-D, ND-M, and SET, respectively; SE = 0.0104). In conclusion, restricting time of pasture access from the morning to afternoon milking appeared to favorably affect efficiency of energy utilization for lactation, not relating to

Table 1709.

Table 1. Equations used to predict energy requirements for maintenance and gain in indigenous goats.

Equation[1]	Parameter estimates		SE	σ^2_e	P-value
Maintenance					
[1] HP, kJ/kgEBW$^{0.75}$ =β_0×e$^{(\beta1\times MEI)}$	β_0	344.1	14.6	2052.9	<0.01
	β_1	0.000883	0.000042		<0.01
[2] Retained CP, g/kg EBW$^{0.75}$=β_2+ β_3×CP intake	β_2	1.091	0.435	0.439	0.041
	β_3	0.282	0.0369		<0.01
Gain					
[3] Energy, MJ=β_4×EBW$^{\beta5}$	β_4	8.63	1.94	346.0	<0.01
	β_5	1.01	0.0801		<0.01
[4] Protein, g=β_6×EBW$^{\beta7}$	β_6	134.5	16.1	33514	<0.01
	β_7	1.14	0.0423		<0.01

[1]The empty BW (EBW) was computed as the BW at slaughter minus the weight of the contents of the digestive tract, bladder, and biliary vesicle; Linear equations and Nonlinear equations were fitted using PROC MIXED and NLMIXED of SAS (v. 9.4, SAS Institute Inc., Cary, NC), respectively.

internal parasitism, but rather by limiting time spent and heat energy associated with grazing.

Key Words: dairy goats, energy, grazing

1709 Energy and protein requirements of indigenous goats. A. K. Almeida*[1], K. T. Resende[1], I. A. M. A. Teixeira[1], S. D. A. Ribeiro[2], M. T. Rodrigues[3], and J. A. Garcia[3], *[1]UNESP, Univ. Estadual Paulista, Department of Animal Science, Jaboticabal, Brazil, [2]Capritec, Espirito Santo do Pinhal, Brazil, [3]Universidade Federal de Vicosa, Vicosa, Brazil.*

The objective of this study was to estimate energy requirements of indigenous goats weighing from 5 to 25 kg of body weight (BW). Goats were weaned at 79 ± 4.4 days after the beginning of experiment. Milk and solid diet intake were recorded daily. Total ration had 11.0 MJ/kg ME and 144 g/kg CP (DM basis). To determine energy maintenance requirements, 33 goats weighing 4.90 ± 0.302 kg of initial BW were used. Ten goats were slaughtered to estimate body energy and protein at the beginning of the experiment, then retained energy. The remaining goats were randomly assigned to two DM intake levels: ad libitum and restricted-fed (1.20X maintenance). Heat production was calculated as the difference between ME intake and retained energy (RE, kJ/kgEBW$^{0.75}$). Net energy requirement for maintenance (NE_m) was estimated as β_0 of relationship between HP and MEI (Table 1, Eq.[1]). Metabolizable energy required for maintenance (ME_m) was calculated iteratively, when HP = MEI. Efficiency of energy utilization for maintenance (k_m) was calculated as NE_m/ME_m. A linear regression of retained CP on CP intake (g CP/kg EBW$^{0.75}$) was used to calculate net protein requirements for maintenance (NP_m). The intercept of regression (Table 1, Eq.[2]) was assumed to be the endogenous and metabolic losses of N×6.25, which represented the NP_m. Net energy and protein requirement for gain (NE_g and NP_g, respectively) were obtained using 26 goats fed ad libitum randomly slaughtered at 5.40 ± 0.484 kg BW (n = 10), 15.8 ± 0.655 kg BW (n = 10), and 26.3 ± 1.27 kg BW (n = 6). The first derivative of allometric equation (used to calculate energy and protein contents in the EBW; Table 1, Eq. [3] and [4]) with respect to EBW yielded estimates of the NE_g and NP_g. A Monte Carlo-based method was used to simulate variation of NE_g and NP_g. Estimated NE_m was 344.1 ± 14.6 kJ/kgEBW$^{0.75}$, resulting in 568.4 kJ/kgEBW$^{0.75}$ ME_m, thus k_m was 0.605. The NP_m was 1.091 ± 0.435 g CP/kgEBW$^{0.75}$·at NI = 0. The CP intake required for maintenance, at which retained CP = 0, was 3.87 g CP/kgEBW$^{0.75}$. The growth phase, NE_g ranged from 8.59 ± 0.555 to 8.75 ± 0.821 MJ/kg and NP_g increased increased from 186.6 ± 5.25 to 230.8 ± 10.4 g CP/kg of empty weight gain in indigenous goats weighing from 5 to 25 kg BW. It is expected that indigenous goats are later maturing animals. That would explain the lack of significant increase in NE_g as BW increased. We thank FAPESP for financial support (grant No. 2014/14939-0, 2014/14734-9, 2015/26000-5).

Key Words: comparative slaughter, gain, maintenance.

1710 Nutrient content of crop residues selected by grazing goats. J. Mendoza*[1], L. Gaytan[1], M. Mellado[2], O. Angel[1], and I. Chavarria[1], *[1]Autonomous Agrarian University Antonio Narro, Torreon, Coahuila, Mexico, [2]Autonomous Agrarian University Antonio Narro, Saltillo, Coahuila, Mexico.*

In Mexico, the majority of goats are exploited extensively, so their diet depends on native vegetation on rangelands, and occasionally crop residues. There is no information on the nutritional quality of different crop residues used by goats. Therefore, the objective of this study was to determine the nutrient content of two crop residues: alfalfa roots (goats grazed in a plowed crop of alfalfa) and oats (straw), selected by mixed breed goats (crossbred dairy goats) grazing in these crop fields. The collection of forage selected by goats was carried out by 10 multiparous goats, which carried a plastic

rope (1.5 m long and 0.5 cm in diameter) tied around their neck. Forage was collected directly from their oral cavity by separating the jaws with the hands, without impeding their grazing activity. Goats were restrained momentarily by holding them with the rope attached to their neck. This procedure was repeated about every 10 min for 3 hours a day, collecting approximately 300 g of forage (green matter) during 5 days (collections were made by one person per goat). A portion of this material was washed immediately with distilled water and was used for the determination of minerals. The data analysis was performed using analysis of variance (ANOVA) using the PROC GLM procedure of SAS. Ash content of goat diets grazing the alfalfa residue was higher ($P < 0.01$) (14.6 ± 1.7 vs. 11.0 ± 0.8) than goats grazing oat residues. NDF was higher ($P < 0.05$) in the alfalfa forage (predominantly roots) selected by goats (57.0 ± 1.9 vs. 53.6 ± 3.9) compared with diets of goats grazing oat residues. The protein content was higher ($P < 0.05$) in forage selected by goats on the oat residues (9.4 ± 1.0) compared to alfalfa residues (8.0 ± 1.2). The Ca, Cu, Mn, and Fe concentrations were higher ($P < 0.01$) in the goat diets grazing on alfalfa residues compared to oat residues. It was concluded that goats grazing on oat residues select diets higher in nutrients compared to diets selected on plowed alfalfa (high root consumption). However, goats ingesting alfalfa residues, mainly roots, had access to higher levels of minerals.

Key Words: alfalfa, NDF, nutritional quality, oats, protein

1711 Genomic evaluation and population structure of eleven Russian sheep breeds. T. E. Deniskova[1], A. V. Dotsev[1], K. Wimmers[2], H. Reyer[2], V. R. Kharzinova*[1], E. A. Gladyr[1], G. Brem[1,3], and N. A. Zinovieva[3], *[1]L.K. Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Genome Biology, Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [3]Institute of Animal Breeding and Genetics, VMU, Vienna, Austria.*

Availability of high-density SNP arrays created an opportunity to understand current genetic structure and differentiation of sheep breeds and to find ways for their improving via whole genome analysis. A wide range of sheep breeds including wool, meat, milk types, and dual- and multi-purpose breeds was established in Russia. Although the breeds have unique gene pool and are a part of national heritage, they have not been genotyped yet and there is no information of their polymorphism at genome level. In this regard, our aim was to evaluate genetic diversity and population structure of some Russian sheep breeds. We used OvineSNP50K BeadChip to genotype 141 sheep of 11 breeds including Romanov (ROM, n = 22), Baikal fine-fleeced (ZBL, n = 12), Tuvan short fat tailed (TUV, n = 16), Kuibyshev (KUI, n = 11), Soviet Merino (SVM, n = 10), Kuchugur (KCH, n = 12), Karakul (KAR, n = 16), North Caucasian merino (NCM, n = 11), Russian long haired (RLH, n = 11), Stavropol (STA, n = 10), and Manych merino (MAN, n = 10). Quality control (QC) of SNPs and summary statistics were performed in PLINK v1.07. R v3.2.3 was used to create input files and visualize the data. After QC overall 48,842 SNPs (90%) were involved in the further analysis, 47,980 (or 98.3% from detected) were polymorphic. The highest polymorphism level among the breeds was identified in ZBL (97.4%), whereas KCH, RLH, STA were characterized by 93.4, 93.7, and 93.8% of polymorphic loci, respectively. Observed heterozygosity was 0.370 ranging from 0.361 in ROM to 0.398 in ZBL. All breeds were characterized by heterozygote excess ranging from 0.84 in ROM to 9.78% in KCH. The minor allele frequency was 0.305 overall for all breeds. The MDS analysis showed pattern corresponding breeds productivity type. Merino breeds (STA, SVM, MAN, ZBL) with close NCM group and semi-fine fleeced clade of RLH and KUI clustered separately from KAR and TUV with coarse wool. Multi-purpose KCH occupied an equidistant position. The most remote group was ROM, probably, due to their unique genetic traits such as extremely high prolificacy and adaptability to any conditions of keeping and feeding. Our study represents the initial phase of large-scale SNP genotyping of Russian sheep breeds. The research was conducted under financial support of Russian Scientific Foundation (project N° 14-36-00039).

Key Words: genetic diversity, sheep breeds, whole-genome studies

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1712 Plate waste and artificial rearing of orphaned lambs versus ewe reared lambs. A. DiPastina* and D. J. R. Cherney*, Cornell University, Ithaca, NY.*

In this study, our objective was to determine the possible use of breakfast plate waste from a university dining hall as a supplement to lamb creep feed other than as compost and to evaluate gain of artificially versus ewe reared lambs. Twelve ewes bearing twins were selected. Twins were given 177 mL of ewe's colostrum each on day 0 immediately after birth and again 4 hours later, and then were randomly assigned to groups. Groups consisted of 12 lambs reared with their dams (NR), 12 artificially reared on milk replacer (AR). Half of each set of lambs were fed a standard creep feed (SC). The other lambs were fed a creep feed containing about 15% plate waste, which replaced some of corn and soybean meal of the standard creep (PW). Both creep feeds contained the same amount of crude protein, neutral detergent fiber, and total digestible nutrients (20.8 ± 3.11%, 23.9 ± 6.22%, and 79 ± 2.12% TDN, respectively). A 2 x 2 factorial was used to compare rearing methods and creep feed treatments for all 24 lambs. The AR lambs were housed in 0.9 x 0.9 meter pens in pairs. The NR lambs were housed with their dams in 1.5 x 1.5 m pens with access to a 0.6 x 1.5 m creep area. Lambs

were weighed daily from days 0 to 30. Lambs weighed 3.76 ± 0.712 kg at birth. Creep feed was offered starting at 10 d of age. Creep feed was weighed 3x daily, and more added if necessary. Creep feed intake did not differ between AR and NR lambs, but AR lambs grew at a greater rate (0.28 kg/d) versus NR lambs (0.27 kg/d; $P < 0.05$). Lambs offered SC consumed more (20.24 ± 11.17 g/d) than lambs offered PW feed (8.83 ± 8.21 g/d; $P < 0.05$). Artificially grown lambs fed SC grew faster ($P < 0.01$) but consumed less milk replacer per day (1.75 ± 0.75 L/day) than PW fed lambs (2.93 ± 1.14 L/day). Lambs fed PW consumed feed at a more accelerated rate past 20 d than what lambs consumed on SC, suggesting possible acceptability issues that decreased over time with the PW. Results indicate that AR lambs can have growth rates greater than or similar to NR lambs, but intensive management is required. In addition, PW produced acceptable growth rates in lambs pre-weaning, but PW use needs continued research to assess issues such as acceptability.

Key Words: orphan lambs, plate waste

1713 Effects of corn silage levels on methane emissions and blood metabolite concentrations of drying-off Xinong Saanen dairy goats. P. Wang*[1], Y. Xue[2], G. Ma[1], and J. Luo[1], *[1]Alltech-NWAFU Animal Science Research Alliance, College of Animal Science and Technology, Northwest A&F University, Yangling, China, [2]Alltech, Lexington, KY.*

The objective of this study was to determine the effects of increasing corn silage level in drying-off Xinong Saanen dairy goats on methane emissions and blood metabolites concentrations. Twenty-one drying-off Xinong Saanen dairy goats (3.36 ± 0.95 yr old; BW = 64 ± 9.19 kg) were randomly allocated to 3 treatments with 7 goats per treatment (one goat of MS treatment got fever and excluded) and were fed 3 levels of corn silage with 2 7-d periods: 0.33 kg/d for LS, 0.47 kg/d for MS, 0.55 kg/d for HS (DM basis), respectively. Goats were fed twice daily by pens. Concentrate, corn silage, and alfalfa hay were provided separately. Concentrates were offered at 0.58 kg/goat daily, and alfalfa hay was ad libitum. Methane emissions were measured on 2 7-d periods using 3 polymethyl methacrylate chambers (length × width × height = 1.2 m × 0.6 m × 1.0 m; bottom is open). One of 7 goats for each treatment was placed in the chamber for 30 min (1200 h-1230 h) during gas sampling day, and temperature was recorded simultaneously. Daily methane emission rates were estimated based on the emission rate of 1200 h-1230 h and the percentage of 1200 h-1230 h methane production in daily methane production. Blood serum samples were collected once on the last day of the experiment to analyze concentrations of blood urea nitrogen (BUN), glucose (GLU), total protein (TP), β-hydroxybutyrate (BOHA), NEFA, and triglyceride (TG). Data were analyzed by GLM and treatment means were compared by LSD test ($P \leq 0.05$). Methane emission rate ranged from 9.90-11.89 g/d, 452.37-508.51 mg/d per kg metabolic body weight (MBW), 7.55-8.52 g/kg DMI. Increasing corn silage intake showed the potential to reduce methane emission rate (9.90 ± 4.00 g/d for HS, 10.58 ± 1.84 g/d for MS, and 11.89 ± 2.03 g/d for LS), although no significant differences were found. The relatively higher methane emission of LS was in accordance with higher hay intakes (0.50 ± 0.06 kg/goat for LS vs. 0.19 ± 0.09 kg/goat for HS, 0.20 ± 0.09 kg/goat for MS). Serum concentrations of BUN, GLU, TP, BOHA, and NEFA were not affected by corn silage intake, whereas serum TG concentration increased with increasing corn silage level ($P < 0.05$). These results indicated that increasing corn silage level potentially reduced methane emissions with accordingly decreased hay intakes.

Key Words: corn silage, dairy goat, methane

1714 Inclusion of a by-product of *Myrtus communis* in the diet of lactating sheep: Performance and health. A. Nudda*[1], G. Battacone[1], P. Nicolussi[2], F. Correddu[1], G. Pulina[1], and P. Bonelli[2], *[1]Dipartimento di Agraria, University of Sassari, Sassari, Italy, [2]Istituto Zooprofilatico Sperimentale della Sardegna, Sassari, Italy.*

By-product resulting from myrtle liqueur preparation of *Myrtus communis* berries could represent a suitable source of polyphenolic compounds. The present study aimed to investigate the effect of dietary supplementation of exhausted berries of *Myrtus communis* (EBM) on milk production and composition, blood metabolic profile and the efficiency of nitrogen utilization in lactating dairy ewes. Thirty Sarda dairy ewes were randomly assigned to 3 dietary treatments consisting of a control diet (CON), a diet supplemented with 50 g/d per head of EMB (EMB50), or a diet supplemented with 100 g/d per head of EMB (EMB100). The study lasted 13 wk, with a 2 wk adaptation period and an 11 wk experimental period. Milk yield was measured and milk samples were collected weekly and analyzed for fat, protein, and milk urea content (MU). Blood samples were collected on d 0, 15, 30, 45, and 60 of the experiment and analyzed for hematological parameters, albumin, alkaline phosphatase (ALP), bilirubin, creatinine, gamma glutamyltransferase (GGT), aspartate aminotransferase (AST), alanine aminotransferase (ALT), protein, blood urea (BU), and serum protein fractions. The urinary N excretion was estimated. Dietary treatments did not affect milk yield and composition, except for MU, which decreased as the dose of EMB in the diet increased (41.5, 37.6, 32.4, respectively; $P < 0.05$). Diet influenced blood urea content (BU), which decreased with the inclusion of EMB in the diet (72.4, 61.3, 59.0, respectively; $P < 0.05$). The urinary N excretion was reduced by the EMB supplementation (19.9, 17.8, 14.9, respectively; $P < 0.05$). The reduction in MU, BU, and estimated urinary excretion suggests that the use of EMB might reduce N emissions. The results on milk production

and composition and hematological parameters suggests that EMB can be included in the diet of dairy ewes without adverse effects on performance and health status.

Key Words: blood parameters, by-product, lactating sheep

1715 Genetic parameter estimates for productivity of the Katahdin and Hampshire ewe and its components. J. G. Pérez-Álvarez, F. A. Rodríguez-Almeida*, and J. Domínguez-Viveros, *Universidad Autónoma de Chihuahua, Chihuahua, Mexico.*

Productivity of the ewe is one of the most important economic traits in lamb production, and predicted as a biological index could facilitate selection decisions for genetic improvement if not negatively related to any of its components. In order to estimate genetic parameters for total weight of lamb weaned at 75 d per lambing ewe (TWW) and its components [average weaning weight (AWW), number of lambs born (NLB), and number of lambs weaned (NLW)] in two distinct breeds, 4439 and 1076 records from 3166 Katahdin (KT) and 646 Hampshire (HS) ewes with progeny from 556 and 72 sires in 91 and 10 flocks in México, respectively, were analyzed. Because NLB and NLW were about the same in HS, NLW was not analyzed for this breed. Weaning weights were adjusted to a female equivalent base for each breed by type of birth and region, prior to the calculation of TWW and AWW. Heritability and genetic correlations were estimated by bi- and tri-variate analyses with the MTDFREML software. The models included the fixed effects of contemporary group-season-year-flock and the linear and quadratic covariate age of the ewe at lambing, and the direct additive genetic and permanent environment random effects of the ewe. For TWW and AWW, also the random effect of sire of mating was included, as well as the fixed effects of NLB and NLW for AWW. Parameter estimates were very similar for both breeds. Heritability estimates for TWW, AWW, NLB, and NLW ranged from 0.13 to 0.18, 0.15 to 0.18, 0.10 to 0.16, and 0.14 to 0.16, respectively. The average estimates of r_g of the component traits with TWW in KT and HS were 0.87 and 0.67 for AWW, 0.83 and 0.70 for NLB, and 0.98 for NLW, and between components in KT were 0.98 for NLW and NLB, 0.35 (tri-) and 0.65 (bi-variate) for AWW and NLW, and around 0 for AWW and NLB in both breeds. Variance for sire of mating random effects as proportion of phenotypic variance were consistently moderate (0.16 and 0.25 for TWW and AWW, respectively) only for the HS breed. In conclusion, a moderate genetic response to selection is expected for the KT and HS ewe productivity without adverse effects in any of its component traits.

Key Words: ewe productivity, genetic correlation, heritability

1716 Effects of protected methionine supplementation during dry period of seasonally synchronized goats on blood parameters and the subsequent lactation. *F*. Piccioli-Cappelli[1], A. Minuti*, M. Maiocchi, M. Mezzetti, and E. Trevisi, *Università Cattolica del Sacro Cuore, Piacenza, Italy.*

At the end of pregnancy, goats experience a marked body fat mobilization and inflammatory events that may increase the risks of ketosis and oxidative stress and impair health. It is recognized that methionine (Met), often deficient in the diet of ruminants, acts as a donor of thiol groups, which are essential in alleviating the negative effects of stress and inflammation. The aim was to study the effects of feeding protected Met (Timet®, Vetagro, RE, Italy) during the dry period to double its content in metabolizable protein. Fourteen Saanen goats were divided into 2 groups of 7 goats each. During the last month of pregnancy the control (CTRL) group received 320 g of soya meal (Met = 0.2% DM) and the treatment (TRAT) group received 300 g of a protein supplement containing Timet® (Met = 0.4% DM). Both groups were fed hay ad libitum and the supplement resulted in a diet with the same energy content (1.4 Mcal/kg DM) and protein (CP 14.2% DM). Blood samples were collected every 7 d and milk samples on 7th and 14th d of lactation. Data were analyzed using Proc. Mixed of SAS. Before kidding, at blood level TRAT compared with CTRL goats had lower concentrations of urea, NEFA (0.22 vs. 0.37 mmol/L, $P < 0.10$), indicating a lower mobilization of body reserves and lower BHB (0.34 vs. 0.48 mmol/L, $P < 0.07$), indicating lower ketogenesis. Altogether these data indicate a higher availability of glucose in TRAT goats. TRAT compared to CTRL goats had a better liver metabolism (i.e., higher concentrations of albumin 35.4 vs. 33.9 g/L, $P < 0.10$), and this could result in a more favorable condition concerning both inflammatory status (lower levels of haptoglobin, 0.13 vs. 0.41 g/L) and oxidative stress (lower levels of reactive oxygen metabolites, 16.7 vs. 19.0 mg H_2O_2/dL) resulted numerically, although not statistically, different. During the first two weeks of lactation these responses likely allowed the TRAT group to yield more milk (2.83 vs. 2.18 kg/d, $P < 0.12$) and lactose (137 vs. 98 g/d, $P < 0.05$); moreover, milk from TRAT treated goats had a significantly lower somatic cells count (2.72 vs. 3.13 logN/mL, $P < 0.05$). Thus, the data indicate that supplementation of Met in late gestation can help goats to mitigate the frequent adverse metabolic and inflammatory conditions that characterize this physiological phase, and to improve the beginning of the lactation cycle.

Key Words: goat, inflammation, metionine, pregnancy

1717 Responses of hair sheep breeds to high heat load index conditions. D. Tadesse*, R. Puchala, T. A. Gipson, Y. Tsukahara, and A. L. Goetsch, *American Institute for Goat Research, Langston University, Langston, OK.*

Fourteen Dorper (D; 59 ± 3.2 kg), 13 Katahdin (K; 58 ± 2.5 kg), and 8 St. Croix (SC; 50 ± 3.0 kg) female sheep (> 1.5 yr) were used to evaluate responses to high heat load index (HLI) conditions. After 4 wk of thermoneutral conditions (70 HLI), in sequential 2-wk periods daytime HLI was regulated near 85, 90, and 95 and that at night was 70, 77, and 81, respectively. Data were analyzed with a mixed model containing breed, week within period, measurement time (0700, 1300, and 1700 h), three-way interactions, and baseline covariates. Rectal temperature (RT) at 1300 and 1700 h was lowest for SC (38.36, 38.87, and 38.96 for D, 38.31, 38.85, and 38.87 for K, and 38.29, 38.64, and 38.66 °C for SC at 0700, 1300, and 1700 h, respectively; SE = 0.046). A similar interaction ($P = 0.052$) occurred for panting score (PS, 0-4.5; 0.10, 0.64, and 0.54 for D, 0.09, 0.70, and 0.58 for K, 0.02, 0.42, and 0.40 for SC at 0700, 1300, and 1700 h, respectively; SE = 0.064). Breed differences in PS resulted from highest HLI in period 3 (0.07, 0.17, and 1.03 for D, 0.08, 0.15, and 1.14 for K, 0.04, 0.06, and 0.73 for SC in period 1, 2, and 3, respectively; SE = 0.080). Period, week, and time interacted ($P < 0.001$) in respiration rate (RR) (period 1: 41, 102, and 97 in wk 1, 50, 124, and 115 in wk 2; period 2: 56, 158, and 124 in wk 1, 65, 160, and 134 in wk 2; period 3: 76, 219, and 161 in wk 1, 130, 164, and 148 in wk 2 at 0700, 1300, and 1700 h, respectively; SE = 6.6). There was a corresponding interaction ($P < 0.001$) in RR:RT as an index of energy expended to minimize RT (period 1: 0.40, 1.00, and 0.96 in wk 1, 0.05, 1.22, and 1.14 in wk 2; period 2: 0.57, 1.55, and 1.22 in wk 1, 0.66, 1.58, and 1.31 in wk 2; period 3: 0.75, 2.14, and 1.58 in wk 1, 1.28, 1.61, and 1.44 in wk 2 at 0700, 1300, and 1700 h, respectively; SE = 0.064). In conclusion, some measures suggest higher tolerance of high HLI by SC than D or K. There appeared to be considerable adaptation in RR from wk 1 to 2 of period 3 to minimize RT in the early afternoon, which was at least partially facilitated by higher RR in the early morning before HLI increased.

Key Words: hair sheep, heat, temperature

1718 In vitro efficacy of three novel compounds on development and survival of gastrointestinal nematode larvae in feces of sheep. J. E. Miller*[1], V. Kelly[2], and J. M. Burke[3], *[1]Louisiana State University, Baton Rouge, [2]Louisiana State University School of Veterinary Medicine, Baton Rouge, [3]USDA-ARS, Booneville, AR.*

Gastrointestinal nematode (GIN) parasites are a major constraint to profitable sheep production. The long-term use of anthelmintics has resulted in GIN populations developing resistance to those available. The objective of this study was to determine the efficacy of three novel compounds on development and survival of GIN larvae in feces of sheep. Feces were collected directly from the rectum of 10 lambs and combined to make one large sample. This sample was homogenized by thorough mixing by hand and five 2-g subsamples were randomly selected for determination of fecal egg count (FEC) using the McMaster technique. Fifty 5-g subsamples were then randomly selected and individual fecal cultures were made by mixing with an equivalent volume of vermiculite and adding water to make a soft crumbly culture composition. Three novel synthetic compounds (Bedoukian Research, Inc.) similar to natural flavor/fragrance application compounds were diluted 1:10, 1:1,000, and 1:10,000. Five mL of water (control) and each dilution of the compounds were thoroughly mixed with a culture, making 5 replicates/dilution. Cultures were incubated at 27°C for 2 wk, after which, they were processed by a baermann procedure to recover infective larvae (L3). The number of L3 were counted to estimate L3/g of feces. The mean FEC (3530 ± 231) indicated that the GIN eggs were evenly distributed in the homogenized fecal mass, so all subsamples were considered to have equivalent FEC. The control larval recovery was 814 L3/g, and recovery for all the dilutions of the 3 compounds was < 10 L3/g. This indicated very high efficacy of L3 reduction (over 98.7%, $P < 0.05$). These novel compounds may be a viable treatment to aid in the control of GIN infection by reducing development and survival of larvae in feces, thus reducing pasture infectivity.

Key Words: control, nematodes, sheep

1719 Recovery of fibroblast cells up to 65 d of postmortem storage of sheep ear skin at 4°C. M. Singh* and X. Ma, *Fort Valley State University, Fort Valley, GA.*

Animal cloning technology has renewed interest in tissue storage, since these tissues can be used to reintroduce lost genetics back into the breeding pool in animal agriculture, preserve genetic diversity, and revive endangered species. Several studies have demonstrated that cell survival decreases with increasing postmortem tissue storage. However, the limits of time interval within which live cells can be recovered

from animal tissues postmortem have not been adequately studied. The objective of this study was to evaluate the time limits of cell survival in sheep skin tissues stored at 4°C after the death of the animal. Outgrowth of cells around small tissue explants in cultures was used as a measure of cell recovery. Ear skin was procured from the university slaughter house from six random but healthy animals and stored at 4°C in the lab. We cultured 2–3 mm^2explants (n = 60) after 0, 10, 20, 27, 30, 35, 38, 41, 45, 50, 55, 60, 65, and 70 d of tissue storage. DMEM media supplemented with 10% FBS and 50 units/mL of penicillin and 50 µg/mL of streptomycin was used. Twelve dishes (60 mm) for each time point were used. After 10 d of culture in a CO_2incubator, outgrowth of fibroblast-like cells around the explants was scored. Out of 481 explants that adhered to dish surface, 374 exhibited outgrowth. Our results showed outgrowth of cells up to 65 d of postmortem storage. In general, the number of outgrowing cells decreased with increasing postmortem storage time. To test the differences between cell cultures obtained from postmortem fresh and stored tissues, we established secondary cultures from primary cells of 0-dpm and 65-dpm time points from selected cell lines and studied their growth profile (p5 level) which showed similar morphology and growth curves. The karyotype analysis of 65 dpm tissue derived cells revealed a normal female karyotype without any genetic aberrations. Both cultures have been passaged up to 33 times which exhibit similar morphology; however, they grew very slowly. These results suggest that live cells can be recovered from skin tissues of sheep and perhaps other animals for more than 2 mo after their death with comparable growth profiles.

Key Words: cell culture, fibroblast cells, postmortem tissue storage, sheep, skin

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1720 Morphometric measurements and body weight affected by breed, age, and sex in the Sindh goat breed populations of Pakistan. M. Moaeen-ud-Din[*1], G. Bilal[1], J. M. Reecy[2], M. S. Khan[3], and S. Razzaq[1], *[1]PMAS-Arid Agriculture University, Rawalpindi, Pakistan, [2]Iowa State University, Ames, [3]University of Agriculture, Faisalabad, Pakistan.*

Sindh province is harbor of maximum goat breeds in Pakistan. However, there is scarcity of information regarding the indigenous goat breeds of Sindh province on morphometric measurements and weight. Therefore, the current study was designed to study the effects of age, sex, and breed on body weight and body measurements of ten goat breeds in their respective breeding tracts. A survey was performed in breeding tracts of ten goat breeds of Sindh viz. Kamori, Tapri, Bugi-Turi, Pateri, Kachan, Jattan, Lohri, Chappar, Barri, and Thari. During the current study HyderAbad, Matiyari, Hala, Methi, Umer kot, Tharparkar, Thatha, Badin, Dadu, and Mirpur Khas districts of Sindh province were visited. Data were collected and arranged according to age class (class 1: 1–6 mo, class 2: 7–12months, class 3: 13–18 mo, class 4: 19–24 mo, class 5: 25–36 mo, class 6; 37–48 mo, class 7: 49–60 mo, class 8: > 60 mo), sex, and breed. Data were analyzed using Mixed Procedure by REML methodology in SAS (Version 9.2) to investigate the effect of breed, age, and sex on body weight and body measurements. Overall breeds did differ for live body weight, heart girth, length, height, and chest length ($P < 0.05$). However, there was no difference among breeds in term of pubic bone length ($P < 0.05$). Kamori had mean body weight of 67.58 ± 1.41 kg, followed by Pateri (50.01 ± 1.50kg), Bugi-Turi (44.13 ± 1.33kg), Barri (43.50 ± 1.60kg), Kachan (42.50 ± 1.60kg), Tapri (39.33 ± 1.55kg), Jattan (38.63 ± 1.51kg), Chappar (38.03 ± 1.49kg), Lohri (35.41 ± 1.60kg), and Thari (33.94 ± 1.45kg). There was significant difference among age class for all the body measurement and body weight ($P < 0.05$) except for pubic bone length. Overall male goats showed higher body weight and height. The present study revealed variations in body measurements and body weight across age, sex, and breed in Sindh for the first time. As goats are mainly raised for meat production in the area, Kamori goat showed highest body weight followed by Pateri, Bugi-Turi, Barri, Kachan, Tapri, Jattan, Chappar, Lohri, and Thari. Moreover, if breeds are to selected for mutton based on body weight, then Kamori are followed by Pateri, Bugi-Turi, Barri, Kachan, Tapri, Jattan, Chappar, Lohri, and Thari. This could be useful information if a selection program is to be launched in the future to improve meat production in the province.

Key Words: AJK, goat breeds, body measurements, body weight

1721 Effects of supplementing olive pomace as a feed additive on weight gain in *Capris aegagrus hircus*. P. Urso*, M. M. Beverly, S. F. Kelley, M. J. Anderson, J. L. Leatherwood, K. J. Stutts, and S. Nair, *Sam Houston State University, Huntsville, TX.*

In the livestock industry, feed is one of the highest variables affecting the cost of production. A producer's goal is to find the least costly feedstuff that is effective in meeting nutrient requirements of livestock, particularly during winter months. Olive pomace is a by-product of the olive oil industry and could be considered as a potential livestock feedstuff to be used as an energy supplement due to its high fat content (15%). The objective of our study was to determine if olive pomace could be used as an acceptable low cost feedstuff to maintain weight during the colder winter months. To accomplish this 28 Spanish influence goats were fed (2% of body weight, BW) varying amounts of fermented pomace with a protein pellet to meet maintenance requirements. The four test groups (n = 7) consisted of a 3:1, 1:1, and 1:3 olive pomace to concentrate ratio (O:C) as well as a control containing no pomace. All groups received molasses at 0.5% BW

to improve the palatability of the feed and to further homogenize the ration to discourage selective eating of the mixture. Does were fed in herring bone style runs every morning for 49 d. The average daily gain (ADG) for the 1:3, 1:1, 3:1, and control groups were 0.0370, 0.0166, 0.0119, and 0.0262 kg/day, respectively, with no difference detected between groups ($P > 0.88$). The similar ADG across groups suggests that pomace can be an effective feed additive to reduce feed costs. A difference ($P < 0.01$) in consumption rates was detected between treatments with the 3:1 group consuming more feed with an average of 0.785 kg/day compared to the control at 0.694 kg/day. Additionally, olive pomace may be considered as a cost effective supplement to reduce costs for maintenance rations. Using ANOVA, cost efficiency of the test groups were compared. Rations costs were calculated at $0.153/g for the 3:1 ration compared to $0.6386/kg for the pelleted control ration. On average, this difference in input cost can reduce a producer's cost of feed by $13.53/hd over a 49 d maintenance feeding period ($P < 0.01$) by feeding olive pomace. While further research is needed to determine the optimum levels of olive pomace feeding, it remains a viable alterative to high cost feedstuffs.

Key Words: goats, olive, pomace

1722 Genetic and non-genetic effects on performance traits in a U.S. population of dairy sheep.

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There are relatively few dairy sheep operations in the U.S., but the industry is growing. Genetic improvement in dairy flocks has come through "breeding-up" ewes of common meat and wool breeds to European dairy breeds with imported rams and semen. This process has led to a crossbred domestic dairy sheep population consisting of East Friesian (EF), Lacaune (LA), and non-dairy (Meat) breeds. The objectives of this research were to: 1) determine the non-genetic factors affecting ewe performance, 2) estimate genetic parameters of and among traits, and 3) evaluate the genetic trends in traits of economic importance. Data were obtained from flock records collected at the Spooner Ag Research Station, University of Wisconsin-Madison from 1995–2015. There were 5438 records on number of lambs born per ewe lambing (NLB) and 4763 records on 180-d adjusted milk (MY), fat (FY), and protein (PY) yield, and percentage fat (%F) and protein (%P). There were 1969 and 1688 ewes with NLB and lactation records, respectively. The two multiple trait repeatability models jointly analyzed NLB, MY, FY, and PY or NLB, MY, %F, and %P. The significant fixed effects were trait dependent but included a proportion of EF and LA breeding, EFxLA and LAxMeat specific retained heterosis coefficients, age of ewe at lambing, and production year. The estimated heritabilities were 0.08 ± 0.02, 0.30 ± 0.04, 0.26 ± 0.04, 0.29 ± 0.04, 0.53 ± 0.04, and 0.61 ± 0.04 for NLB, MY, FY, PY, %F, and %P, respectively. NLB had a negative genetic correlation with %F (−0.25 ± 0.12). However, all other estimates of genetic correlations between NLB and lactation traits were low. The yield traits had high genetic correlations with each other (0.90 ± 0.02 between MY and FY, 0.96 ± 0.01 between MY and PY, and 0.93 ± 0.01 between FY and PY). There were unfavorable genetic correlations of −0.29 ± 0.08 between MY and %F and −0.35 ± 0.08 between MY and %P. The genetic correlation between %F and %P was high (0.60 ± 0.05). The regression of MY predicted breeding value on ewe year of birth revealed an average genetic improvement of 2.60 ± 0.12 kg yr^{-1} from 1995 to 2014 in this population. Due to the current restrictions and difficulties surrounding importation of foreign germplasm, a national dairy sheep genetic evaluation program is key to the continued improvement of U.S. flocks.

Key Words: crossbreeding, dairy sheep, genetic parameters

1723 Effects of high concentrations of crude glycerin on feed intake and ruminal parameters of sheep.

E. H. C. B. van Cleef*[1,2], M. T. C. Almeida[1,2], E. S. Castro Filho[1], I. Monsignati[1], H. L. Perez[1,2], and J. M. B. Ezequiel[1], *[1]São Paulo State University, Jaboticabal, Brazil, [2]FAPESP, São Paulo, Brazil.*

Eight ruminally-cannulated crossbred (Santa Ines × Dorper) male sheep (64.5 ± 8.5 kg) were used to evaluate the effects of high concentrations of crude glycerin on dry matter intake, and ruminal parameters. Animals were assigned to a replicated 4 × 4 Latin square design and, in pairs, were fed one of the four experimental diets. Isonitrogenous (18.4% CP) and isoenergetic (2.7 Mcal ME/kg DM) diets were composed of corn silage, soybean hulls, soybean meal, mineral premix, and crude glycerin replacing 0 (G0), 10 (G10), 20 (G20), or 30% (G30) corn cracked grain (DM basis), in a roughage:concentrate ratio of 40:60. Crude glycerin totally replaced corn grain in G30, and contained 83% glycerol, 95% DM, 6% salt, and less than 0.01% methanol. Each experimental period lasted 21 d (14 d adaptation and 7 d data collection). Animals were fed twice daily (0700 and 1900 h), and feed delivered and refused were weighed every morning to assess DMI. Ruminal pH, ammonia nitrogen (NH_3–N), and short-chain fatty acids (SCFA; acetate [C2], propionate [C3], butyrate, isobutyrate, valerate, and isovalerate) were evaluated at 0, 2, 4, 8, 10, and 12 h after feeding. No interaction time of observation × treatments was observed. The DM intake tended to show a quadratic effect ($P = 0.09$), with greater values observed for

G10 and G20 (1375 and 1336 g/d, respectively). Ruminal pH tended to linearly increase ($P = 0.07$), with values from 6.0 (G0) to 6.2 (G30). A tendency for a quadratic effect of ruminal concentrations of NH_3–N ($P = 0.06$) was observed, with lesser values for treatments with intermediate levels of crude glycerin (9.6 and 10.2 mg/dL, respectively for G10 and G20). Crude glycerin inclusion linearly decreased total SCFA ($P < 0.0001$), acetic acid ($P < 0.0001$), butyric acid ($P = 0.0004$), isobutyric acid ($P = 0.0007$), isovaleric acid ($P = 0.003$), and C2:C3 ratio ($P < 0.0001$). The production of propionic and valeric acids were not influenced by treatments (average = 8.7 and 0.5 mg/dL); however, the proportion of propionate linearly increased from 21 to 34% of total SCFA produced. The inclusion of up to 30% crude glycerin in diets for crossbred sheep promotes quadratic effect on DM intake and ruminal concentrations of NH_3–N, changes SCFA profiles and increases ruminal pH.

Key Words: glycerol, rumen, sheep

1724 Serum anti-mullerian hormone as an indicator of fertility in Katahdin ewes. M. Acharya*[1], J. M. Burke[2], E. Smyth[2], L. Ngere[2,3], and R. W. Rorie[1], [1]*Department of Animal Science, Division of Agriculture, University of Arkansas, Fayetteville,* [2]*USDA-ARS, Booneville, AR,* [3]*Oak Ridge Institute for Science and Education, Oak Ridge, TN.*

Individual ewes vary in reproductive performance parameters, such as age at first lambing, twinning rate, and ability to breed during off-season. Previous studies indicate that anti-mullerian hormone (AMH) in circulation reflects the total pool of follicles within the ovaries, and is positively correlated with fertility. In this study, retrospective analysis was used to determine if AMH could serve as an indicator of ewe fecundity. Serum samples were collected from 152 Katahdin ewes ranging from 0.5 to 7 yr of age, their pregnancy and lambing rate recorded, and estimated breeding values obtained from the National Sheep Improvement Program. Anti-mullerian hormone was analyzed using an equine and ovine AMH enzyme-linked immunosorbent assay (ELISA) kit. Continuous variables were analyzed by ANOVA and categorical data by chi-squared, using JMP® (SAS institute) software. Serum AMH ranged from 0.04 to 0.39 ng/mL, with mean of 0.17 ng/mL. Mean serum AMH was similar ($P = 0.37$) across all ewe age groups (< 1, 1 to 2, 2 to 3, and > 4 yr). The distribution of AMH concentrations was divided into quartiles (AMH Q1 through Q4, with the Q1 lowest and Q4 the highest). There was no relationship (fall; $P = 0.65$; summer; $P = 0.11$) between AMH quartile and mean number of lambs born (NLB) from fall and summer breeding. No correlation ($P = 0.39$) was found between individual estimated breeding value for NLB and serum AMH concentration. A significant correlation ($P < 0.01$; $r = 0.411$) existed between mean NLB per individual ewe during summer (0.79) and fall (1.44). Overall pregnancy rate was higher ($P < 0.01$) for fall (79%) than summer (48%) breeding. It was noted that 25/68 (36.8%) of ewes < 2 yr of age fell into the lowest AMH quartile (Q1) as compared with 13/84 (15.5%) for older ewes. Similarity of AMH among different ewe age groups and a lower percentage of older ewes in AMH Q1 could reflect particular selection criteria.

Key Words: anti-mullerian hormone, ewes, reproductive performance

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1725 Fatty acid composition of different fat depots from hair and wool x hair crossbred lambs supplemented with highly digestible fiber containing agro-byproducts on pasture. C. Tripp*[1], J. H. Lee[1], S. Wildeus[2], A. Discua[1], and D. Kafle[1], [1]*Fort Valley State University, Fort Valley, GA,* [2]*Virginia State University, Petersburg.*

Agro-byproducts such as soy hull and corn gluten have been recognized as economical sources of feeds for small ruminants because they can provide supplemental nutrients for small ruminants with highly digestible fiber. However, their effect on the fatty acid profile of different fat depots in lambs has not been completely studied. This study was conducted to determine the fatty acid composition of different fat depots from grazing lambs supplemented with highly digestible fiber containing agro-byproducts. Thirty-six 7.5-mo-old purebred hair (Barbados Blackbelly and St. Croix) and crossbred wool (Dorset) x hair lambs grazed predominantly Jesup tall fescue pasture. Lambs were randomly assigned to a pasture-only, or a soy hull (SH) or corn gluten feed (CGF) supplemented group balanced by breed type. Supplement was provided at 2% of BW daily at individual feeding stations. After 77 d of grazing, lambs were slaughtered using standard procedures. Intramuscular, subcutaneous, and kidney fats were obtained from each carcass. Total lipids from each fat depot sample were extracted by the chloroform-methanol method. Extracted lipids were prepared for the fatty acid methyl esters (FAME) and then analyzed by a gas chromatography. All data were analyzed as a completely randomized design with a 2 × 3 factorial treatment arrangement: breed type (pure- or cross-bred) and diet (pasture-only, pasture plus SH or CGF) as main effects. The fatty acid profiles of different fat depots from lambs were significantly influenced by supplementation. Compared with lambs supplemented with SH or CGF, pasture-only fed lambs had higher concentrations of γ-linolenic (C18:3n6; 0.50 or 0.52 vs. 0.64%), arachidonic (C20:4n6; 2.10 or 2.06 vs. 3.31%), eicosapentaenoic (C20:5n3; 0.46 or 0.36 vs. 1.06%), and docosahexaenoic (C22:6n3; 0.55 or 0.52 vs. 1.27%) acids, but lower ($P < 0.05$) concentrations of palmitic (C16:0; 17.0 or 18.1 vs. 15.9%) and oleic (C18:1n9; 33.8 or 32.8 vs. 29.1%) acids in intramuscular fat; higher ($P < 0.05$) concentrations of myristoleic (C14:1n5), palmitoleic

(C16:1n7), α-linolenic (C18:3n3; 1.80 or 1.24 vs. 2.84%), and C18:3n6 (0.83 or 0.65 vs. 2.66%) acids, but a lower ($P < 0.01$) concentration of C18:1n9 in subcutaneous fat; and a higher ($P < 0.01$) concentration of C14:1n5, but a lower concentration of C18:1n9 in kidney fat. The results indicate that fresh lamb from pasture only fed-lambs might have healthier fatty acid profiles compared with that from lambs supplemented with soy hull or corn gluten feed.

Key Words: agro-byproduct, fatty acid, lamb

SMALL RUMINANT SYMPOSIUM: ENHANCING SMALL RUMINANT PROFITABILITY

1726 Profitability of small ruminant production systems.

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The prolonged decline in U.S. sheep numbers is well documented. Well known reasons for the decline include dwindling U.S. demand for lamb, relative prices for competing meats, the rise of man-made fibers competing with wool, discontinuation of the U.S. Wool Incentive payment program, grazing allotment policies for public lands, and restrictions on predator control. Another critically important force behind falling U.S. sheep numbers has been rising costs resulting in unprofitable conditions, forcing producers to reduce the size of their flocks or exit the industry. Using extension sheep production budgets, this study examines and compares sheep production costs across various states representing conventional sheep production based on an average flock size with costs and returns on a per ewe basis. The weighted total variable cost was $124.44 per ewe in 2015 and ranged from $148 per ewe in Kentucky to $118 per ewe in Wyoming. Receipts were the highest in the Eastern region at $179 per ewe and were the lowest in Texas at $98 per ewe. Net returns ranged from a-$41 to $21 per ewe in Texas and Kentucky, respectively. Costs between regions reflected significant differences in production systems. For example, feed made up just over 50% of total variable costs in Texas and 22% of total variable costs in Wyoming. Hired labor made up 37% of total variable costs in Wyoming or $44 per ewe. Predator control costs were $10.50 per ewe in Texas but only $1-$2 in the other regions. The results highlight the variable nature of the cost of sheep production and the range of production systems across the country. Policy changes that affect hired labor costs, for example, affect Wyoming and Western region production more than smaller flocks in the East with little, if any, hired labor. New technologies or predator control systems would be likely to see the greatest returns in Texas and the Southwest or in the Mountain West. Changes in public land grazing policies would have the biggest effect in the West. Positive returns in Kentucky indicate opportunities for industry expansion in the Eastern half of the U.S.

Key Words: cost of production, net returns, production systems, sheep

1727 Contribution of hair sheep to small ruminant profitability.

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Hair sheep numbers in the United States have increased dramatically in the past twenty years as documented by breed registry data. Characteristics promoted by hair sheep producers include: moderate or small framed, easy care, parasite resistant, twinning, productivity in extensive systems, aseasonal breeders, and adapted to heat and humidity. These descriptors suggest that hair sheep have the potential to add to the profitability of small ruminant production in the USA. Two hair sheep breeds rank among the top six breeds for numbers of sheep registered in the USA from 2002 to 2015 (Table 1 for 2003–2015). The increase in hair sheep registrations occurred while the vast majority of wool sheep registries experienced declines of 25–75% in their registration numbers from 1990 to 2015. Research results from three research stations will be discussed since they document productivity of hair sheep and hair sheep crosses. These stations include USDA ARS Meat Animal Research Center in Nebraska, USDA ARS Small Farm Research Center in Arkansas, and Texas A&M Agrilife Research Center in San Angelo, Texas. Data from these stations and other university studies find that the weights of weaned and finished hair sheep lambs are well suited to markets and regions of the country that reward the non-traditional or light lamb market. In the Nebraska and Arkansas production systems, hair sheep genetics produced 150–200% lamb crops in forage-based systems compared to annual NASS reports of 110% for the United States. In west Texas, research results indicate that lamb markets differentially impact hair sheep (Dorper) and wool sheep (Rambouillet) producers based on corn prices and weather (Sheep and Goat Research Journal, In Press). During drought years, Dorpers wean significantly more lambs. When corn prices are high, Dorpers bring premium prices for the light lamb, non-traditional markets. When corn prices are low, wool feeder lambs bring premium prices. A significant percentage of the hair sheep operations, using breed association membership, are located in regions of the country where sheep numbers have traditionally been low, especially the Southeastern region. It is suggested that lack of shearers, decreased quality and quantify of wool, resistance to parasites (documented by Virginia Tech, LSU, USDA Booneville, among others) and adapted to heat and humidity help with popularity of these breeds in this region.

Key Words: breed registry, hair, sheep

1728 Contribution of newer goat breeds to small ruminant profitability. R. Browning, Jr.*[1] and M. L. Leite-Browning[2], [1]*Tennessee State University, Nashville,* [2]*Alabama A&M University, Huntsville.*

Profitability in commercial meat goat enterprises is affected by animal productivity, market value, and input costs. Productivity indicators include doe reproductive output, kid growth rate, carcass merit, and hardiness. Breed choice(s) can affect these profit factors and set the path to profit or loss. Meat goat breed options are scant compared to other ruminant livestock sectors in the US. The South African Boer goat was a highly visible new breed introduced in the 1990s to enhance meat production of the US herd base of primarily Spanish-type goats. This model has been repeated worldwide. New Zealand Kiko goats were also imported by US interests in the 1990s. New breeds are usually introduced with a focus on improving growth and end-products (e.g., meat, milk, fiber) while overlooking fitness traits (health and reproduction) that may be greater profit drivers, especially if doelings are retained for future breeding. Successful new breed introductions require some level of adaptation to destination environments, particularly in low-input systems. Loss of native or naturalized local genotypes possessing desirable fitness levels while pursuing improved growth or end-product traits is a global concern. This was true after large-scale crossbreeding of naturalized Spanish goats with imported Boer commenced. Research indicated that Boer germplasm generated an insignificant to negative impact on doe fitness compared to the Spanish maternal base. Reductions in doe reproductive output, wellness, and stayability point to lowered expected enterprise profitability. Health and stayability problems increase input costs. Economic analysis demonstrated lower annual net return for Boer does (-$52.25) compared to Spanish does ($7.18) in a low-input setting. Some relative increases in weight were evident using Boer at various research stations, but improvements in carcass merit were not so obvious. One carcass trait noticeably improved by the Boer influence was conformation score. Improved conformation score can increase market value. Across performance traits, other data suggests that Kiko goats may be a favored import over Boer for increasing commercial herd profitability. The newest breed garnering attention among US producers is the South African Savanna. Like Boer and Kiko in the 1990s, current industry use of Savanna is preceding objective characterization. The newer breeds have increased industry popularity, but not necessarily profitability. Proper selection and use of new and established breeds in meat goat mating systems is important for profitability in a low-input commercial setting. Managing around poor meat goat breed choices is probably not profitable or sustainable.

Key Words: breed, meat goat, profitability

1729 Contribution of forage production systems to small ruminant profitability. R. Ehrhardt*, *Michigan State University, East Lansing.*

Improving forage utilization is a key consideration in increasing production efficiency and decreasing the cost of production in a small ruminant farming systems. In much of North America, winter dormancy and to a lesser extent, slow growth in mid-summer, creates barriers in both forage availability and quality in perennial-based grazing/forage production systems for small ruminants. To better understand how to optimize forage systems for sheep production in the upper Midwest USA, a series of grazing studies were conducted with sheep over a 3 yr period to examine forage utilization, animal performance, and cost of production on annual, short-term perennial, and perennial pastures. These pastures were evaluated as part of a 3 yr pasture rotation system and compared to a perennial only system. This rotation was established in year 1 by converting perennial pastures to annual crops between after attaining approximately 60% of historical seasonal biomass production (mid-June conversion). Annual crops evaluated included warm season grasses, brassicas, and their mixtures. In year 2 a short-term perennial pasture consisting of red clover, ryegrass, and chicory was established in early spring into the annual forage residue from year 1. In late summer of year 3, a perennial pasture was reestablished. The perennial pasture used as a base of comparison consisted of a mixture of alfalfa, endophyte free tall fescue and orchard grass. Animal performance on these pastures and within these systems was measured by the growth performance of lambs post-weaning expressed on a lamb (g/day) and land basis (kg/hectare). Individual lamb gains on brassica (310 g/d) and short-term perennial (278 g/d) pastures approached that of the same genotype fed a concentrate diet fed in confinement (330 g/d). On a land basis, seasonal gains on short-term perennial pasture excelled (1430–1640 kg/ha) over other pastures. The cost of lamb gain was calculated for each pasture ranking lowest to highest were short term perennial < perennial < brassica monocultures < brassica/warm season mixes < warm season monocultures. In summary, complimentary pasture rotation systems offer value to small ruminant production by reducing the cost of gain, allowing opportunities for finishing on pasture, improving parasite management, improving soil health, and overall system productivity and profitability.

Key Words: sheep, goats, forages, grazing

SWINE SPECIES

1730 Probiotic treatment using *Bacillus subtilis* PB6 improves the growth performance, intestinal morphology, enzyme activities and barrier function in low birth weight piglets. L. Hu, L. Che**, X. Peng, Q. Xu, Z. Fang, S. Xu, Y. Lin, and D. Wu, *Institute of Animal Nutrition, Sichuan Agricultural University, Chengdu, China.*

This study aimed to investigate the effects of *Bacillus subtilis* PB6 supplementation in milk formula on growth performance, intestinal development, and immune function in low birth weight (LBW) piglets. Piglets with a birth weight near the mean litter birth weight (SD 0.5) were identified as normal birth weight (NBW), whereas those with at least 1.5 SD lower birth weight were defined as LBW. Fourteen pairs of NBW and LBW piglets (7 d old) were randomly assigned to receive the formula milk or formula milk with *Bacillus subtilis* PB6 for a period of 21 d. At Day 28, blood samples, intestinal tissues, and digesta were collected at necropsy and analyzed for morphology, digestive enzyme activities, immune cells, gene, and protein expressions as well as microbial population. Data were analyzed by SPSS software using the MIXED procedure. Regardless of the diet, LBW decreased the average daily dry matter intake (−31%, $P <$ 0.001) and the average daily growth (−28%, $P < 0.001$). Moreover, LBW decreased plasma concentration of immunoglobulin A (−17%, $P < 0.001$), interleukin-1β (−12%, $P =$ 0.006), the count (−33%, $P = 0.021$) and percentage (−13%, $P = 0.025$) of blood lymphocytes compared to NBW piglets. LBW decreased the villous height (−8%, $P = 0.039$) and enzyme activity of maltase (−24%, $P = 0.011$), as well as the mRNA abundances of *Toll-like receptor 9* (−34%, $P = 0.020$) and *Toll-interacting protein* (−21%, $P = 0.001$) in ileum. Regardless of body weight, the supplementation of *Bacillus subtilis* PB6 markedly decreased the feed:gain ratio (−10%, $P = 0.034$), which could be related to the better intestinal morphology, increased enzyme activities of maltase (+19%, $P = 0.082$) and sucrase (+23%, $P = 0.095$) in jejunum. Moreover, the protein abundances of *Zonula occludens-1* and *Claudin-1* (+33~54%, $P < 0.05$) in ileum, as well as the copy number of *Bacillus* ($P = 0.01$) in colonic digesta were increased in piglets supplemented with *Bacillus subtilis* PB6 relative to piglets with control diet. Our results indicated that LBW impaired the growth and intestinal development as well as immunity of piglets, however, dietary supplementation of *Bacillus subtilis* PB6 improved the growth performance with better intestinal development and barrier function in both NBW and LBW piglets.

Key Words: immunity, low birth weight, probiotic

1731 Dietary nucleotides supplementation improves the intestinal development and immune function of low birth weight piglets. L. Hu, L. Che**, X. Peng, Q. Xu, Z. Fang, S. Xu, Y. Lin, and D. Wu*, Institute of Animal Nutrition, Sichuan Agricultural University, Chengdu, China.*

This study aimed to determine whether dietary nucleotides supplementation could improve growth performance, intestinal development, and immune function of low birth weight (LBW) piglets. Piglets with a birth weight near the mean litter birth weight (SD 0.5) were identified as normal birth weight (NBW), whereas those with at least 1.5 SD lower birth weight were defined as LBW. Fourteen pairs of NBW and LBW piglets (7 d old) were randomly assigned to receive a liquid milk-based control diet (CON diet) or diet supplemented with nucleotides (NT diet) for a period of 21 d. NT diet was formulated by adding 0.74% nucleotides in CON diet, the pattern of nucleotides (5'-AMP, CMP, GMP, IMP, UMP) was similar as that in sow milk. Data were analyzed by SPSS software using the MIXED procedure. Compared with NBW piglets, LBW piglets had significantly lower average daily dry matter intake ($P = 0.001$) and average daily gain ($P < 0.001$). Moreover, LBW decreased the villous height ($P = 0.008$) and villi: crypt ratio ($P = 0.014$) in duodenum, as well as maltase ($P = 0.033$) activity in jejunum. In addition, LBW decreased the serum concentrations of immunoglobulin A ($P < 0.001$), interleukin-1β ($P = 0.017$) and interleukin-10 ($P = 0.008$), as well as the percentage of peripheral lymphocytes ($P = 0.015$). Meanwhile, the downregulation of innate immunity-related genes such as *Toll-interacting protein* (TOLLIP) ($P = 0.012$) and *Toll-like receptor* (TLR) 2 ($P = 0.073$) was observed in the ileum of LBW relative to NBW piglets. Regardless of birth weight, however, feeding NT diet decreased ($P = 0.001$) the feed:gain ratio, increased villous height in duodenum ($P = 0.036$), activities of lactase ($P = 0.019$) and maltase ($P = 0.055$) in jejunum, also increased count of peripheral leukocytes ($P = 0.039$), serum concentrations of immunoglobulin A ($P = 0.001$), and interleukin-1β ($P = 0.019$) as well as gene expressions of *TLR-9*, *TLR-4*, and *TOLLIP* (all $P < 0.05$) in ileum. In addition, the protein expressions of *Claudin-1* and *Zonula occludens-1* ($P < 0.05$) in ileum were markedly increased by feeding NT diet relative to CON diet. Our results indicated that LBW impaired the growth performance, intestinal and immune function, but dietary supplementation of nucleotides improved the growth performance, digestive capability, and immunity.

Key Words: immunity, low birth weight, nucleotides

1732 Effect of supplemented mineral phosphorus and fermentable substrates on gut microbiota composition and metabolites, phytate hydrolysis, and health status of growing pigs. C. M. E. Heyer*, S. Schmucker, E. Weiss, M. Eklund, T. Aumiller, E. Graeter, T. Hofmann, M. Rodehutscord, L. E. Hoelzle, J. Seifert, V. Stefanski, and R. Mosenthin, *University of Hohenheim, Institute of Animal Science, Stuttgart, Germany.*

The present study examined the impact of diets with varying CaP levels and fermentable substrates on intestinal CaP concentration, phytate (*myo*-inositol hexakisphosphate, $InsP_6$) hydrolysis, the intestinal microbiota, and the immune system in pigs. In 2 consecutive experiments, 31 growing pigs (55 ± 4kg) were allotted to a 2 × 2 factorial arrangement with 4 treatment groups, and were fed either a corn-soybean meal or a corn-pea based diet with differences in digestibility, each with 2 different CaP levels (low vs. high, supplemented with monocalcium phosphate). After 3 wks of adaptation to the diets, all pigs were immunized twice with keyhole limpet hemocyanin (KLH) (wk 4 and 6) and blood samples were taken 2 wks after the second immunization. In wk 8, the amount of anti-KLH IgG and anti-KLH IgM were analyzed in blood samples. After slaughtering in wk 9, jejunal and cecal digesta were analyzed for Ca, P, and inositol phosphate isomers, determination of 16S rRNA gene copy numbers by qPCR and bacterial metabolite analyses. Pigs fed the low-CaP diets showed lower plasma anti-KLH IgG concentrations ($P < 0.05$). The low-CaP level promoted jejunal *Bifidobacterium* spp. ($P < 0.01$). For the pea diets, jejunal *Lactobacillus* spp. were lower ($P < 0.05$). In the cecum, *Eubacterium rectale* and *Roseburia* spp. ($P < 0.05$) were lower for the low-CaP diets. For the pea diets, the caecal *Eubacterium rectale* and *Bifidobacterium* spp. ($P < 0.05$) were lower. In the cecum, total SCFA, acetate, and propionate ($P < 0.01$) were lower for the low-CaP diets. Acetate and butyrate ($P < 0.05$) in caecal digesta were lower for the pea diets. The P net absorption in the jejunum and cecum was lower ($P < 0.01$) for the low-CaP diets. In addition, the $InsP_6$ hydrolysis in digesta samples was not affected by the dietary treatment, nevertheless the $InsP_6$ concentration in the jejunum was lower for the pea ($P < 0.05$) and low-CaP diets ($P < 0.05$). In conclusion, the present study demonstrated that CaP and fermentable substrates modulate the adaptive immune response and the intestinal microbiota, and sufficiently high amounts of CaP may be required to support the adaptive immune response, beneficial saccharolytic bacteria and SCFA production. It needs to be further elucidated whether variations in P digestion and/or absorption might explain the complex relationship between P, the immune system, and the microbial ecosystem.

Key Words: immune system, intestinal microbiota, phosphorus, pig

1733 Sexual development and boar taint in male pigs selected for divergent residual feed intake. A. Prunier*[1], S. Parois[1], N. Le Floc'h[1], and H. Gilbert[2], *[1]PEGASE, Agrocampus Ouest, INRA, Saint-Gilles, France, [2]GenPhyse, Université de Toulouse, INRA, INPT, INPT-ENV, Castanet-Tolosan, France.*

Improving feed efficiency and rearing entire male pigs are relevant strategies to reduce feed cost and environmental waste in pig production. The major constraint for rearing entire male pigs being boar taint, an experiment was performed to determine the consequences of a divergent selection on residual feed intake (RFI: low RFI = LRFI; high RFI = HRFI) on pubertal development, and boar taint. Forty-one purebred French Large White male pigs in the course of a divergent selection experiment for RFI (10th generation of selection, $n = 20$ or 21 per line) were recruited. Blood samples were drawn at 125, 140, 154, and 168 ± 1 d of age (mean ± SD) for plasma estradiol (E2) and testosterone (T) determination by EIA. At slaughter at 177 ± 4 d of age (108 ± 14 kg liveweight), a backfat sample was collected in the neck for androstenone and skatole determination by HPLC and genital tract was removed for testes and Cowper gland weighing after tissue trimming. All data were analyzed by ANOVA using R, including line as a fixed effect. Plasma E2 and T were log transformed for normalization and analyzed using a repeated in time model with nlme. Fat androstenone and skatole were analyzed using a generalized mixed model with lme4. Other data were analyzed using lm. Growth rate, age, and liveweight did not differ between lines ($P > 0.1$). Testes weight was similar in both lines (LRFI: 527 ± 23 g; HRFI: 471 ± 33 g, $P > 0.1$) whereas Cowper glands were heavier in LRFI pigs (176 ± 10 g vs. 100 ± 8 g). Fat androstenone (1.97 ± 0.31 vs. 0.56 ± 0.08 μg/g pure fat) and skatole (0.14 ± 0.02 vs. 0.05 ± 0.01 μg/g pure fat) were also higher in LRFI pigs ($P < 0.001$). The interaction age x line for E2 and T was not significant ($P > 0.1$). Across ages, plasma T (5.0 ± 0.9 vs. 2.7 ± 0.7 ng/mL plasma) and E (25.5 ± 2.9 vs. 11.4 ± 1.0 pg/mL plasma) were also higher in LRFI than in HRFI pigs ($P < 0.001$). In both lines, both hormones increased with age ($P < 0.001$). Overall, these data suggest a lower testicular activity in the HRFI than in the LRFI line which is positive for meat quality but may be detrimental to the reproductive function in the HRFI line.

Key Words: androstenone, boar, estradiol, feed efficiency, testosterone

1734 Effects of dietary live yeast supplementation on growth and immunological parameters of weaned piglets challenged with *Escherichia coli* K88.

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This study aimed to investigate the effects of dietary live yeast (*Saccharomyces cerevisiae*, Phileo Lesaffre Animal Care, France) supplementation on growth performance and immunological parameters of piglets challenged with enterotoxigenic *Escherichia coli* K88. A total of 180 weaned piglets (6.39 ± 0.05 kg) were randomly allocated into 5 treatments with 6 pens and 6 piglets (3 barrows and 3 gilts) per pen, receiving the control (CON) diet, diets supplemented with antibiotics plus ZnO (ABT-ZnO:2250 mg/kg of ZnO, 20 mg/kg Colistin and 75 mg/kg Aureomycin), live yeast at 1 (LY1), 2.5 (LY2.5), or 5 g/kg (LY5) for a period of 2 wk. On Day 8, six piglets from CON group received sterilized Luria Broth as control ($n = 6$), while another 30 piglets from CON ($n = 6$), antibiotic plus ZnO ($n = 6$), LY1($n = 6$), LY2.5 ($n = 6$), and LY5 ($n = 6$) groups, were orally challenged with Luria Broth containing $1x10^{11}$ cfu of *E. Coli* K88. Body weights and pen feed disappearance were recorded weekly to determine ADG, ADFI, and F:G. On d 10, blood, ileum, and mesenteric lymph node (MLN) tissue samples were collected at necropsy and analyzed for immunological parameters. Data were analyzed by SPSS software using the GLM procedure. Pigs fed ABT-ZnO diet had higher ($P < 0.05$) ADG and ADFI than pigs fed CON, LY1, and LY5 diets during the first week, while ADFI and F:G were similar between pigs fed ABT-ZnO and LY2.5 diets. Moreover, the ADG of pigs fed LY1 diet was similar to pigs fed ABT-ZnO diet during the second week. Compared with the pigs fed ABT-ZnO diet and non-challenged pigs, pigs fed LY2.5 and LY5 diets had higher ($P < 0.05$) plasma concentration of immunoglobulin G. Relative to the non-challenged pigs, moreover, the plasma concentration of Pig Major Acute Phase Protein (PMAPP) was increased ($P < 0.05$) in the challenged pigs fed CON diet, but PMAPP had not been markedly affected in the pigs previously fed ABT-ZnO and LY5 diets. Relative to the non-challenged pigs, *E. coli* K88 challenge up-regulated ($P < 0.05$) the mRNA abundances of toll-like receptor 4 (TLR-4), toll-like receptor 9 (TLR-9), myeloid differentiation factor 88 (MyD88), tumor necrosis factor receptor-associated factor 6 (TRAF-6), and interleukin-6 (IL-6) in ileum, however, those genes were downregulated by feeding LY5 diet. In conclusion, pigs fed live yeast diet had similar ADFI and F:G as pigs fed ABT-ZnO diet during the first week, the higher inclusion of live yeast could improve immunological parameters of piglets challenged with *E. coli* K88.

Key Words: immunity, intestine, live yeast

1735 Assessment of the age of lesions on the pig carcass at the abattoir through spectrophotometric color assessment and gene expression analysis.

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The presence of skin lesions downgrades carcass value and indicates poor animal welfare preslaughter. The aim of this study was to assess the age of lesions on the carcass at slaughter through spectrophotometric color assessment and gene expression of the following genes involved in tissue inflammation and repair: CCL2, IL6, ITGA3, MMP1, and SERPINE1. A total of 96 barrows (100 ± 10kg), allotted into 8 pens of 12 pigs each, were used. Over a three day period, each pig was mixed four times: in the finishing pen 2 d before slaughter, at loading, and in the lairage pen at the abattoir. Fighting- and mounting-type lesions were selected through visual assessment and video validation. Twenty lesions and control skins (with no lesions) per age group (total of 80 lesions and control skins) were selected, with each group consisting of 1, 4, 24, and 48 h old lesions. Data and skin samples were collected at the abattoir. For gene expression analysis, a skin biopsy of 4 mm was taken on each lesion and control skin at bleeding. After extraction, RNA was analyzed by qPCR to evaluate gene expression involved in tissue inflammation and repair. In the cooler, the color of each lesions and control skin was assessed through Minolta spectrophotometer. Delta values for each lesion were calculated between color and gene expression values obtained from the lesioned and control skin. Statistical analyses were performed using the mixing procedure of SAS, with log transformation applied to gene expression data. The time of infliction had an effect on Minolta L* and a* values ($P < 0.01$ for both), with 1 h old lesions being darker (higher-DL* value) than 4 and 24–48 h old ones ($P < 0.05$) and redder (higher Da* value; $P < 0.01$) than 24–48 h old lesions. The different lesions age resulted in a different expression of CCL2 and IL6 cytokines ($P < 0.001$), and other genes involved in tissue repair and remodeling (MMP1, ITGA3, SERPINE1) whose genetic expression was greater ($P < 0.01$) in 1 h old lesions compared with 24–48 h old ones. Furthermore, when compared with 4 h old lesions, 1 h old lesions presented a greater expression of CCL2 and ITGA3 ($P < 0.01$), and MMP1 ($P < 0.05$). To conclude, the spectrophotometric color assessment and the analysis of inflammatory and tissue repair gene expression in the carcass lesions at slaughter may be reliable methods to discriminate between fresh and older lesions at the abattoir.

Key Words: age, pigs, skin lesions

1736 Blood plasma replacement by hydrolyzed yeast in weaned piglets' diets. J. A. Rivera*[1], L. F. Araújo[2], R. L. D. C. Barbalho[3], M. A. Bonato[3], L. A. Vitagliano[4], G. D. Santos[3], and M. L. Cuadros[5], *[1]Faculdade de Medicina Veterinária e Zootecnia–VNP/FMVZ/USP, Pirassununga, Brazil, [2]University of Sao Paulo, Pirassununga, Brazil, [3]ICC Brazil, Sao Paulo, Brazil, [4]Universidade de São Paulo, Pirassununga, Brazil, [5]Veterinary Medical, Universidad Peruana Cayetano Heredia, Lima, Peru.*

The aim of this study was to evaluate partial levels or complete substitution of blood plasma by hydrolyzed yeast as a source of nucleotides in piglets' diets. For this, 1600 weaned piglets (± 21 d of age) Agroceres PIC® distributed in a randomized block design with 4 treatments and 10 replicates of 40 animals each. The nursery phase was divided in four: pre-initial I: 22 to 28 d; pre-initial II: 29 to 35 d; initial I: 36 to 47 d; and initial II: 48 to 63 d. The treatments consisted of different inclusions of plasma and hydrolyzed yeast (*Saccharomyces cerevisiae*) [HY] (Hilyses®-from ICC Brazil Company): 1- Control–conventional diet provided at the farm, with normal levels of plasma (6, 4, 2, and 0%- in the respective phases); 2- Diet with plasma reduction (3, 2, 1, 0) + HY (4, 3, 2, and 0%); 3- Diet with plasma reduction (1.5, 1, 0.5 and 0%) + HY (6, 4.5, 3, and 0%); 4- Diet without plasma + HY (8, 6, 4, and 0%). The piglets begin receiving the experimental diets after weaning until the end of this phase (± 66 d). The feed intake (FI) and body weight were measured at the end of each phase. Based on this, FI (g/d), body weight gain (BWG, g/d) and feed conversion ratio (FCR, g/g) were calculated. Mortality were daily observed and noted. Data obtained were analyzed with GLM (SAS) procedure and means were compared by Tukey test ($P = 0.05$). In phase pre-initial 1 the control treatment (no replacement) resulted in better ($P < 0.05$) FI and BWG, when compared to other treatments. However, during phase pre-initial 2, treatments with the larger proportion of HY (3 and 4) showed an increase ($P < 0.05$) in FI (26.3 and 13.7%, respectively); in phase initial 1, improved ($P < 0.05$) BWG (30.8%, for both treatments) and FCR (−17.4 and −17.3%, respectively). Considering the total period, the treatment 3 improved numerically (not statistically) FI (4.1%), BWG (8%), FCR (−2.3%), and mortality (−83.3%). The analysis of the data allow us to conclude that, in commercial farm conditions, the replacement of blood plasma by hydrolyzed yeast as a source of nucleotides is a viable alternative, and may even improve FI, BWG, FCR, and mortality.

Key Words: nucleotides, nursery, nutrition, *Saccharomyces cerevisiae*

1737 Effects of dietary energy on muscle growth of low birth weight neonatal pigs. Y. Chen*, S. R. McCauley, K. R. Oliver, R. P. Rhoads, and S. W. El-Kadi, *Virginia Tech, Blacksburg.*

Increasing the efficiency of nutrient utilization in farm animals remains one of the most important means to increasing profitability. It is well documented that increasing energy intake increases insulin-like growth factor I (IGF-I) concentration in animals. In addition, our previous data suggest that IGF-I signaling is compromised in muscle of low birth weight (LBWT) compared to normal birth weight (NBWT) neonatal pigs. We hypothesized that LBWT pigs have a higher energy requirement compared to their NBWT siblings. Twelve pairs of 7-d old, sex matched LBWT (1.73 ± 0.24 kg) and NBWT (2.42 ± 0.29 kg) pigs from the same litters were used. Pigs were fed either a low (LE) or high energy (HE) isonitrogenous diets, that contained 80 or 100% of NRC metabolizable energy requirement for 14 d. Body composition was determined by dual energy X-ray absorptiometry before and 13 d after initiation of feeding. On the last day of the study, pigs were euthanized to collect blood, and weigh and sample muscles. Plasma IGF-I concentration was measured using a commercial ELISA kit, and muscle mRNA expression by real-time PCR. Body weight was lower for LBWT than NBWT pigs throughout the study ($P \leq 0.05$). Lean and fat deposition increased with feeding in both LBWT and NBWT pigs, but was lower in LBWT compared with their NBWT littermates ($P \leq 0.05$). Longissimus dorsi (LD), gastrocnemius, semitendinosus and soleus muscle weights were lower in LBWT compared to NBWT pigs ($P \leq 0.05$). However, there was no effect of diet energy content on body composition and muscle weights. Plasma IGF-I concentration in LBWT pigs was lower than NBWT when pigs were fed LE diet, but increased to similar level as the NBWT group when pigs were fed the HE diet ($P \leq 0.05$). Gene expression of IGF-I, IGF-I receptor, and IGF binding protein 3 and 5 were lower in the LD muscle of LBWT compared with NBWT pigs fed the LE diet, while the mRNA abundance of these proteins was similar in LBWT and NBWT pigs fed the HE diet ($P \leq 0.05$). These results suggest that although increasing dietary energy content increased plasma IGF-I concentration and muscle mRNA expression of IGF-I and IGF binding protein 3 and 5 in LBWT pigs, the increase in growth was only modest indicating that other macronutrients may be limiting growth.

Key Words: dietary energy, LBWT, muscle growth

1738 Prediction of the concentration of androstenone in backfat from boar carcasses using indicators of sexual development. A. Prunier*[1], S. Parois[1], A. Faouën[1], and C. Larzul[2], *[1]PEGASE, Agrocampus Ouest, INRA, Saint-Gilles, France, [2]GenPhyse, Université de Toulouse, INRA, INPT, INPT-ENV, Castanet-Tolosan, France.*

Predicting fat androstenone concentration using a rapid and cheap method applied to live pigs is needed for efficient genetic selection against boar taint. Piétrain x (Large White x Landrace) boars were slaughtered either at 119 ± 4 kg live weight and 168 ± 1 d of age (S1, n = 48) or at 116 ± 4 kg and 174 ± 1 d of age (S2, n = 42). Blood and saliva samples were collected on D 0 (S1: 29 d, S2: 35 d before slaughter) and D 27 (S1: 2 d, S2: 8 d before slaughter) to measure plasma concentrations of estradiol and testosterone and salivary concentration of estrone by EIA. A backfat sample was collected on live pigs by biopsy on D 27 and on carcasses at slaughter to measure concentration of androstenone by HPLC. Testes and Cowper glands were weighed at slaughter after tissue trimming. Data were analyzed using the R MASS package. When necessary, variables were log or square root transformed for normalization. Predictive models of fat androstenone at slaughter were established with the modlin function. Plasma estradiol and fat androstenone on D 27, taken separately, were good predictors of fat androstenone at slaughter (mean R^2 between measured and predicted values was 0.48 and 0.43, respectively for each predictor) in S1 pigs. The quality of the prediction decreased between S1 and S2 pigs despite inclusion of salivary estrone in the equation with estradiol. To conclude, plasma estradiol can be considered as a good predictor of fat androstenone at slaughter if the delay between blood collection and slaughter is short.

Key Words: estradiol, estrone, genital tract

1739 Effects of dietary ramie (*Bochmeria nivea*) powder at different levels on carcass traits, muscle fiber characteristics, and muscular free amino acid profile of Chinese indigenous finishing pigs. Y. Tang*, *Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China.*

The experiment was conducted to investigate the effects of containing different levels of ramie powder in finishing pig diets on carcass traits, muscle fiber characteristics, and muscular free amino acid (FAA) profile. A total of 150 Xiangcun Black pigs, a Chinese local breed, with initial body weight (70.71 ± 1.21 kg) were used in a 50-d feeding study. Pigs were randomly allotted to 1 of 5 isonitrogenous and isoenergetic diets (corn-soybean meal-based) containing 0, 3, 6, 9, or 12% ramie. There are 6 replicate pens per treatment with 5 pigs per pen. On d 50, a subsample of 40 pigs (8 pigs per treatment) was harvested and carcass traits were calculated. Measurements of diameter and density of myofibers in longissimus dorsi muscle (LM) were taken. Muscle samples including LM and biceps femoris muscle (BM) were analyzed for myosin heavy chain (MyHC) mRNA expression level and FAA profile. The data were analyzed by SPSS 18.0 software with ANOVA analysis. Polynomial contrasts were performed to determine linear and quadratic effects. The level of P < 0.05 was the criterion for statistical significance. Overall, increasing dietary ramie reduced (linear, P < 0.05; 34.09 to 25.02 mm) the backfat thickness and increased (linear, P < 0.05; 23.46 to 32.38 cm2) the loin-eye area of the finishing pigs. A quadratic effect of MyHC IIb mRNA expression level in the LM was also observed as the dietary ramie added (P < 0.05), and the lowest value (0.77) was noted in 9% ramie group, along with the increased (P < 0.05) density of myofibers with a quadratic effect, but diameter of myofibers in the LM was linearly reduced (P < 0.05, 74.06 to 67.07 μm). Inclusion of ramie powder in the diet could up-regulate MyHC I mRNA expression level in the BM (quadratic, P < 0.05), with the highest point (1.77) in 9% ramie group. In addition, increasing dietary ramie linearly lowered (P < 0.05) the contents of essential amino acid (EAA) and total amino acid (TAA) in the LM, while linearly heightened (P < 0.05) both contents in the BM. In conclusion, these results suggested that ramie is an effective and unconventional feed crop to improve carcass traits and muscle fiber characteristics, and the underlying mechanism may be partly due to the alteration in MyHC gene expression levels and muscular FAA profile induced by dietary ramie.

Key Words: carcass trait, finishing pig, free amino acid, myofiber, ramie

1740 Effects of different sources and routes of administration of copper and vitamins A and D on gut volatile fatty acids and gene expression involved in regulation of innate and acquired immunity in piglets. L. Lo Verso*[1], J. J. Matte[1], G. Talbot[1], J. Lapointe[1], N. Bissonnette[1], F. Guay[2], N. Gagnon[1], B. Ouattara[1], and M. Lessard[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, Canada, [2]Universite Laval, Quebec City, Canada.*

Placental and colostral transfers of copper and vitamins A and D are limited in pig species (Matte et al., 2014, JAS 92-Suppl. 2:153). Because these micronutrients can influence intestinal microbiota and development of immunocompetence, the aim of the study was to evaluate the influence of different neonatal supplementation strategies on volatile fatty acid (VFA) concentration, pH, and modulation of cytokine gene expression in piglets' gut. Within each litter from 5 sows, 10 newborn piglets were allocated to one of the following combinations of sources and routes of micronutrient administrations: oral vitamin D3, retinol-acetate and $CuSO_4$ (T1); oral

25-OH-D3, β-carotene and Cu-yeast (T2); exposure to UVB light (20 min every second day), oral retinol-palmitate and Cu-gluconate (T3); intramuscular vitamin D3 and retinol-propionate and oral Cu-acetate (T4); oral saline (CTL). Oral or intramuscular provisions corresponded to 12 mg of copper and 70 and 12 MIU of vitamins A and D, respectively. This design was repeated with 5 other sows fed daily supplements of 25-OH-D3 (4 MIU), β-carotene (24 MIU), and Cu-yeast (45 mg) from 90 d of gestation to 21 d of lactation. At 23 d of age, 2 d after weaning, 5 repetitions of a combination of sow and piglet factorial treatments were sacrificed: caecal pH was recorded and digesta samples from cecum and mid-colon were taken to measure VFA concentrations. Mesenteric lymph nodes and jejunal and ileal mucosal samples were collected for measurement of cytokine gene expression by quantitative real-time PCR. Supplementation to sows significantly reduced caecal pH ($P < 0.01$) and increased both caecal ($P < 0.05$) and colonic ($P < 0.01$) VFA concentrations. Within piglet treatments, caecal VFA concentration was higher in T3 than in T4 ($P < 0.05$), but no difference was detected among other groups. For cytokine gene expression, jejunal IL-10 expression was reduced in T2 compared to T1, T3, or T4 groups ($P < 0.05$), while supplementation to sows increased gene expression of IL-22 ($P < 0.01$), IL-1β ($P < 0.05$), and IL-8 ($P < 0.05$) in the mesenteric lymph nodes. These results indicated that sow supplementation in combination with exposure to UVB light and oral supplementation of vitamins D and A and copper was an efficient administration method to modulate intestinal production of VFA by microbiota and cytokine gene expression compared to CTL. These results are in line with data indicating that copper and vitamins A and D statuses of neonatal piglets are increased by oral supplementation or UVB light (results not shown).

Key Words: copper, gut, piglets, retinol, vitamin D

1741 Comparison of transport characteristics of ferrous sulfate and iron glycine chelate across IPEC-J2 cell monolayers. *S. Fang*, College of Animal Science, Zhejiang University, HangZhou, China.*

The study was conducted to compare the transport characteristics of ferrous sulfate ($FeSO_4$) and iron glycine chelate (Fe-Gly) across porcine jejunal cell line (IPEC-J2) monolayers. IPEC-J2 cells were seeded onto the 6-well transwell collagen-coated PTFE filters and evaluated for study use on the 19–22th days. The trans-epithelial electrical resistance (TEER) value of 7510.92 ± 1586.44Ω·cm^2 was observed, a transportation percentage (0.92%) of fluorescein sodium could meet the requirements of tightness. The AKP activity in the apical side (AP) had significant higher than the basolateral side (BL) ($p < 0.01$), which means the IPEC-J2 cells has well polarity. These cell monolayers were used for the transport studies. For transport study, sample solutions containing different iron concentrations (5, 10, and 20 μmol/L) were added to AP and a buffer was added to BL. Different times (0–120 min) and temperatures (37°C, 4°C) were designed to study the effects on transportation in the same iron concentration (10 μmol/L). Samples were removed from the buffer and the iron concentrations were analyzed by atomic absorption spectrophotometer. Triplicate wells were used for each treatment. The results showed that transports of Fe-Gly and $FeSO_4$ across IPEC-J2 cell monolayers are linear increased as time went on ($R^2 = 0.9518$, $R^2 = 0.9428$, respectively). Iron transport amount of Fe-Gly and $FeSO_4$ under 37°C are significant higher than those under 4°C ($P < 0.05$), so did the apparent permeability coefficient (*Papp*). These results suggest that the absorption of Fe-Gly and $FeSO_4$ in IPEC-J2 cells may through active transport. However, no concentration-dependent iron transport was found, at concentration of 5 and 10μmol/L, iron transport in Fe-Gly treatment was higher than $FeSO_4$, at concentration of 20μmol/L, transport amount of both iron sources significantly reduced ($P < 0.05$), iron transport amount in Fe-Gly treatment was significant lower than $FeSO_4$ ($P < 0.05$). Distinct absorption mechanism may account for the transport difference between these two iron sources at different concentrations.

Key Words: IPEC-J2; absorption; ferrous sulfate; iron glycine chelate; active transport

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1742 Studing of population structure of European wild boar (*Sus scrofa*) and its subspecies, inhabiting Russia. A. A. Traspov[1], O. V. Kostyunina[1], I. A. Domsky[2], A. V. Ekonomov[2], A. A. Sermyagin[*1], and N. A. Zinovieva[1], *[1]L.K.Ernst Institute of Animal Husbandry, Moscow, Russian Federation, [2]Institute of Hunting and Fur-farming named after professor B.M. Zhitkov, Kirov, Russian Federation.*

Genetic studies help to shed a light on the topic but it embraces various aspects including economic, social, and technical issues. Genetic structure of wild boars from Russia can represent flexible territorial clusterization on large geographical areas. In this study, we performed whole-genome SNP analysis of wild boars inhabiting the Russian Federation. Forty animals represent 11 regional subpopulations of the wild boars. They were genotyped using Porcine 60K BeadChip (Illumina Inc., USA). All populations belong to European part of Russia, including Arkhangelsk, Chelyabinsk, Kirov, Krasnodar, Kurgan, Novgorod, Smolensk, Tumen, Udmurtia, Vladimir, and Volgograd regions. We used PLINK v1.09 to obtain Multi-Dimensions Scaling matrix (MDS) and pairwise clustering based on IBS distances. Neighbor Joining tree provided by MEGA v.7 software, based on Tamura-Nei model. In addition, we evaluated population structure of wild boars using ADMIXTURE 1.20 package and calculated pairwise differences and F-statistics between subpopulations. Visualization of data was performed by R. Analysis of spatial distribution showed that at least four groups of animals, which belong

to Arkhangelsk, Kirov, Novgorod, and Vladimir subpopulations, performed separated clustering. Another seven subpopulations have formed a huge single group. We could observe the exchange of single animals between Smolensk and Arkhangelsk subpopulations. The same result was shown by NJ-tree dendrogram and IBS-clustering matrix—most part of animals formed main core with minor branches. Analysis of admixture was performed for the number of clusters (K) from 2 to 7. Analysis of population structure performed for the clusters number K = 2 and 3 according to obtained lowest values of CV errors (0.76395 and 1.42878, respectively) and showed high divergence of the Arkhangelsk subpopulation among all other subpopulations. The presence of clusters may probably indicate the existence of wild boar subspecies. There are no Asian subspecies of wild boar in the European territory of Russia, so we can presume that Arkhangelsk wild boar subpopulation belongs to European-Caucasian subspecies of wild boar. This is the first large-scale analysis of the Russian wild boars performed on whole-genome level. Studies will be continued with involving wild boars inhabiting the whole area of distribution of this species in Russia.

Key Words: phylogenetic, population studies, wild boar

1743 Supplementation with a blend of capsicum and artificial sweetener improves performance of growing and finishing pigs. C. Ionescu*, C. Soulet, C. Bruneau, and E. H. Wall, *Pancosma, Geneva, Switzerland.*

Supplementation of piglets with the artificial sweetener SUCRAM® increases intestinal expression of sodium-glucose co-transporter-1, glucose uptake, and mucosal growth. Both SUCRAM® and capsicum oleoresin improve efficiency of growth in pigs; however, responses to the two additives fed in combination have not been described. The objective of this experiment was to determine the effects of such a blend on feed intake and performance of growing and finishing pigs exposed to a dietary energy challenge. Pigs (PIC380 x Large White/Landrace; n = 252 barrows & 252 gilts) were housed in 24 pens under 12-h artificial lighting, were blocked by BW and gender, and were randomly assigned to two treatments (n = 21 pigs per pen; 12 pens per treatment) during grower and finishing phases (Grower 1: 25–50 kg; Grower 2: 50–75 kg; Grower 3: 75–100 kg; Finsher: 100–129 kg). Dietary treatments were: 1) Low-NE which was a standard diet formulated to meet NRC recommendations, with wheat millrun added to decrease net energy by 100 kcal NE/kg; and 2) Low-NE + supplementation with a blend of capsicum oleoresin and SUCRAM® (CAPS-SUC; 75 g/ton; TakTik® X-Hit; Pancosma, Geneva, Switzerland). Diets were fed ad libitum as mash feed and disappearance of feed was measured by a robotic recording system. Pigs and remaining feed were weighed at the end of each feeding phase to calculate daily gain and daily feed intake, respectively. Mortality, pulls, and health records were monitored; growth performance, days to market weight, and carcass characteristics were measured. Inclusion of CAPS-SUC in the Low-NE diet increased daily gain in both the Grower 1 (949 vs. 974 g/d; $P < 0.05$) and Finisher phases (921 vs. 938 g/d; $P < 0.05$). This appeared to be partly driven by feed intake, which was numerically increased with CAPS-SUC when all phases were considered (2.70 vs. 2.85 g/d; $P < 0.20$). Feed ÷ gain was not affected by treatment across all phases (2.98 vs. 2.97; $P > 0.80$). Removals and deaths were not affected by treatment ($P > 0.50$). Carcass weight was increased (101.7 vs. 102.5 kg; $P \leq 0.05$) and days to slaughter were decreased (18.2 vs. 16.7; $P \leq 0.10$) with CAPS-SUC. Feed costs were not affected by treatment ($0.72 vs. $0.73/kg; $P > 0.20$). The results of this study indicate that CAPS-SUC can improve performance of growing and finishing pigs when a dietary challenge is introduced.

Key Words: feed additive, phytonutrient, Sucram

1744 Effects of different sources and routes of administration of copper and vitamins A and D on piglets gut microbiota. G. Talbot[1], M. Lessard[*1], E. Yergeau[2], N. Gagnon[1], L. Lo Verso[1], J. Lapointe[1], N. Bissonnette[1], D. Bueno Dalto[1], B. Ouattara[1], F. Guay[3], and J. J. Matte[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke Research and Development Centre, Sherbrooke, Canada, [2]Université du Québec, Centre INRS-Institut Armand-Frappier, Laval, Canada, [3]Universite Laval, Quebec City, Canada.*

Placental and colostral transfers of copper and vitamins A and D micronutrients from dams to neonates are limited in pig species (Matte et al., 2014, JAS 92-Suppl. 2:153). The aim of the study was to evaluate the influence of different perinatal micronutrient supplementation strategies on piglets' gut microbiota. Within each litter from 5 sows, 10 newborn piglets were allocated to one of the following combinations of sources and routes of micronutrient administrations: oral vitamin D3, retinol-acetate and $CuSO_4$ (T1); oral 25-OH-vitamin D3, β-carotene and Cu-yeast (T2); exposure to UVB light (20 min every second day), oral retinol-palmitate and Cu-gluconate (T3); intramuscular vitamin D3 and retinol-propionate and oral Cu-acetate (T4); oral saline (CTL). Oral or intramuscular provisions corresponded to 12 mg of copper and 70 and 12 MIU of vitamins A and D, respectively. This design was repeated with 5 other sows fed daily extra supplements of 25-OH-vitamin D3 (4 MIU), β-carotene (24 MIU) and Cu-yeast (45 mg) from 90 d of gestation to 21 d of lactation. At 21 d of age, feces were collected and piglets were weaned. At 23 d of age, 5 repetitions of a combination of sow and piglet factorial treatments were sacrificed and feces and content from mid-jejunum, ileum, mid-colon, and rectum were collected to characterize gut microbiota. Bacterial communities were analyzed by sequencing the V3-V4 regions of

16S rRNA genes on an Illumina MiSeq. Bioinformatic analyses were performed on our internal data analysis pipeline and statistics were performed in R. The analysis of bacterial community composition at the class level revealed that sow supplementation significantly increased the relative abundance of *Bacilli* in feces at d 21 ($P = 0.04$) but not at d 23. Gut microbiota diversity significantly differed ($P = 0.03$) according to supplemental treatments provided to piglets. However there was no piglet treatment effect on gut microbiota based on PCoA analyses. The Shannon diversity of jejunal and ileal microbiota was significantly ($P < 0.05$) decreased when supplementation was given to sows. Sow supplementation also significantly increased *Bacilli* in both jejunum and ileum ($P < 0.001$, both). The study demonstrated that piglet gut microbiota can be modulated by daily extra supplementation of vitamins A and D and organic copper to sows during late pregnancy and lactation periods. Further studies are thus warranted to study mechanisms of action explaining the impact of such maternal micronutrient supplementation on bacterial colonization in piglets gut.

Key Words: copper, gut microbiota, piglets, retinol, vitamin D

1745 Diurnal heat stress reduces nursery-grower pig performance and intestinal integrity.

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Heat stress negatively affects performance and intestinal integrity of livestock. Our objective was to characterize the effects of diurnal heat stress on nursery-grower pig performance and intestinal integrity. Forty-eight individually penned crossbred gilts (21 ± 2.0 kg BW) were randomly assigned across two environmental treatments (thermal neutral (TN) or diurnal heat stress (HS), $n = 24$/trt) at the Iowa State University Swine Nutrition Farm. All pigs were allowed ad libitum access to water and a corn-soybean diet that met or exceeded NRC (2012) requirements. After a thermal neutral acclimation period, 24 pigs (HS) were exposed to 3 d of diurnal heat stress with 6 h in HS conditions (38°C; 40–60% humidity) and 18 h in thermal neutral conditions (32°C; 40–60% humidity). The remaining 24 TN pigs were maintained for these 3 d under thermal neutral conditions (28°C; 40–60% humidity). Pig rectal temperature (Tr), respiration rates (RR), BW changes, and feed disappearance were recorded over the environmental treatment. Blood samples were collected at the end of the 3 d environmental treatment and metabolites, endotoxin, cytokines, and acute phase proteins were evaluated. All pigs were sacrificed after the 3 d environmental treatment and ex vivo ileum integrity was assessed in Ussing chambers by measuring transepithelial resistance (TER), FITC-dextran (FD4), and FITC-LPS permeability. As expected, HS pig Tr were increased on average 2°C over the 3 d period ($P < 0.05$) and RR increased from 50 to 150 breathes per min (TN verses HS, respectively, $P < 0.01$). Compared to TN, HS pigs had a 30% reduction in ADFI and a 76% reduction in ADG over the 3 d environmental treatment ($P < 0.05$). Gain to feed was also reduced due to HS compared to TN (0.16 verses 0.55, $P = 0.016$). Ileum TER was significantly decreased ($P = 0.04$), FTIC-LPS ($P < 0.01$) and FD4 ($P = 0.015$) permeability increased due to HS compared to TN pigs. Serum endotoxin was significantly elevated due to HS ($P = 0.031$) and there was a reduction in LPS-binding protein ($P = 0.06$) and tumor necrosis factor α ($P = 0.04$) in HS compared to TN pigs. Overall, HS reduced blood insulin concentrations by 50% ($P = 0.02$), but did not affect blood glucose concentrations ($P = 0.47$). Altogether, short exposure to diurnal heat stress significantly reduced pig performance and intestinal integrity compared to those exposed to thermal neutral conditions.

Key Words: heat stress, intestine, pig

1746 Effect of diet composition on piglet growth and digestibility responses to a high dietary canola content.

G. A. Mejicanos*, *University of Manitoba, Winnipeg, Canada.*

Soybean meal (SBM) and canola meal (CM) are the most extensively used protein supplements in the feed industry, whereas corn and wheat are the main sources of energy in swine diets in North America. Although recent studies show that piglets can handle relatively high levels of CM, it is unclear whether this ability depends on the cereal base the diet. Thus, the aim of the study was to determine whether the composition of the main feed ingredients in the basal diet influences pig response to high dietary CM inclusion as indicated by growth performance and apparent total tract digestibility (ATTD) measurements. Ninety-six pigs [(Yorkshire-Landrace) x Duroc)] with an initial BW of 6.63 + 0.028 kg (barrows) and 6.78 + 0.036 kg (gilts) were used in this 28-d feeding study. There were 8 replicate pens per treatment each with 3 pigs. Pigs were randomly allotted to one of four dietary treatment: 1) Corn-SBM; a corn-SBM based diet, 2) Corn+20%CM; a corn-SBM diet with SBM partially replaced by 20% CM, 3) Wheat-SBM; a wheat-SBM based diet, and 4) Wheat+20% CM, a wheat-SBM diet with SBM partially replaced by 20% of CM. A two phase feeding program was used (phase 1, 1 to 14 d post-weaning and phase 2, 15 to 28 d post-weaning). Average daily gain (ADG), average daily feed intake (ADFI), and feed efficiency (G:F) were recorded weekly. Freshly voided fecal samples were collected on d 21 and 27 to determine ATTD of CP and energy. Data were analyzed as a randomized complete block design using MIXED procedure of SAS. No significant differences were observed in ADFI, ADG, and FBW among treatments ($P > 0.10$). Pigs

fed on the wheat + 20% CM diet had higher G:F ratio compared with those fed on the corn-SBM diet (0.95 vs. 0.79, $P < 0.01$) during phase 1. However, the corn-SBM diet had higher ATTD of CP and energy compared with piglets fed the corn+20% CM, wheat-SBM, and wheat+20% CM diets (96.6 vs. 89.0, 90.9, and 87.2%; and, 95.3 vs. 89.6, 90.8, and 86.9%, $P < 0.01$) during phase 2. In conclusion, results indicated that the composition of the main feed ingredients in the basal diet influences feed efficiency, likewise protein and energy digestibility when CM is included at 20% level without affecting voluntary feed intake and ADG.

Key Words: canola meal, diet composition, digestibility

TEACHING UNDERGRADUATE AND GRADUATE EDUCATION

1747 Increase in demand for hands-on instruction in animal science curriculum.

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In animal science programs across the United States, the fraction of undergraduate students that have livestock experience before entering college is diminishing. Students in many programs clamor for hands-on experiences with animals and livestock, as it is relevant to their program of study, and may provide a competitive advantage in applying to a veterinary program. An experimental course was proposed for two primary purposes; first to address the specific demand encountered in the Department of Animal Sciences at Colorado State University, and second to provide greater pre-employment training and experience in course development and instruction for a doctoral student wishing to pursue an academic path. With guidance from the department head, a course description, outline, and schedule were constructed and presented to the departmental curriculum committee. Upon receiving authorization for the course to be listed on an experimental basis, registration was made available to the first ten students to enroll. The three credit course consisted of two lectures per week and one lab. Students were guided through an introduction to classical behaviorism and ethology, moving on to species specific behaviors of the major livestock species. Information was presented first in lecture, and reinforced through lab exercises. In labs, students were introduced to concepts through expert demonstration of animal handling or management techniques, and then practiced the skill with close supervision. Students had several opportunities to increase their proficiency with specific skills before they were given a practical assessment. Students were assessed on their assimilation of lecture material through traditional written exams, as well as in class and take home quizzes. Evaluation of the course was conducted with questions ranked in a 5-point Likert scale to assess student perceptions and effectiveness of the course to achieve university learning goals. Students felt this course was an important part of their academic experience, and indicated that the exposure to the livestock species and various sectors of the livestock industry they were exposed to in this course was an invaluable experience. Finally, students felt that the size of the class provided optimum opportunity for students to receive instruction, practice, and demonstrate proficiencies.

Key Words: hands-on instruction, livestock experience, livestock handling, proficiency

1748 Adding a student-generated summary of main points to a lecture as a learning tool in an advanced nutrition course.

S. L. Hansen*, *Iowa State University, Ames.*

Learning-centered classrooms encourage students to focus on the thinking required to master a concept. Previous work has suggested that increasing the number of focused engagement activities such as Turn To Your Partner (TTYP) within a class period enhances student retention of information in an advanced animal science course. The TTYP activity allows at least 3 opportunities to think about the learning, as the student generates his/her own answer, discusses it with a partner, and participates in whole class discussion. Starting each class period with a defined set of learning outcomes provides focus to the lecture and provides an outline from which students can study. Similarly, a structured ending to a class period that includes a review of the most salient points from a lecture could be beneficial to student learning. Students in a senior level animal nutrition course ($n = 34$ students) were asked to generate overall summary statements at the end of lecture ($n = 23$ lectures in the semester). During the last 5 min of class, students were asked to compile summary points from the lecture using the TTYP format. Students were given approximately 2 min to generate a list of 3 to 5 primary summary points from the day's lecture material or discussion. They were then allowed to work with a partner for another minute, and then brought back to group discussion. Students were held accountable for their learning by being called on at random to share what they and their partner had identified as a critical summary point for the day's material. This continued until all points were exhausted. Critical opportunities for student development included the opportunity for the instructor to correct misconceptions, and for students to develop better note taking and summarizing skills. Students gave feedback halfway through the semester and 80% specifically mentioned that summary point generation was a factor in class that positively affected their learning. Twenty-three students completed the final anonymous course evaluation, and 87% replied to the question "what helped your learning most in this class"? Of those replies, 100% indicated the TTYP and summary exercise were beneficial in their learning. Including

a summary exercise at the end of each class was a positive addition to an advanced nutrition course and contributed to the success of students.

Key Words: learning, summary points, undergraduate

1749 Teaching animal welfare via competitive judging contests. C. B. Shivley*[1], F. B. Garry[2], and T. Grandin[1], [1]*Colorado State University, Fort Collins,* [2]*Colorado State University, College of Veterinary Medicine and Biomedical Sciences, Fort Collins.*

The scientific study of animal welfare involves complex assessments of an animal's physical health, emotional state, and the naturalness of its environment. As the public becomes more aware of animal welfare, the demand for students knowledgeable about animal welfare science is increasing, yet many universities provide little training in this field. The Animal Welfare Judging and Assessment Contest (AWJAC) was created in 2002 at Michigan State University with support from Purdue University to teach students how to assess and critique the welfare of animals used for food production, research, companionship, and other human purposes. Each year at the annual competition, computer-based scenarios on four pre-determined animal species are presented to the students with information on performance, health, physiology, handling, and behavior of the animals. The students evaluate the scenarios to determine which facility has the best welfare, and defend their decision through oral reasons presented to judges. The competition now has undergraduate, graduate, and veterinary divisions. The 2015 competition was held at Ohio State University with 25 teams and 105 individuals competing. A course was created at Colorado State University (CSU) in 2012 to prepare students for the competition, and can serve as an example of how to teach students about animal welfare assessment. The course teaches students about general animal welfare principles, provides in depth training on the four featured species through guest lecturers, field trips, and review of the scientific literature, and develops public speaking skills. The CSU teams have continued to be successful at the contest, and in 2015 CSU won first place in the graduate division, as well as numerous individual awards. The contest combined with the course provides learning opportunities about the growing field of animal welfare science.

Key Words: animal welfare, judging teams, welfare assessment

1750 Integrated program for reducing bovine respiratory disease complex (BRDC) in cattle, coordinated agricultural project (CAP): Translation of multi-omics research results into teaching programs. M. G. Thomas*[1], R. M. Enns[1], R. Hagevoort[2], J. S. Neibergs[3], A. L. Van Eenennaam[4], H. L. Neibergs[5], and J. E. Womack[6], [1]*Department of Animal Sciences, Colorado State University, Fort Collins,* [2]*New Mexico State University, Dairy Extension, Clovis,* [3]*Washington State University, Pullman,* [4]*University of California, Davis,* [5]*Department of Animal Sciences, Washington State University, Pullman,* [6]*Texas A&M University, College Station.*

Bovine respiratory disease complex is a common cause of morbidity and mortality in cattle, especially young animals exposed to stress. This disease is considered a complex because of numerous pathogens, environmental and management factors of the beef and dairy industries. Susceptibility to BRDC is also considered a complex trait as it is very polygenic. The general research objective of this CAP is to use genomic approaches to identify chromosome regions associated with susceptibility to BRDC. The genomic approaches described in the research publications from this CAP involve multiple types of data and results, such as genome-wide association and SNP-chip data, DNA and RNA sequencing, quantitative genetics and many physiological measures of the immune system. The results will be translated to beef and dairy industries via selective breeding tools and methods for disease prevention and management. These types of tools are known as genome-assisted EPD and PTA. A translational effort of research findings, which also includes cattle health and behavior results, is encompassed in multiple teaching and extension efforts described on this website: http://www.brdcomplex.org/. Examples of the genomic translational educational effort include the Herd Health and Breeding and Genetics modules within the U.S. Dairy Education and Training Consortium (USDETC) and two online graduate courses titled: I) Applied Disease Management for BRD and II) Genetics and Genomics of BRD in Cattle. Within these activities, students learn about the various types of omics data and how these data are used in the calculations of genome-assisted estimated breeding values. This CAP is now in its latter years of funding, and the research team is

successfully publishing results. Therefore, quality multi-omics information is available to teach students about various types of omics data and how these data can be used in genetic improvement programs for traits that are currently difficult to measure in beef and dairy production systems. In summary, the education component of the BRDC-CAP (USDA-AFRI 2011–68004–30367) involves cross-disciplinary learning opportunities that coincide with the multi-omics research of susceptibility to BRDC.

Key Words: cattle, genomics, respiratory disease, teaching

1751 A novel approach to adviser training for relational skills. *A. L. Robinson* and H. D. Tyler, Iowa State University, Ames.*

The Iowa State University College of Agriculture and Life Sciences Dean's Task Force on First Year Student Success recommended that workshops should be developed to enhance relational skills of academic advisers. The topic of the first workshop developed was "Student Issues: Recognition and Referral". In contrast to other workshops covering similar topics, this workshop incorporated undergraduate students that had overcome a variety of barriers to their success. We maintained a small interactive workshop approach, limiting adviser enrollment to 12 advisers per workshop and incorporating an equal (or greater) number of students. During the 3-hour workshop, participants discussed common barriers to assisting students during a brief presentation on common student issues, effective communication skills for advisers, and campus and community resources available for referral. In addition, students assisted in role-playing exercises designed to simulate adviser meetings with a student in crisis, and the session ended with a panel discussion allowing advisers to ask questions directly to any of the students or the session leaders. Over 50 advisers from across campus have attended these workshops, and the session was also replicated at a regional meeting of the National Academy of Academic Advising. Advisers attending these workshops provided feedback through a survey at the end of the session rating six different aspects of the workshop on a 1–10 scale. Ratings for each aspect of the program ranged from 8.5 to 9.2, with advisers rating the student panel and student role-playing as the most impactful aspects of the workshop at 9.2/10 and 8.8/10, respectively. These data suggest that relational workshops for advisers are more impactful when a student perspective is included. Adviser comments reflected that many advisers lack confidence in their ability to respond appropriately to a student in crisis, and that their confidence increased as a result of participating in this workshop. In summary, adviser participation in relational workshops that include student participants enhances adviser confidence in their ability to recognize student issues and respond appropriately and effectively; these skills ultimately should improve student retention and success.

Key Words: academic advising, student success

1752 The effect of a real-world learning project on students' knowledge retention: A comparative study. L. M. White*, *New Mexico State University, Las Cruces.*

To be successful in many undergraduate disciplines, students must retain base knowledge from lower level courses and apply that knowledge in upper level courses. Students may benefit and realize the importance of mastering basic concepts from the opportunity to utilize base knowledge in a real-world setting. Objectives of this project were to compare students ability to retain information after completing a real-world learning project (RWLP) to base knowledge retained from exams students took during the semester, and finally to determine student's perception of the RWLP. Incoming freshmen (n = 52, 79% female, 96% animal science majors) enrolled in an introductory equine science course worked independently to create a RWLP, specifically an educational bulletin (EB) for eight main topics studied during the course. The main topics were identified by the instructors as the most important topics to learn in an introductory horse science class, and included: identification, behavior, health, nutrition, activities, hoof care, parasite/disease, and reproduction. Students completed two assessments after the course was completed, the regular course exam quiz (REQ) which contained questions (n = 16; 2 questions from each main topic) the students had previously completed on exams and the educational bulletin quiz (EBQ) which contained questions (n = 16; 2 questions from each main topic) that were generated by the instructors from each student's EB. Students also completed a 3-question survey (Likert scale 1–5) regarding the influence of the EB on their understanding of the material, retention of material presented in class, and overall impression of the EB. Student scores on the REQ and EBQ were correlated (r = 0.54 and r = 0.39, respectively) to final course grade, but not to gender ($-0.05 < r < 0.05$). Students performed better ($P < 0.0001$) on questions from the EBQ compared to questions from the REQ. Students indicated they enjoyed completing the EB and perceived that they better understood basic information and expected to better retain the material as a direct result (4.5 ± 0.1, 4.72 ± 0.1, and 4.5 ± 0.4 on a 5 point scale, respectively). Students benefited from completing the EB project by better retaining key concepts taught during an introductory equine science course and the project was highly thought of by students. Disciplines that require students to retain key concepts from lower level courses for later use in upper level courses could benefit from a RWLP like the EB.

Key Words: base knowledge retention, real-world learning project, undergraduate learning

1753 Utilization of concept mapping as a tool to qualitatively assess knowledge of college seniors in a companion animal management course.

C. L. Morris*, *Iowa State University, Ames.*

Concept mapping is a visual technique to facilitate integration of new information with previously learned material. This study was designed to evaluate the effectiveness of concept mapping as a novel method to qualitatively assess student critical thinking and understanding in a discussion-based senior level companion animal management course. Students over 3 semesters (n = 106) provided feedback after completing 9 total concept maps (3 per semester) following 3 main informational course units (n = 318 maps). A novel quantitative rubric was established, consisting of 3 categories each having 4 point levels, including Organization and Presentation, Content and Concepts, Knowledge of Concept Relationships, and Understanding Through Connections. Students completed the initial portion of maps before unit introduction and they were collected and held by the instructor (not graded) until the conclusion of the unit when they were returned to students for completion in a different color ink. Students were asked 4 anonymous questions about the maps using a standard 1–5 Likert type scale (1 = Strongly Agree and 5 = Strongly Disagree): 1) Concept maps made me think about information I already knew; 2) Concept maps helped me learn new material; 3) I liked Concept maps as an evaluation tool; 4) Concept maps were effective forms of assessment for this course. Additionally, students could submit comments regarding concept maps. A total of 87 of 106 students provided written feedback. Question score means were 1.27, 1.68, 1.45, and 1.55 for the four questions, respectively, and 94% of respondent comments were positive. Five students indicated they did not like the mapping activity and preferred essays or traditional exams. Sixty-seven percent of comments indicated maps improved learning because students were able to focus on how material specifically related to them and their existing knowledge base rather than worrying about stress of memorizing facts for exams. The words "less stressful" specifically appeared in 60% of written comments. This highlights the value of using concept mapping to develop critical thinking skills in a discussion-based class where traditional exams may not be effective. High rate of return of student feedback and consistency of positive responses from students underscore the value of this technique for qualitative assessment of knowledge and learning in a senior-level discussion-based companion animal course.

Key Words: companion animal, concept mapping, teaching

1754 Spanish for animal health and care: Toward a certificate program in field-specific Spanish.

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There is increasing awareness of the need for basic field-specific communication skills in Spanish on the part of animal science and veterinary professionals working with livestock operations. Between 80% and 90% of the workforce in such establishments is comprised of Spanish-speaking immigrants with low English proficiency and minimal formal education. Until now, the ways in which this language barrier has been approached have not been informed by the growing body of research on Languages for Specific Purposes (LSP). The objective of this presentation is to detail the interdisciplinary approach to the curriculum development and implementation of a basic "Spanish for Animal Health and Care" class leading to a certificate program designed to cater to the specific language needs of future animal scientists and veterinarians. The curriculum is based on a needs analysis, which includes non-structured interviews of Spanish-speaking workers on livestock farms and livestock farm professionals, the recording of a livestock workers' safety meeting, as well as the creation of a specialized, domain-specific corpus. All course materials consist of module-specific packages of video and audio recordings, interactive hands-on materials, a library of relevant images, and a corpus of authentic texts, from which targeted vocabulary and grammatical forms are derived. The curriculum is divided into 3 performance-based units: describing and comparing animals' physical and behavioral traits, mock-trainings of new hires wherein students describe the 'why' of farm procedures, and a mock-veterinary consultation which includes descriptions of abnormal animal behavior/physicality and recommendations for care. Formal mid-term assessments demonstrate increased development of functional language proficiency by indicating ascension on the American Council on the Teaching of Foreign Languages (ACTFL) proficiency scale from novice-mid toward novice-high. Communicative tasks that form the performance-based assessments require elaborated, context-specific sentence-length discourse, which is imperative for novice-high proficiency on the ACTFL scale. Informal student evaluations report gratitude and excitement about working toward field-specific functional proficiency in Spanish, which may factor into the current class average of 87.48%. Additionally, a survey completed by 257 students in CSU's professional veterinary program revealed that 93.5% of students are interested in learning basic Spanish language skills specific to their future professional needs. 92.8% of those surveyed and 100% of students currently taking the beginner

Spanish course report that they would like to pursue a certificate program in Spanish for Animal Health and Care.

Key Words: curriculum development, languages for specific purposes, Spanish language proficiency

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1755 Characterization of students' educational background and subsequent use of relevant teaching methods enhances student engagement and success in introductory animal science course. J. Adcock*[1], Q. S. Baptiste[1], and M. Knights[2], [1]*Berea College, Berea, KY,* [2]*West Virginia University, Morgantown.*

One of the most challenging dilemmas a teacher faces when designing lessons for their class is the variation of prior knowledge of their students. This is especially true in introductory Animal Science courses, where students from a variety of backgrounds and knowledge levels are placed in the same course. Some of these students probably grew up around livestock or taken Animal Science courses in high school, while others may have never had these opportunities. In an effort to reach as many students as possible, teachers must either choose to cover the basics or start at the level of the majority of the class. The first option is best for those who do not have prior knowledge, but does not permit others to advance their education. The second allows advancement for some, but leaves others behind. Thus, a survey was conducted to characterize the educational background of potential Animal Science students and to determine adoptable teaching methods that were currently being used by agriculture educators in West Virginia and Kentucky high schools. Data revealed an even divide of the sexes (Male: 56.52 vs. Female: 43.48%) among participating students with 56.52 and 26.09% of whom live in rural non-farm and farm area, respectively. Most students enrolled in Animal Science class to be in Future Farmers of America (30.43%), to pursue agriculture/animal science career (34.78%), or were just interested in animal systems (26.09%). Weighted averages of students surveyed scaled responses (0 = least to 5 = most) indicated that the majority of students claimed they had the least amount of knowledge about abstract knowledge based topics of the digestive systems (3.77), nutrition (3.77), and genetics (3.83). Indeed, the surveyed teachers' responses also indicate that the most challenging topics to teach were nutrition and genetics. Teaching strategies that were reportedly most effective included, hands-on learning, project-based experiences, active learning experiences, and varying the speaker, technology, and interactions within the learning environment. Subsequent use of the foregoing information to modify an introductory Animal Science class with students of widely diverse educational background and experiences at Berea College resulted in increased (50%) student engagement and a significant increase (16.67%) in overall student satisfaction with the course as compared to when it was taught 2 yr prior. Conclusively, the characterization of students' educational background and subsequent use of relevant teaching methods can enhance teaching effectiveness.

Key Words: educational background, teaching effectiveness, teaching methods

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1756 Impact of a global food security assignment on agricultural sciences students' education and career interests. K. Matthews* and O. Bolden-Tiller, *Tuskegee University, Tuskegee, AL*

As we approach 2050, the challenge of producing enough wholesome, nutritious food for the world population is of increasing concern. Although the solution has yet to be identified, it is clear that to address this issue a well-trained workforce that understands the issue of global food security and its causes is required. Therefore, this study sought to assess the impact of a global food security assignment on freshman animal science students' understanding of global food security and their desire to pursue careers that address this issue. To address this objective, 48 students majoring in animal science at Tuskegee University completed a Likert scale survey (1 = Strongly Disagree, 2 = Disagree, 3 = Neutral, 4 = Agree and 5 = Strongly Agree) following the completion of a global food security writing assignment. The results of the survey indicated that after completing the global food security assignment, students had an increased understanding of global food security (4.3/5.0) as well as its causes (4.6/5). Before the global food security assignment, students indicated that they had not considered pursuing a career to assist with global food security (2.4/5.0); however, after the assignment, the students were more likely (3.5/5.0) to pursue a career that addresses global food security. These findings indicate that once students are educated about agro-issues, such as global food security, they are more likely to pursue educational and career opportunities that allow them to address said issues.

Key Words: food security, students, survey

1757 Student perspectives on agricultural study abroad programs. M. M. Beverly*, S. F. Kelley, P. Urso, M. J. Anderson, J. L. Leatherwood, and K. J. Stutts, *Sam Houston State University, Huntsville, TX.*

The globalization of the US economy and agriculture products warrants agricultural programs to enrich the learning environment beyond agricultural systems in the United States, but to embrace international systems and markets, as well. International agriculture classes combined with study abroad programs have a positive effect toward students' understanding of global agriculture systems with a broadened cultural awareness. It is the study abroad experience that allows students to immerse themselves in cultural differences and obtain an understanding of different agricultural systems and policies governing food production in other countries. In the

summer of 2015, sixteen students from Sam Houston State University (62% female, 38% male, 20–24 yr of age) participated in pre-/post-surveys regarding a study abroad trip to France and Italy. In the pre-survey, 21% of the students predicted that the international experience would enhance their self-confidence/problem solving skills and on their return these characteristics increased to 40%. Students' predicted an increased knowledge in international animal regulations and practices and the post-survey verified that prediction by being 50% more confident in European Union (EU) animal agriculture practices, 62% more confident in EU animal welfare policies, and 62.5% more likely to have knowledge surrounding EU agriculture and animal organizations. When asked to if the study abroad experience increased their desire to travel abroad, 93% responded "very much". Only 2% would consider changing their academic major due to their study abroad experience. Students' responded overwhelmingly (100%) that they would recommend the program to a friend. Comments of students were: life changing, traveling with fellow students added to the experience, meeting people with the same passion for agriculture, and amazing, once in a lifetime trip. While there are many obstacles within study abroad trips, the expansion of knowledge for students is beneficial.

Key Words: international, study abroad, travel course

1758 Curriculum development for animal disaster planning.
K. Franks, S. F. Kelley*, and M. M. Beverly, *Sam Houston State University, Huntsville, TX.*

Disaster preparedness is mandated by the federal government in the United States. Until the passing of the Pet Evacuation and Transportation Standards (PETS) Act in 2006, animals were not addressed in disaster planning except in the scope of livestock disease outbreaks and the need to protect our food supply. Disasters can be defined as "sudden-onset occasions that seriously disrupt social routines…" Hurricanes, tornadoes, wildfires, droughts, floods, severe blizzards, chemical spills, industrial explosions, and other incidents are types of potential disasters. Disasters can cause anxiety, depression, stress, and fear as well as financial strains and physical injuries for both human and animal. The cattle industry has a more than $88 billion dollar a year impact, while the horse industry produces more than $39 million a year direct impact on the U.S. economy. Companion animals are a vital part of our economy as well, with owners spending in excess of $50 million a year on pets and their care. Society acknowledges the importance of the human-animal bond and its impact on mental health while studies have also shown the same effect on the mental health of animals during times of stress and separation from their owners. The Federal Emergency Management Agency (FEMA), a division of the Department of Homeland Security, provides information to understand disaster preparedness and implementation, while developing curriculum to enrich agricultural program curriculum and education students on disaster planning and preparedness. Sam Houston State University has developed a course to address the need of the gap in education when dealing with these issues. The course focuses on risk assessment, to allow the student to learn the importance of focusing resources in strategic need areas and learn where mitigation efforts would be most beneficial. Topics also include: planning for mass die off and/or mass euthanasia, mass evacuation events, and a how-to plan for the evacuation and housing of companion animals, horses, and other types of livestock. This course provides a strong foundation on how to be prepared for man-made and natural disasters.

Key Words: agriculture, disaster planning, preparedness

1759 Application of a survey instrument for assessing student demographics and interests in an animal and dairy sciences career planning course.
M. C. Nicodemus*, *Mississippi State University, Mississippi State.*

Recent changes to the Mississippi State University Animal and Dairy Sciences (ADS) curriculum was designed to address the needs of today's students preparing to enter into the animal industry. The new curriculum includes the addition of a sophomore/junior level 1 h lecture course, ADS 2111 ADS Career Planning, focused on developing life skills needed for preparing for an animal science career. The course includes resume building and skill development in interviewing along with skills in job searches and preparation needed for building a strong background to impress potential employers. The course includes speakers and industry interaction along with career research activities and group discussions. To better develop and expand the new course, a survey instrument was applied to determine student demographics and interests. Students enrolled in both the spring and fall 2015 ADS 2111 ADS Career Planning course (n = 58) were asked to take a researcher-developed survey consisting of 10 questions compiled of both open-ended and forced choice questions. The majority of students taking the course were ADS majors (98%), and of those, over half (58%) were expecting to go to veterinary college, while 27% had expectations of attending graduate school. These ongoing degrees require a GPA of 3.0 or higher in which only 17% of the students in the course had a GPA below these requirements. As for practical industry experience, 88% of the students have performed an animal science internship or will be carrying out one in the coming semester. Over half of the students (54%) planned to focus their career in companion animals, including equine. ADS 1113 Animal Science was reported by 43% as being the most useful course taken at this point in their academic career. As for future courses, 39% reported the course they looked forward to most taking was the internship course,

ADS 4420 ADS Internship. As for the student's assessment of the ADS 2111 ADS Career Planning course and what activities they felt were the most useful, almost half (48%) reported the development of a resume and cover letter was the most useful in their academic career with 71% admitting they had not done a cover letter before the course. In conclusion, through the survey insight was given on what would be beneficial to adding to the course and what topics in the course are worthy of expanding according to the students' interests and background.

Key Words: assessment, career planning, demographics,

1760 Evaluation of learning outcomes in a dairy science section of a science, technology, engineering, and math retention program. K. A. Dolecheck* and J. M. Bewley, *University of Kentucky, Lexington.*

The mission of the University of Kentucky's STEMCats program is to 1) increase retention of STEM students, 2) increase awareness of non-traditional STEM careers, 3) create an opportunity for early exposure to research, 4) diversify the student population in STEM majors, and 5) increase faculty development. Freshmen students accepted into the program spend their second semester of the year-long program working with a research lab to gain hands-on experience. The objective of this study was to evaluate learning outcomes of students participating in the first dairy section of the program. Nine students with no previous research experience were enrolled in the Spring 2016 STEMCats dairy section. At the beginning of the semester, each student completed a nine-question survey that asked them to rank their understanding of different research aspects on a 1 (low) to 5 (high) Likert scale. The survey was re-administered either five (n = 5) or six (n = 4) weeks later. Based on a paired sample t test, understanding increased between the first and second survey in the areas of "how to design a research study" (mean ± SD increase = 1.4 ± 1.2 points; $P < 0.01$), "understanding of statistical analysis" (mean ± SD increase = 1.1 ± 0.8 points; $P < 0.01$), "how to create a research poster or presentation" (mean ± SD increase = 1.6 ± 1.3 points; $P < 0.01$), "how to find research papers" (mean ± SD increase = 0.9 ± 0.9 points; $P = 0.02$), and "how to analyze other's research" (mean ± SD increase = 1.4 ± 1.5 points; $P = 0.02$). Understanding did not increase in the areas of "how to create and support/refute a hypothesis" (mean ± SD increase = 0.7 ± 1.3 points; $P = 0.17$), "how to conduct a research study" (mean ± SD increase = 1.1 ± 1.5 points; $P = 0.05$), "how to write a research abstract" (mean ± SD increase = 1.1 ± 1.7 points; $P = 0.08$), and "how to explain research to others" (mean ± SD increase = 1.1 ± 1.7 points; $P = 0.08$). Students in the STEMCats dairy section will re-take the survey again at the end of the semester to re-evaluate learning outcomes. These results can be used to analyze and adjust teaching methods for future lab sections and can serve as an example to other universities considering similar programs.

Key Words: STEM, undergraduate education, undergraduate research

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1761 Student assessment of curriculum efficacy in a beef systems management course. C. E. Andresen*, E. L. Lundy, D. D. Loy, and P. J. Gunn, *Department of Animal Science, Iowa State University, Ames.*

In 2013, a modified Delphi process was utilized to conduct a needs assessment and guide curriculum reconfiguration of the senior-level beef systems management course at Iowa State University. Stakeholders-guided assessment of course objectives was accomplished through a series of surveys designed to identify subject-matter areas in which beef students need to be proficient. The result was a list of 25 subject-matter areas that were emphasized when redesigning course curriculum. In no particular order, subject areas included: history of beef production, current events, advocacy, allied industry relationships, technology utilization, business planning, record keeping, economics/risk management, employee management, management of input costs, marketing, break-evens, health, nutrition, grading systems, calculating production costs, facility design, beef quality assurance, implants and feed additives, EPDs, grazing management, reproduction, beef interactions with environment, alternative business schemes, and use of beef-based software. The objective of this study was to evaluate how students' perceived importance and knowledge of these stakeholder-derived subject-matter areas changed as a result of the course. The subject-matter areas were presented to students in an anonymous survey at the beginning and end of the course for 4 consecutive semesters. Students were asked to rank the subject-matter areas in order of perceived importance (1–25; 1 = most important, 25 = least important) and indicate their perceived knowledge of each outcome (1–4; 1 = no knowledge, 4 = expert). Data were analyzed using the MIXED procedures of SAS. In both pre- and post-course surveys, students identified business planning as the most important subject and history of beef production as the least important subject in the course. Compared to pre-course surveys, end-of-course surveys ranked beef production history ($P = 0.01$) and current events ($P = 0.04$) lower. No differences were noted between pre- and post-course survey rankings of the other 23 subject-matter areas. As a result of the course, students' perceived knowledge was increased in 22 of 25 subject-matter areas ($P < 0.01$). Although numeric increases in knowledge were noted for history of beef production, allied industry relationships, and record keeping, students did not perceive a significant change in knowledge base for these areas ($P \geq 0.07$). Thus, a renewed emphasis will be placed on these areas in future semesters. These data indicate that the curriculum revision of the senior-level beef management course at

Iowa State University has been successful in educating students on stakeholder-guided course outcomes.

Key Words: beef, curriculum revision, survey

TEACHING UNDERGRADUATE AND GRADUATE EDUCATION SYMPOSIUM: ANIMAL SCIENCE EDUCATION IN THE CURRENT ENVIRONMENT

1762 Introduction to learning theories and implications for classroom design. M. Clement*, *Berry College, Mount Berry, GA.*

Today's students may be underprepared for both graduate and undergraduate coursework, yet they seek to become professionals in their fields. Frustration on the part of all who teach in higher education has led to the question, "How do we teach today's students such that they master the content?" The answers to this question come from three areas: looking at traditional course design, backward by design, and transparent teaching. Additionally, the steps of lesson design and engagement techniques are important. Traditionally, professors planned a course by choosing a classic text, planning lectures, and hoping for the best. Traditional teaching can work, when the lessons are planned with visuals, informal assessments, and explicit teaching. Backward by design, also called understanding by design (Grant Wiggins and Jay McTighe's work), implies that an instructor look at the biggest, most important outcomes of a course, and then plan ways to get students to achieve those outcomes. Transparent teaching, as defined by Mary-Ann Winklemes, includes task, purpose, and criteria. Explicit explanations, crystal-clear aligned assessments, and a rationale of what is taught can improve student achievement. When much content must be mastered by students in order for them to progress to graduate school, or to begin their professional lives, explicit direct instruction can be powerful. Well-crafted, well-taught lessons achieve that end. Strategies for a single lesson include a focus, presentation of material, application/practice of material, and review/assessment. The knowledge base of learning continues to expand rapidly, and research-based methods of teaching do exist. The work of Brown, Roediger, and McDaniel has challenged traditional thought on how students learn, and influenced how professors can teach such that today's students can learn. All of these strategies can be used at all levels of teaching in animal science, to prepare the next generation of professionals in the field.

Key Words: college students, learning theory, teaching strategy

1763 Beyond veterinary school: Helping animal science students explore other career opportunities. J. A. Sterle*[1], H. D. Tyler[1], and J. Daniel[2], *[1]Iowa State University, Ames, [2]Department of Animal Science, Berry College, Mt. Berry, GA,*

A large percentage of students entering undergraduate animal science programs have a desire to become a veterinarian. For example, at Berry College, a private school in northwest Georgia with an animal science program, 81 ± 0.6% of the incoming freshmen (n = 194) for the last 2 yr have indicated a desire to become a veterinarian. Animal science is an appropriate undergraduate major for students interested in veterinary science, and animal science programs should help those students to successfully obtain those goals, however many students come from a background with little experience or knowledge of opportunities for a career working with animals other than veterinary medicine. At Berry College, 69 ± 1.5% of the incoming freshmen for the last 2 yr reported coming from an urban or suburban area, and only 14 ± 1.9% reported living on a farm. While more freshmen report being from a farm at Iowa State University (29.15% in 2014 and 42% in 2015), the trend is still similar. These urban and non-farm students have a desire to work with animals, but limited knowledge of the opportunities available as indicated by the fact that 25 ± 2.9% of the incoming freshmen at Berry College indicated having no experience working with their primary animal of interest. To help students further define where their passion may lie, steps have been implemented in the Department of Animal Science at Iowa State University to inform incoming and freshmen students about the diversity of careers in animal science. During campus visits with high school students and families, the vast array of opportunities surrounding careers in Animal Science are discussed briefly. More discussion follows during Freshmen Orientation, and also during ANS 110: Orientation in Animal Science. Freshmen and transfer students enrolled in ANS 110 were asked to indicate their interest in various careers at the beginning and again at the end of the semester. At the beginning of the semester, 62% (315 responding) indicated that veterinary school was their primary interest. The last week of class, only 43% (296 responding) responded that this was still at the top of their interests. Even more interesting was the increased interest in graduate school (8% in September vs. 17% in November). Identifying interests earlier in their collegiate career will allow students to take advantage of internships and other experiences more closely related to their interest.

Key Words: prevet, teaching, undergraduate

1764 A different approach in pedagogical model: Flipped classrooms. M. G. Maquivar[*1] and A. Ahmadzadeh[2], [1]*Department of Animal Sciences, Washington State University, Pullman,* [2]*University of Idaho, Moscow.*

New data indicate that undergraduate students are currently different from those 15 yr ago, their needs are different and they are more immersed in technological tools. As technology advances educators should learn more how to use these resources and pedagogical methodologies to enhance and promote active learning. Flipped classroom is a new pedagogical method developed to use different resources to create an environment where students take responsibility for their own learning. The end goal of this approach is to personalize learning and promote a more solid learning meeting the educational expectations of the new generation of undergraduate students. The concept of blended learning within flipped classrooms involves student participation through online or outside-classroom delivery of content and instruction that allows students to have some control over their time, effort, location and pace of delivery while using the traditional method of face-to-face classroom participation. The role of instructors in the classroom changes with the flipped classroom methodology, the faculty member is no longer the sole source of knowledge and information, instead, the instructor is a facilitator for students that allows students to take responsibility for much of their learning and knowledge attainment. The flipped classroom allows increasing interaction and personalized content time between students and faculty, promotes critical thinking, increase constructivist learning, engaged students in the course, and provides and incentives students to prepare for class. The adoption of this pedagogical approach is slow and the courses have to be well designed and carefully planned to avoid student frustration and dissatisfaction with the course, however, there is no doubt that flipped classroom and/or blended learning approaches addresses students learning needs.

Key Words: flipped classroom, personalized learning

1765 Teaching evaluations and other alternatives to assess good teaching and learning. K. G. Odde*, *Kansas State University, Manhattan.*

Animal Science departments have long strived for excellence in teaching. Quality teaching programs have been difficult to maintain because of reduced state funding, changing demographics of students, loss of livestock units that support teaching, and greater emphasis on extramurally funded research. Building and sustaining a culture whereby teaching receives respect similar to other mission areas is critical. Trends in higher education are toward "the research institution", since research is thought to drive more funding into the institution. However, the rapid increases in tuition rates in most institutions has made attracting students a high priority. Critical to building outstanding teaching programs is properly assessing teaching quality. The literature results on student evaluation of teaching as a tool for effectively evaluating and improving teaching are mixed. Some studies indicate that student evaluations can be useful and that results are positively correlated with learning, while others raise concerns about gender bias in student evaluations. Student evaluation of teaching is a useful tool, but has limitations. Peer evaluation of teaching can also be an effective tool in improving teaching quality.

Key Words: assessing teaching and learning, teaching evaluations

TOXIC PLANTS SYMPOSIUM

1766 Is there a difference between exposures to one or two plant toxins? K. D. Welch*, *USDA, ARS, Poisonous Plant Research Laboratory, Logan, UT.*

The majority of the plants in a given rangeland provide valuable forage for livestock species. However, plants that can poison livestock are very much a part of our rangelands. In this regard, most rangelands contain more than one poisonous plant. Frequently, much is known regarding the toxicity of individual plants and their effects on livestock. However, little is known regarding the effect of co-exposure to multiple toxic plants or even the effect of multiple toxins from an individual plant. Mixture toxicology, or the study of the co-exposure to multiple toxins, can result in additive, synergistic, or antagonistic effects. This presentation will highlight some of the recent research from the Poisonous Plant Research Lab wherein the effect of co-administering multiple plant toxins from the same plant and the effect of co-administration of different poisonous plants has been evaluated. A better understanding of the effect of co-exposure to multiple poisonous plants, and the mixture toxicology involved, will be useful in developing more beneficial management recommendations

for ranchers.

Key Words: cattle, death camas, larkspur, methyllycaconitine, mixture toxicology, multiple toxins, poisonous plants, sheep, zygacine

1767 Resistance to toxic plants: The right animal at the right time in the right pasture. B. T. Green[*1], K. D. Welch[1], J. W. Keele[2], T. G. McDaneld[2], and J. A. Pfister[3], *[1]USDA, ARS, Poisonous Plant Research Laboratory, Logan, UT, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [3]USDA ARS Poisonous Plant Research Laboratory, Logan, UT*

Neurotoxic poisonous plants negatively impact livestock on many western rangelands, which results in annual economic losses of millions of dollars from animal deaths, increased management and treatment costs, and if animals are deferred from grazing, the underutilization of otherwise highly nutritious pastures and rangelands. One potential solution to the problem of toxic plants is to identify and select animals that are "resistant" to neurotoxic plants. Research at the Poisonous Plant Research Laboratory (PPRL) has focused on the physiological effects of two plant species, larkspur (*Delphinium* spp.) and lupine (*Lupinus* spp.). There are significant differences in the susceptibility of cattle breeds to larkspur and lupine. For example, when Angus and Hereford cattle were orally dosed with 8 mg/kg d-(methylsuccinimido) anthranoyllycoctonine (MSAL)-type alkaloids in the form of dried ground larkspur, Angus were significantly more resistant to the larkspur-induced fatigue ($P < 0.0001$, Two-tailed *t* test, 33 Angus versus 48 Line 1 Herefords). Breed differences have also been observed for lupine which causes birth defects in cattle by the inhibition of fetal movement. For example, when six pregnant Angus and five pregnant Holstein heifers were orally dosed with 1.1 g/kg dried ground *Lupinus leucophyllus* and fetal activity monitored via transrectal ultrasonography, there were significantly more fetal movements in Holstein heifers at eight and 12 h after oral dosing than the Angus heifers ($P = 0.0430$ and 0.0001 for eight and twelve hours after oral dosing, respectively, linear mixed model analysis). These results provide the basis for phenotypes, which can then be used in the development of a genetic test to facilitate selection of resistant animals, which can then be used to manage the risk of toxic plants.

Key Words: cattle, d-(methylsuccinimido) anthranoyllycoctonine, larkspur, lupine,

1768 Using divergent selection and genomics to uncover genetic variation underlying larkspur tolerance and susceptibility in cattle. J. W. Keele[*1], T. G. McDaneld[1], L. A. Kuehn[1], W. M. Snelling[1], R. G. Tait, Jr.[1], K. D. Welch[2], and B. T. Green[2], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]USDA, ARS, Poisonous Plant Research Laboratory, Logan, UT.*

In the Rocky Mountain region of western US, selection for larkspur tolerance would reduce mortality of cattle from larkspur poisoning and increase opportunity to utilize pastures at peak nutrient availability resulting in increased sustainability of beef production. Previous research indicated that there are breed differences for tolerance to toxic larkspur. Our objective was to estimate heritability for larkspur tolerance within breed and evaluate the potential for increasing larkspur tolerance through artificial selection. Larkspur challenge was administered to 141 yearling steers (32 Angus, 13 Brahman, 49 Line 1 Hereford, 33 Holstein, and 14 Jersey) with a standardized dose of dried ground larkspur suspended in water and gavaged directly into the rumen. Larkspur tolerance was measured at 24 h after dosing as the length of time (up to 40 min maximum) in which the animal could sustain walking at 6.44 km/h while being led behind a tractor on a circular track. High-density SNP arrays (770,000 or 30,000 SNP) were used to genotype each steer and genotypes were used to compute the genomic relationship matrix which is a precursor to estimating heritability. Larkspur tolerance heritability estimates were similar whether estimated with REML (0.36 ± 0.30; $P = 0.10$) or Bayesian Monte Carlo Markov chain (MCMC) (0.42 ± 0.23; MCMC posterior distribution 2.5, 25, 50, 75, and 97.5th percentiles were 0.035, 0.24, 0.40, 0.59, and 0.90). To evaluate the potential for using our larkspur challenge data to calculate EBV of an untested population, we computed genomic relationship coefficients between 190 previously genotyped (but untested for larkspur tolerance and comprising the same 5 breeds in this study) cattle and the 141 steers tested for larkspur tolerance. Because of uncertainty in the heritability estimate, EBV were computed for each iteration of the MCMC to average over all possible values for heritability and weight by the appropriate posterior density. The most extreme EBV were for target animals with the strongest genetic ties to tested animals. Simulations indicated that divergent selection of parents can more than double the power for estimating heritability. Our results indicate that selection for larkspur tolerance should be effective. The rate of selection response will critically depend on challenging and testing animals with strong genetic ties to candidates for selection. Genetic ties can either be estimated from SNP genotypes or computed from common ancestry. USDA is an equal opportunity provider and employer.

Key Words: cattle, larkspur, plant toxins

1769 The relationship between swainsonine-containing plants and endophytic fungi. D. Cook*, D. R. Gardner, and J. A. Pfister, *USDA, ARS, Poisonous Plant Research Laboratory, Logan, UT.*

Swainsonine, an indolizidine alkaloid with significant physiological activity, is an α-mannosidase and mannosidase II inhibitor that alters glycoprotein processing and causes lysosomal storage disease. Swainsonine is present in a number of plant families worldwide including the Convolvulaceae, Fabaceae, and Malvaceae and causes severe toxicosis in livestock grazing these plants. The three families of swainsonine containing plants are represented by six genera of plants: *Ipomoea*, *Turbina*, *Astragalus*, *Oxytropis*, *Swainsona*, and *Sida*. Two families of fungal endophytes, Pleosporaceae and Chaetothyriaceae, that produce swainsonine have been isolated from the Fabaceae and Convolvulaceae swainsonine-containing plants, respectively. Data will be presented in regard to these plant endophyte relationships. Additionally data will be presented characterizing this interaction and the influence of environment and genotype in determining swainsonine concentrations in planta. Furthermore we will present data further exploring the diversity of plants containing swainsonine and their associated endophytes.

Key Words: locoweed, morning glory, swainsonine,

1770 Alleviation and mitigation of fescue toxicosis. G. E. Aiken*, *USDA-ARS, Forage-Animal Production Research Unit, Lexington, KY.*

Tall fescue (*Lolium arundinaceum* L.) is a cool-season perennial grass that is utilized as a forage on approximately 16 million hectares of the USA, primarily in the transition zone between the temperate northeast and subtropical southeast. A fungal endophyte (*Epicloë coenophialia*) that infects most plants of the most widely grown cultivar, Kentucky 31 produces alkaloids that impart the plant with tolerances to environmental stresses, but also produces ergot alkaloids that causes a toxicosis. The signs of "fescue toxicosis" include maintaining rough hair coats during the summer, elevated body temperature, labored respiration, and decreased prolactin concentrations. Ergot alkaloids bind α adrenergic receptors in peripheral vasculature of ruminants that disrupts thermoregulation and makes them vulnerable to severe heat stress at onset of moderate air temperatures. Calf weight gain can be very low on toxic tall fescue, which has limited the use of fescue for stocker production. Although the grass is primarily used for cow-calf production, calving percentages, milk yields, and weaning weights can be reduced on toxic endophyte-infected tall fescue. Non-toxic endophyte tall fescues have been commercially released that demonstrate to alleviate fescue toxicosis. Other technologies, such as chemical seedhead suppression, feeding soy hulls, and overseeding with red clover also have shown to mitigate fescue toxicosis. Evaluations of the efficacy of these new technologies in enhancing cattle performance and well-being on toxic endophyte-infected tall fescue will be presented and discussed.

Key Words: endophytes, *Epicloë coenophialia*, fescue toxicosis, *Lolium arundinaceum*, tall fescue

1771 Effects of high selenium forages on reproduction in sheep. Z. Davis*, *ARS USDA, Logan, UT.*

High Se-containing forages grow on seleniferous soils in many parts of world and can cause acute or chronic selenosis in livestock. Anecdotal reports of decreased reproductive rates in livestock grazing seleniferous forages have been reported and it has been speculated that reproductive failure is one of the initial changes of Se poisoning. However, there is very limited if any information in the literature on the effects on selenium on reproduction in livestock. The objective of this research was to determine the effect of high Se forages on reproduction in ewes and rams. Ewes were randomly divided into three groups (n = 10) and fed a control alfalfa pellet (< 0.3 ppm Se) or a high Se-containing alfalfa pellet that contained either 10 or 30 ppm Se for 12 wk. Feeding of the pellets began 6 wk before exposing the ewes to rams. Each ewe was exposed to two rams twice each day for two complete reproductive cycles. After the first cycle, significantly (P < 0.05) more ewes were pregnant in the control group (10/10) than in the 10 ppm Se (6/10) and 30 ppm Se (6/10) groups. After a second cycle 9/10 and 6/10 were pregnant in the 10 and 30 ppm Se groups, respectively. In a second study rams were randomly divided into two groups (n = 10) were they were fed either a control alfalfa pellet (containing < 0.3 ppm Se) or a high Se-containing alfalfa pellet (~25 ppm Se) for twelve weeks during which time semen samples were collected weekly. After twelve weeks of being fed high Se pellets, one testicle from each ram was surgically removed, the rams were then fed a control alfalfa pellet diet (containing < 0.3 ppm Se) and allowed to recover for 8 wk at which time the second testicle was surgically removed for histological analysis. Rams fed the high Se-containing alfalfa pellet had a decrease in sperm motility and an increase in the percentage of abnormal sperm. These negative effects were reversed after the rams were fed the regular alfalfa pellets for 8 wk. None of the sheep in either study demonstrated any clinical signs of Se poisoning during the study. In summary, high selenium feeds negatively affect reproduction in both ewes and rams.

Key Words: reproduction, selenium, sheep

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